

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 10, 2003, 16:24:59 ; Search time 3400 Seconds  
(without alignments)  
5342.316 Million cell updates/sec

Title: US-09-719-601-5  
Perfect score: 2438  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database :

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40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match % | Score | Length | DB ID | Description         |
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| 2          | 99.5          | 2425  | 3016   | 9     | AF126799 Homo sapi  |
| 3          | 99.5          | 2425  | 3083   | 6     | BD127375 Primer fo  |
| 4          | 99.5          | 2425  | 3083   | 9     | AK074933 Homo sapi  |
| 5          | 99.5          | 2425  | 3149   | 9     | AF084559 Homo sapi  |
| 6          | 99.5          | 2425  | 4089   | 6     | AX035941 Sequence   |
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| 9          | 2189          | 89.8  | 1508   | 10    | AF126798 Mus muscu  |
| 10         | 2186          | 89.7  | 1335   | 6     | AX253297 Sequence   |
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| 17         | 1935          | 79.4  | 2257   | 6     | BD082655 Methods a  |
| 18         | 1935          | 79.4  | 2257   | 6     | BD092934 Methods a  |
| 19         | 1703          | 69.2  | 2621   | 9     | HSM800210 Homo sapi |
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| 24         | 1662          | 68.2  | 1498   | 5     | AF478472 Salmo sal  |
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| 37         | 1560.5        | 64.0  | 1757   | 6     | AX035942 Sequence   |
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| 40         | 1551.5        | 63.6  | 1818   | 10    | AB041560 Mus muscu  |
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| 45         | 1515          | 62.1  | 1928   | 6     | AR264714 Sequence   |

ALIGNMENTS

RESULT 1









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REFERENCE
AUTHORS      2 (bases 1 to 3083)
TITLE        Isogai, T. and Otsuki, T.
JOURNAL      Direct Submission
COMMENT      Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
              Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0912, Japan
              (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
              NEDO human cDNA sequencing project supported by Ministry of
              Economy, Trade and Industry of Japan; cDNA full insert sequencing:
              Research Association for Biotechnology; cDNA library construction:
              Institute of Medical Science, University of Tokyo, Laboratory of
              Genome Structure, Human Genome Center; cDNA 5' - & 3' - end one pass
              sequencing and clone selection: Helix Research Institute (supported
              by Japan Key Technology Center etc.).

FEATURES
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LOCUS

AF084559 3149 bp mRNA linear PRI 12-OCT-2000

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141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyraPheGlyAsnGlyTrpIlePro 160  
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RESULT 6
AX035941 4089 bp DNA linear PAT 15-NOV-2000
LOCUS Sequence 2 from Patent EP1035207.
DEFINITION AX035941
ACCESSION AX035941
VERSION AX035941.1 GI:11191483
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1. Marquardt, A. and Weber, B.H.
TITLE Cdna molecules of the members of gene family encoding human fatty
acid desaturases and their use in diagnosis and therapy
JOURNAL Patent: EP 1035207-A 2 13-SEP-2000;
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Score: 2425.00 Matches: 442
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 99.47% Indels: 0
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US-09-719-601-5 (1-444) x AX035941 (1-4089)
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RESULT 7
BD091695 1335 bp DNA linear PAT 27-AUG-2002
LOCUS Process for producing lipid and microorganism secreting lipid.
DEFINITION BD091695
ACCESSION BD091695
VERSION BD091695.1 GI:22637306
KEYWORDS WO 0175069-A/1.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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| 517   | Db |  | ATCGTCATGGAAGCATCGCTGGTTTCATCCCTCGTACTTCGGCAATGGCTGGATTCCC      | 576  |
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| 577   | Db |  | ACCGTCATCAACGGCTTTGCTCTGCTACCTCCCAAGGCCAAGCTGGATGGCTACAACAT     | 636  |
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| 637   | Db |  | GATTATGGCCACCTTTCGTCTATAAGAAATCCATATGGAACCAACATTTGTCCACAAGTTT   | 696  |
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| 697   | Db |  | GTCATTGGCCACCTTAAAGGGTGCTCCGCCAACTGGTGAACCAATCGACATTTCCAGCAC    | 756  |
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| 817   | Db |  | CTTGGAGAGTGGCAGCCCTTCGAGTATGCAAGAAGAGCTGAATATCTGCCCTACACAC      | 876  |
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| 997   | Db |  | AGCTACTATGAGGTTTCTTCTACACTATATCCCTTTCTATGGCATCTTGGGAGCCCTG      | 1056 |
| 321   | QY |  | LeuPheLeuAsnPheIleArgPheLeuGluSerHisTtpPheValTtpValThrGlnMet    | 340  |
| 1057  | Db |  | GTTTCTCTCAACTTATCAGGTCTCTGGAGGCCACTGGTTGTGTGGTGCACACAGATG       | 1116 |
| 341   | QY |  | AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTtpPheSerSerGlnLeu    | 360  |
| 1117  | Db |  | AACACATCTCATGAGAGATTGATCTTGATCTACTACCGGAGCTGGTTTCAGCAGCAGCTG    | 1176 |
| 361   | QY |  | ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTtpPheSerGlyHisLeuAsn    | 380  |
| 1177  | Db |  | GCACCCACCTGCATGTGGAGCAGTCTTCTTCATGACTGGTTCAGCGGACACTCAAT        | 1236 |
| 381   | QY |  | PheGlnIleGluHisIlePheProThrMetProArgHisAsnLeuHisLysIleAla       | 400  |
| 1237  | Db |  | TTCAGAGATTGAGCACCACTCTTCCCACTATGCCAAGACACAATCTGCAACAAGATTGCC    | 1296 |
| 401   | QY |  | ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu    | 420  |
| 1297  | Db |  | CCACTGTGTGAAGTCTCTCTGCCCAAGCATGTCATTAATACCAAGAGAACCGCTGCTG      | 1356 |
| 421   | QY |  | ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTtpLeuAspAla    | 440  |
| 1357  | Db |  | AGGCCCTCTCTCACAATGTGTGATTTCATTGAAGAAGTCTGGGAGCTGTGGCTGGATGCC    | 1416 |
| 441   | QY |  | TyrLeuHisLys 444  |      |
| 1417  | Db |  | TACCTCCACAAA 1428   |      |
| RESULT 9  |    |  |   |      |
| AF126798  |    |  |   |      |
| LOCUS   |    |  |   |      |
| DEFINITION Mus musculus delta-6 fatty acid desaturase mRNA, complete cds. |    |  |   |      |
| ACCESSION AF126798  |    |  |   |      |
| VERSION AF126798.1 GI:4406525   |    |  |   |      |
| linear ROD 21-JUN-2000  |    |  |   |      |







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| QY | 1   | MetGlyLysGlyGlyAsnGlnGlyGluGlyValaAaGluArgGluValSerValProThr     | 20  |
| DB | 93  | ATGGGGAAGGAGGAGAACCCAGGGGAGGGGCGCCGAGCGAGGTGTGCGTGGCCACC         | 152 |
| QY | 21  | PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp     | 40  |
| DB | 153 | TTTCACTCGGGAGGAGATTCAAGAACAATCTCGCACCGACAGGTGGCTGTGCTATTGAC      | 212 |
| QY | 41  | ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyValnArgValIle    | 60  |
| DB | 213 | CGCAAGGTGTTTACAACATCATCCAAATGTTGTCATCCAGCACCCGGGGGGCCAGCGGTGCATC | 272 |
| QY | 61  | GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu     | 80  |
| DB | 273 | GGGCCTACTCGCTGGAGAGATGCACGGATGCCTTCGGCGCTTTCACCCCTGACCTGGAA      | 332 |
| QY | 81  | PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer     | 100 |
| DB | 333 | TTTCGTGGCCAGAGTCTCTTGAACCCCTGCTCATTTGTTGAACGTGCCCGGAGAGGCCACGC   | 392 |

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|------------|--|--|------|
| 559        | Db   | AAAGGGTGCCTCTCCCAACTGGTGGAAATCATCGCCACTTCCAGCACCACGCGCAAGCCCTAAC | 618  |
| 226        | Qy   | ILPheHi slvsAspProAspValAsnMetLeuHi sValPheValLeuGlyVglutpGln    | 245  |
| 619        | Db   | ATCTTCACAAGGATCCCGATGTGAACATGCTGCACGTTGTCTTGGCGCATGGCAG          | 678  |
| 246        | Qy   | ProileGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr     | 265  |
| 679        | Db   | CCCATCGATACGGCAAGAAAGAGCTGAAATACCTGCCCTACATCAATCACCAGCAGAAATAC   | 738  |
| 266        | Qy   | PhePheLeuileGlyProProLeuLeuileProMetTyrPheGlnTyrGlnileleMet      | 285  |
| 739        | Db   | TTCTTCCTGATTGGCGCGCTGCTCATCCCATGTATTTCAGTACCCAGATCATCATG         | 798  |
| 286        | Qy   | ThrMetileValHisLysAsnTrpValAspLeuAlaTrpAlaValserTyrTyrileArg     | 305  |
| 799        | Db   | ACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCTGGGCGGTGAGCTACTACATCCGG    | 858  |
| 306        | Qy   | PhePheileThrTyrileProPheTyrGlyileLeuGlyAlaLeuLeuPheLeuAsnPhe     | 325  |
| 859        | Db   | TTCTTCATCACTACATCCCTTTCATCGGCATCTCTGGAGCCCTCTTCTTCCTCAACTTC      | 918  |
| 326        | Qy   | IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisileValMet     | 345  |
| 919        | Db   | ATCAGGTTCTGGAGAGCCACTGGTTTGTGTGGGTACACAGATGAATCAGATCGTCATG       | 978  |
| 346        | Qy   | GluileAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn     | 365  |
| 979        | Db   | GAGATTGCACGAGGAGGCTACCGTGACTGGTTCAGTACGCCAGCTGACGCCACCTGCAAC     | 1033 |
| 366        | Qy   | ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnileGluHis     | 385  |
| 1039       | Db   | GTGAGCAGTCCCTTCTTCAACGACTGGTTCAGTGAGCACCCTTAACCTCCAGATTGAGCAC    | 1099 |
| 386        | Qy   | HisLeuPheProThrMetProArgHisAsnLeuHisLysileAlaProLeuValLysSer     | 405  |
| 1099       | Db   | CACCTCTCCCAACCATGCCCGGCACAACTTACAAAGATCGCCCGCTGGTGAAGTCT         | 1159 |
| 406        | Qy   | LeuCysAlaLysHisGlyileGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp     | 425  |
| 1159       | Db   | CTATGTGCCAGCAGTGGCATTGAATACCAGGAGAGCCGCTACTGAGGCGCCTGCTGAC       | 1219 |
| 426        | Qy   | IleileArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys        | 444  |
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| DEFINITION | Primer for synthesizing full-length cDNA and use thereof.  |  |      |
| ACCESSION  | BD127406   |  |      |
| VERSION    | BD127406.1 GI:23222351   |  |      |
| KEYWORDS   | JP 2002017375-A/2837.  |  |      |
| SOURCE     | Homo sapiens (human)   |  |      |
| ORGANISM   | Homo sapiens   |  |      |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |  |      |
| AUTHORS    | 1 (bases 1 to 2825)<br>Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.  |  |      |
| TITLE      | Primer for synthesizing full-length cDNA and use thereof   |  |      |
| JOURNAL    | Patent: JP 2002017375-A 2837 22-JAN-2002;  |  |      |
| COMMENT    | HELIX RESEARCH INSTITUTE<br>OS Homo sapiens (human)<br>PN JP 2002017375-A/2837<br>PD 22-JAN-2002<br>PF 07-JUL-2000 JP 20020253172<br>PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO KOGA, H. |  |      |
|            | PI ISHII<br>PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,<br>PI TETSUO Otsuki, HISASHI KOGA   |  |      |

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C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuLeuLeuLeuLeu 140  
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QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTyrTyrAsnHisArgHisPheGlnHis 220  
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DB 487 CAGCCCAAGCTTACATCTTCCACAGGATCCGATGTGAACATGCTGCAGCTGTGTGTT 546  
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DB 667 TACCAGATCATATGACCATGATCGTCCATAAGAACTGGTGGAGCTGGCGCTGGCGCTC 726

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DB 787 CTTTTCTCACTTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTACACAGATG 846  
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeu 360  
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ACCESSION AK074991  
VERSION AK074991.1 GI:22760798  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,  
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,  
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,  
Kojima, S., Nagahara, K., Masuko, Y., Ono, T., Okano, K., Yoshikawa, Y.,  
Notsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and  
Ninomiya, K.  
TITLE NEDO human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2825)  
AUTHORS Isogai, T. and Otsuki, T.  
TITLE Direct Submission  
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,  
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan  
(E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology; cDNA library construction:  
Institute of Medical Science, University of Tokyo, Laboratory of  
Genome Structure, Human Genome Center; cDNA 5' & 3'-end one pass  
sequencing and clone selection: Helix Research Institute (supported  
by Japan Key Technology Center etc.).  
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precursor cells after 2-weeks retinoic acid (RA)
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Alignment Scores:
Pred. No.: 1,86e-189 Length: 2825
Score: 2068.50 Matches: 378
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 3
Query Match: 84.84% Indels: 3
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US-09-719-601-5 (1-444) x AK074991 (1-2825)

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Qy 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 67 TTCGTGGGCAAGTCTTGAAACCCCTGCTGATGGTGAACCTGGCCCGGAGAGCCACG 126

Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
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Db 187 GAGACATGAACCTGTTCAAGACCAACACGCTGTTCTTCCTCTCTCTCTCTCTCTCTCT 246

Qy 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
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DEFINITION Sequence 8 from patent US 6428990.
ACCESSION AR221960
VERSION AR221960.1 GI:23329263
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2257)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 8 06-AUG-2002;
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US-09-719-601-5 (1-444) x AR221960 (1-2257)

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BD082640.1 GI:22628250

KEYWORDS

SOURCE

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ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 2257)

AUTHORS

Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Loenard,A.E.Y.

TITLE

Methods and compositions for synthesis of long chain

JOURNAL

poly-unsaturated fatty acids

Patent: JP 2001523091-A 20 20-NOV-2001;

CAUGENE LLC,ABBOTT LABORATORIES

COMMENT

PN JP 2001523091-A/20

PD 20-NOV-2001

PF 10-APR-1998 JP 1998544053

PR 11-APR-1997 US 08/834655

PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND.

PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD

PC C12N15/53,C12N15/61,C12N9/02,C12N5/10,C12N1/19,C12P7/64 PC

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Best Local Similarity: 81.86% Mismatches: 44

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116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPheLeuLeu 135

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175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194

487 GCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAAAACCAAGTGGAC 546

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667 ATGCTGCACGTGTTTGTCTGGCGAATGGAGGCCCATCGAGTACGGCAAGAAAGCTG 726

255 LysTyrLeuProTyrAsnHisGlnHisGlyLysPhePheLeuIleGlyProProLeuLeu 274

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RESULT 16

BD082640

LOCUS

DEFINITION

Methods and compositions for synthesis of long chain

2257 bp DNA linear PAT 27-AUG-2002

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  Methods and compositions for synthesis of long chain
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ACCESSION
  BD082655
VERSION
  BD082655.1 GI:22628265
KEYWORDS
  JP 2001523092-A/15.
SOURCE
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ORGANISM
  unidentified
REFERENCE
  1 (bases 1 to 2257)
  Knutson,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and

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Leonard,A.E.Y.
Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
Patent: JP 2001523092-A 15 20-NOV-2001;
CAUGENE LLC/ABBOTT LABORATORIES
PN JP 2001523092-A/15
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PI DEBORAH KUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND.
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
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  Query Match: 79.37% Indels: 4
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Db 787 ATCCCATGATTTTTCAGTACCAATCATCATCATCATCATCATCATCATCATCATCATCAT 846
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## RESULT 18

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BD092934
LOCUS 2257 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION BD092934
VERSION BD092934.1 GI:22638545
KEYWORDS JP 2001527395-A/21.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 2257)
AUTHORS Knutson,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and
Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants
JOURNAL Patent: JP 2001527395-A 21-25-DEC-2001;
CAUGENE LLC,ABBOTT LABORATORIES
PN JP 2001527395-A/21
PD 25-DEC-2001
PF 10-APR-1998 JP 1998544175
PR 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR

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DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
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Score: 1935.00 Matches: 352
Percent Similarity: 88.84% Conservative: 30
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US-09-719-601-5 (1-444) x BD092934 (1-2257)

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 1 (bases 1 to 2621)  
 Wambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 Direct Submission  
 Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152  
 Martinsried, GERMANY  
 Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing  
 consortium of the German Genome Project.  
 This clone (DKFZp586C201) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further  
 information about the clone and the sequencing project is available  
 at http://www.mips.biochem.mpg.de/proj/cDNA/.

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 Db 314 GTGTTTGTCTGGCGGAATGGCAGCCCATCGAGTACGGCAAGAGCTGAATACCTTG 373  
 Qy 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMet 277  
 Db 374 CCTACATACACAGCAGCAATACTTCTTCTGATTGGCGCGCTGTCTATCCCATG 433  
 Qy 278 TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297  
 Db 434 TATTTCAGTACCAGATCATCATGACCATGATCGTCATTAAGAACTGGGTGGACCTGGCC 493

QY 298 TplalaValSerTyrTyrIleAArgPhePheHleThrTyrIleProPheTyrGlyIleLeu 317  
 Db 494 TGGGCCCGCTAGCTACTACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCG 553  
 QY 318 GlyAlaLeuLeuPheLeuAenPheIleAArgPheLeuGluSerHisTyrPheValTyrVal 337  
 Db 554 GGAAGCCCTCCCTTTCTCAACCTTCATCAGTTCTCTGGAGGCACTGGTTGTGTGGGTC 613  
 QY 338 ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaIleAArgPheSer 357  
 Db 614 ACACAGATGAATCACATCGTCATGGAGATTGACAGAGCCCTACCGTCACTGGTTCACT 673  
 QY 358 SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTyrPheSerGly 377  
 Db 674 AGCAGCTACAGCCACCTGCAACGTGGAGCAGTCTCTTCTCAACGACTGGTTCACTGGA 733  
 QY 378 HisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHis 397  
 Db 734 CACCTTAACCTTCAGATTGACACCACTCTTCCCAACCATGCCCGGCACAACTTACAC 793  
 QY 398 LysIleAlaProLeuValIlysserLeuCysAlaLysHisGlyIleGluTyrGlnGluLys 417  
 Db 794 AGATCGCCCGCTGGTGAGTCTCTATGTGCCAAGCATGGCTGATTAATACAGGAGAG 853  
 QY 418 ProLeuLeuArgAlaLeuLeuAspIleIleAArgSerLeuLysLysSerGlyLysLeuTyr 437  
 Db 854 CCCTACTAGAGGCCCTGCTGGACATCATCAGGAGCCTGATGAAGTCTGGGAAGCTGTGG 913  
 QY 438 LeuAspAlaTyrLeuHisLys 444  
 Db 914 CTGGAGCCCTACCTTCACAA 934

RESULT 20  
 AY055749 1745 bp mRNA linear VRT 01-OCT-2002  
 LOCUS Sparus aurata putative delta 6-desaturase (FD6D) mRNA, complete cds.  
 DEFINITION  
 ACCESSION AY055749  
 VERSION AY055749.1 GI:23428437  
 KEYWORDS  
 SOURCE Sparus aurata (gilthead seabream)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
 Percoidae; Sparidae; Sparus.  
 1 (bases 1 to 1745)  
 Seiliez,I.; Panerat,S., Kaushik,S. and Bergot,P.  
 Cloning, tissue distribution and nutritional regulation of a delta  
 6-desaturase-like enzyme in gilthead seabream  
 Unpublished  
 2 (bases 1 to 1745)  
 Seiliez,I., Panerat,S., Kaushik,S. and Bergot,P.  
 Direct Submission  
 TITLE  
 JOURNAL Submitted (11-SEP-2001) Fish Nutrition Laboratory, INRA,  
 St-Pee-sur-Nivelle 64310, France  
 FEATURES  
 source Location/Qualifiers  
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 CDS  
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 LTFILSILLATQATQAGWLQHPDFGLSVFKSSNNHLLHKFVIGHLKASANNWNRH

FOHAKPNIFSKDPVNNMLHIFVLGDTQTPVEYGIKKIKYLPYHHOYFLLVGPPLLI  
 PYPHIOIRTMISHDWDIAWSVYTRVLCVVPVLYGLFGSVALISVVRPLESHW  
 FVWVMHMLDMDIDHEKHDPMLTMOQATCNIEKSVNDKFSGLHNFQIEHLFPFM  
 PRNHYLVAPLVHALCEKHGIPYQKTNMQGIVDIRSLKXNSGDLMLDAYLHK"

BASE COUNT 424 a 439 c 445 g 437 t

# Alignment Scores:

Pred. No.: 5,6e-153 Length: 1745  
 Score: 1687.50 Matches: 291  
 Percent Similarity: 79.19% Conservative: 63  
 Best Local Similarity: 65.10% Mismatches: 88  
 Query Match: 69.22% Indels: 5  
 DS: 5 Gaps: 2

US-09-719-601-5 (1-444) x AY055749 (1-1745)

QY 1 MetGlyLysGlyGly-----AsnGlnGlyGluGlyAlaAlaGluAArgGluValSer 17  
 Db 156 ATGGGAGGTGGAGGCCAGCTCACGGAGCCAGGGAGCGGGCAGCGAGCTGGTGGC 215  
 QY 18 ValProThrPheSerTyrGluGluIleGlnLysHisAsnLeuAArgThrAspSerGlyLeu 37  
 Db 216 GTT-----TACCTCGGAGGAGGTGCAGAGCCACAGCAGCAGGAATGACCACTGGCTG 269  
 QY 38 ValIleAspArgLysValTyrAsnIleThrLysTyrPheSerIleGlnHisProGlyGlyGln 57  
 Db 270 GTGATAGATCGAAAGGTCTACACGTCAAAAGTGGGCCAAGAGCACCAGGAGGATTG 329  
 QY 58 ArgValIleGlyHisTyrAlaGlyLysAspAlaThrAspAlaPheAArgAlaPheHisPro 77  
 Db 330 CGGGTCATCAACCTATGCTGGAGAGGATCCAGGAGGCGGTTCATCTGCTTTTCCACCT 389  
 QY 78 AspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGlu 97  
 Db 390 GATTTAAAGTTGTGCAGAAGTTCTGAAGCCCTCTGATTGAGAGCTGGCAGCGAGC 449  
 QY 98 GluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheAArgAlaLeuArg 117  
 Db 450 GAGCCAGCCAGGACCGAAATAAATATCGCGCGGTTCATTAGGATTTCCACACCTTACGT 509  
 QY 118 LysThrAlaGluAAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137  
 Db 510 GCGCAGCGGAGGAGCGAGCGCTGTGTTCCAGCTCAGCGCTGTGTTCTTCTGCTCCACCTG 569  
 QY 138 AlaHisIleIleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGly 157  
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 QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyr 177  
 Db 630 TGGACACTGACCTTTCTGATTTCGATCTCTGCAACTGCTCAGACGCGAGCGGATGG 689  
 QY 178 LeuGlnHisAspTyrGlyHisLysSerValTyrArgLysProLysTyrAsnHisLeuVal 197  
 Db 690 CTGAGCATGACTTCGGCCACTGCTGCTCTTCAAGAGTCCAGCTCGATCATCATTTTG 749  
 QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaIleAsnTyrPheAsnHisArgHis 217  
 Db 750 CACAAAGTTGTTCATCGTTCATTAAAGGAGCGCTCTGCCAACTGGTGGAAATCATCGCAT 809  
 QY 218 PheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237  
 Db 810 TTCAGCATCAGCTTAACCAACATCTTCAGCAGAGGAGCCCTGATGTGTCATGTTGCAC 869  
 QY 238 ValPheValLeuGlyGluTyrGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeu 257  
 Db 870 ATCTTTGTGCTGGAGACACTCAGCCAGTCGAGTACCGCATTAAGAGATCAATAATCTG 929  
 QY 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeuLeuLeuProMet 277  
 Db 930 CCTATCATCACCAGCACCAGTACTTCTCTCTCTCGGACCGCGCTCTCTCATTCAGATT 989

278 TyrPheGlnTyrGlnIlelleMetThrMetIleValHisLysAsnTrpValAspLeuLa 297  
 Db TACTTCACATTCAGATTATTCACCATGATTTCCCGCACGACTGGTGGATCTGGCC 1049  
 298 TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeu 317  
 Db TGGTCTATGCTTACTACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109  
 318 GlyAlaLeuLeuPheLeuAsnPheIleAtgPheLeuGluSerHisTrpPheValTrpVal 337  
 Db GGCTCAGTGGCGCTCATCAGCTTGTGAGGTTTGTGAGAGTCACTGGTTTGTCTGGGTG 1169  
 338 ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSer 357  
 Db ACTCAGATGATCATCTTCGCGATGGATCGATCCAGCAGCAGCAGCAGCAGCAGCAGC 1229  
 358 SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGly 377  
 Db ATGAGTTTACAGCCACTTCACATGAGAGTCCGCTTTCACGACTGGTTTACGCGGA 1289  
 378 HisLeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHis 397  
 Db CACCTCAACTTCAATTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1349  
 398 LysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLys 417  
 Db CTGGTGGCCCGCTTGTCCAGCACTGTGTGAGAAATCGGATCCCTTACCAAGTGAA 1409  
 418 ProLeuLeuArgAlaLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrp 437  
 Db ACAATGTGGCAGGCGCTGTCAGCTTATCAGGTATCAGTGAAGTCACTGAAGAACTCAGG 1469  
 438 LeuAspAlaTyrLeuHisLys 444  
 Db CTGGATGCTTATCCATAAA 1490

RESULT 21  
 AF301910 1866 bp mRNA linear VRT 10-AUG-2001  
 LOCUS Oncorhynchus mykiss putative delta 6-desaturase (FD6D) mRNA,  
 DEFINITION complete cds.  
 VERSION AF301910.1 GI:13447754  
 KEYWORDS  
 SOURCE Oncorhynchus mykiss (rainbow trout)  
 ORGANISM  
 Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 1866)  
 Seilliez,I., Panerlat,S., Kaushik,S. and Bergot,P.  
 Cloning, tissue distribution and nutritional regulation of a  
 delta-6-desaturase-like enzyme in rainbow trout  
 Comp. Biochem. Physiol., B 130, 83-93 (2001)  
 2 (bases 1 to 1866)  
 Seilliez,I., Panerlat,S., Kaushik,S. and Bergot,P.  
 Direct Submission  
 Submitted (30-AUG-2000) Fish Nutrition Laboratory, INRA,  
 St-Pee-sur-Nivelle 64310, France  
 FEATURES  
 Location/Qualifiers  
 1..1866  
 /organism="Oncorhynchus mykiss"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8022"  
 /tissue\_type="liver"  
 1..1866  
 /gene="FD6D"  
 104..1468  
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 /codon\_start=1  
 /product="putative delta 6-desaturase"  
 /protein\_id="AAK26745.1"  
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 LWWGTGWSLTLLCSLMATSSQASQWLDYGLSVCKTSWNVHLKFEVIGHLGA  
 SANWNHRRFQHKAKPNVFSKDPQVNSLVFVLGDKQPEYKIKLKYMFYHQHOFV  
 FLIGPPLVIVPEFTTQIOTFMFSQBNVLDLAWMTFYLRFFCCVYFPFGFVSVALIS  
 FVRLESHWFVWVNTQMHLPMEIDHERHDKWLTQMSATCNIESQFNDFWFSGLHNFQ  
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 YLHK"

BASE COUNT 474 a 444 c 464 g 484 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4,66e-151 Length: 1866  
 Score: 1668.00 Matches: 292  
 Percent Similarity: 81.24% Mismatches: 63  
 Best Local Similarity: 66.82% Indels: 1  
 Query Match: 68.42% Gaps: 0  
 DB: 5

US-09-719-601-5 (1-444) x AF301910 (1-1866)

QY 8 GlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluLeuGln 27  
 Db 156 GGGTTGGGCGCCGATGGAGGGCGAGGTGGCAGTGCA-GTCTACACCTGGGAAGAGGTCCAG 214  
 QY 28 LysHisAsnLeuLeuArgThrAspSerGlyLeuValIleLeuAspArgLysValTyrAsnIleThr 47  
 Db 215 AAGCACTCCACAGAAAGGACAGAGGTGGTGGTTCATCGACAGAGGTCTATAATATTACC 274  
 QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67  
 Db 275 CAGTGGCGAAGACACACCCAGGGGGCATCAGGGGTTCATCAGTCACTTGTCTGGGAAGAT 334  
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 Db 335 GCCACGAGTATTTGTCCGATTCATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 394  
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107  
 Db 395 CGTTGCTGATGGAGAGCTGGACAGCAGAGCCAGCCAGGACCATGGGAAAAACGCA 454  
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 Db 455 GTACTGGTACAGGACTTCCAGGCCCTGGTGCACCGCTGGAGAGGGAGGGTCTCTCCCGT 514  
 QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 Db 515 GCCCGCCCGCTGTTCTTTCAGCCTCTACCTGGGCCACATCTGCTACTAGAGCCCTGGCT 574  
 QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 Db 575 TTGGGCGCTGCTCTGGGTCTGGGGGACGAGCTGGAGCCCTCAGTCACTGCTGTTCCTCCATG 634  
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187  
 Db 635 CTGGCCACATCTCAGTCCAGGCTGGTGGCTGGAGCATGACTAGCCACCTGTGTGCTGCTG 694  
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 Db 695 TGCAGACATCCAGCTGGGAATCACGTACTGCAAGATTTGTCAATGGACACACCTAAGGT 754  
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227  
 Db 755 GCGTCTGCTAACTGGTGGAAACCATGCTCACTTCCAGCACCAGCCTPAGCCCAACCTGTT 814  
 QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlyTrpGlnProIle 247  
 Db 815 AGTAAAGATCTGATGTCAACTCACTGTCATGCTTCTGCTCTGGAGACAAACAGCCTGTA 874  
 QY 248 GluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 267  
 Db 875 GAGTATGGTATAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 934

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Qy 268 LeuileGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleMetThrMet 287
Db 935 CTCATTGGACCTCCACTAGTTATTCAGTGTCTTTTCCATCCAGATATTCAGACCATG 994
Qy 288 IleValHisLysAsnTyrValAspLeuAlaTyrPheValSerTyrTyrIleArgPhePhe 307
Db 995 TTTTCACAGGACCTGGGTGGATCTGGGCTGGGAGACCTTCTACCTTCCTTCTTC 1054
Qy 308 IleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArg 327
Db 1055 TGCTGTACTACCTCTCTCTTGTCTTGTGGCTCGTACGATTCATGCTGCTGACG 1114
Qy 328 PheLeuGluSerHisTyrPheValTyrValThrGlnMetAsnHisIleValMetGluIle 347
Db 1115 TTTTGGAAAGCCACCTGGTTGTATGGTGACCCAGATGATCACTTCTTATGGAGATA 1174
Qy 348 AspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeuThrAlaThrCysAsnValGlu 367
Db 1175 GATCAGAGAGACACAGGACCTGGCTCACCACGCACTTGGTGTGCTGCTGCTGCTG 1234
Qy 368 GlnSerPhePheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHisLeu 387
Db 1235 CAGTCAACCTTCAACGACCTGGTTCAGTGGACACCTCACTTTCAGATTGACACCATCTG 1294
Qy 388 PheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCys 407
Db 1295 TTTCTCTACCATGCTCCCTGATTAACCTACCACTGCTGCTGCTGCTGCTGCTGCTG 1354
Qy 408 AlalyeHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIle 427
Db 1355 GAGAAACATGGACTCTCCCTACCAAGGTCAAGACTTTTGCAGAAAGCCATCATGTGTC 1414
Qy 428 ArgSerLeuLysSerGlyLysLeuTyrPheLeuAspAlaTyrLeuHisLys 444
Db 1415 GGGTCACTGAAGAAGTCAGGGGATCTGTGGCTGGATCGTATCTCCATAAA 1465

RESULT 22
BD127815 2558 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127815
VERSION BD127815.1 GI:23222760
KEYWORDS JP 2002017375-A/3246
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE
JOURNAL Primer for synthesizing full-length cDNA and use thereof
PATENT: JP 2002017375-A 3246 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3246
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P1/02, C12P1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS Location/Qualifiers
source 1..2558

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Alignment Scores:
Pred. No.: 7,148-151 Length: 2558
Score: 1668.00 Matches: 297
Percent Similarity: 59.67% Conservatives: 1
Best Local Similarity: 59.33% Mismatches: 1
Query Match: 68.42% Indels: 0
DB: 6 Gaps: 0
US-09-719-601-5 (1-444) x BD127815 (1-2558)
Qy 146 IleAlaTyrPheThrValPheTyrPheGlyAsnGlyTyrPheProThrLeuIleThrAla 165
Db 1 ATTGCATGGTTTCACTGTCTTTTACTTTGGCAATGGCTGGATTCTCCCTCATCAGCGCC 60
Qy 166 PheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeu 185
Db 61 TTTGTCTTGTCTACCTCTCAGGCCCAAGCTGGATGGCTGACATGATTATGGCCACTG 120
Qy 186 SerValTyrArgLysPheGlyTyrPheAsnHisLeuValHisLysPheValIleGlyHisLeu 205
Db 121 TCTGTCTACAGAAAACCAAGTGGAAACCACTTGTCCACAAATTCATCATTTGGCCACTTA 180
Qy 206 LysGlyAlaSerAlaAsnTyrTyrPheAsnHisArgHisPheGlnHisHisAlaLysProAsn 225
Db 181 AAGGGTGGCTCTGCCCACTGGTGGATCATCGCCACTTCCAGCACCAGCCAGCCTAAC 240
Qy 226 IlePheHisLysAspProAspValAsnValLeuHisValPheValLeuGlyGluTyrGln 245
Db 241 ATCTTCCACAGGATCCCGATGTGAACATGTGCACGTGTGTCTTGTGGCGAATGGCAG 300
Qy 246 ProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
Db 301 CCCATCGAGTACGGCAAGAAAGCTGAATACCTGCCCTACATACCAGCAGCAATAC 360
Qy 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285
Db 361 TTTCTTCTGATTGGGCGCCGCTGCTCATCCCATGTATTTCAGTAGTACCATCATCATG 420
Qy 286 ThrMetIleValHisLysAsnTyrValAspLeuAlaTyrPheValSerTyrTyrIleArg 305
Db 421 ACCATGATCGTCCATAAGAACTGGTGGACCTGGCTGGGCGCTGACCTACTACATCCGG 480
Qy 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 481 TTTCTCATCCTCATCATCCCTTTCTACGGCATCTGGAGCCCTCTTTTCTCAACTTC 540
Qy 326 IleArgPheLeuGluSerHisTyrPheValTyrValThrGlnMetAsnHisIleValMet 345
Db 541 ATCAGGTTCTTGAGAGACCACTGGTTGTGTGGTGCACACAGATGAATCATCGTCATG 600
Qy 346 GluIleAspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 601 GAGATTGACAGAGAGGCTTACCGTACTGTTTCACTAGTACCGAGCTGACAGCCACTGCAAC 660
Qy 366 ValGluGlnSerPhePheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHis 385
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Qy 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 721 CACCTCTTCTCCCATCATGCCCGGCACTTACCAAGATCGCCCGCTGGTGAATGCT 780
Qy 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 781 CTATGTGCCAGCATGGCATTTGAATACAGGGGAAGCGCTTACTGAGGGCCCTCTCTGCAC 840
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LOCUS Homo sapiens cDNA FLJ90444 f1s, clone NT2RP3001159.
DEFINITION AK074925
ACCESSION AK074925
VERSION AK074925.1 GI:22760689
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hito, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahara, K., Masuno, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2558)
AUTHORS Isogai, T. and Otsuki, T.
JOURNAL Direct Submission
COMMENT Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' - & 3' -end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
FEATURES
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precursor cells after 2-weeks retinoic acid (RA)
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Pred. NO.: 7.14e-151 Length: 2558
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Query Match: 68.42% Indels: 0
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Qy 186 SerValTyTrA:GlySProLySTrPAsnHisLeuValHisTyPheValIleGlyHisLeu 205
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Qy 246 ProIleGluTrGlyLysLysLysLeuLysLeuProTyTrAsnHisGlnHisGluTyTr 265
Db 301 CCCATCGAGTAGCGCAAGAGAGAGCTGAATACCTGCCCTACAATCACCAGCAGCAATAC 360
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Db 361 TTCTTCCTGATTTGGCGCGCTCTCATCCCATGTAATTTCCAGTACCCAGATCATCATG 420
Qy 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTrIleArg 305
Db 421 ACCATGATCGTCCATAGAACTGGGTGGACCTGGCTGGCGCTGAGCTACTACTACATCGG 480
Qy 306 PhePheIleThrTrIleProPheTyGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
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Qy 406 LeuCysAlaLysHisGlyIleGluTyTrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
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DEFINITION cds.
ACCESSION AB074149
VERSION AB074149.1 GI:16904664
KEYWORDS Oncorhynchus masou (cherry salmon)
SOURCE Oncorhynchus masou
ORGANISM Oncorhynchus masou
REFERENCE 1 Sirisuy, S., Yoshizaki, G., Kiron, V., Takeuchi, T. and Gen, K.
AUTHORS delta6-desaturase-like cDNA in masou salmon form2
TITLE Unpublished
JOURNAL 2 (bases 1 to 1498)
REFERENCE 1 Sirisuy, S., Yoshizaki, G., Kiron, V., Takeuchi, T. and Gen, K.
AUTHORS Direct Submission
TITLE Submitted (10-NOV-2001) Soranuth Sirisuy, Tokyo University of
JOURNAL Fisheries, Aquatic Bioscience, 4-5-7 Konan, Minato-ku, Tokyo
108-8477, Japan (E-mail: soranuth@yahoo.com, Tel:81-3-5463-0555,
Fax:81-3-5463-0553)
FEATURES Location/Qualifiers

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DB 139 GGAGGGCGAGTGGGAGTGCA-GTCTACACCTGGGAGAGGTCCAGAAGCACTGCCACAG 197
QY 32 gThrAspSerGlyLeuValIleAspArgLysValTyRsnIleThrLysTrpSerIleG 52
DB 198 AAGCGACCACTGGTTGGTCATCGACAGGAGGTCTATATATACCCAGTGGGCGAAGAG 257
QY 52 nHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGluAspAlaThrAspAlaPh 72
DB 258 ACACCGAGGAGCATCAGGTCATCAGTCATCTTCTCGGAGAGATGCCAGGATGATT 317
QY 72 eArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleG 92
DB 318 TGTGCGATTCCATCCCGATTCTAATTTTGTGAGGAAGTTTCTGAAGCGGTTGCTGATTG 377
QY 92 yGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAs 112
DB 378 AGAGCTGGCACCACAGACGCCAGCCAGGACCATCGGAAACACGACTACTGGGGCAGGA 437
QY 112 pPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPh 132
DB 438 CTTCCAGGCGCTCGGCGACCGGTGTAGAGGAGGGGTCTCTCCGTGCGCCGCCCTCTT 497
QY 132 ePheLeuLeuLeuLeuAlaHisIleAlaLeuGluSerLleAlaTTPPheThrValPh 152
DB 498 CTTACGCTCTACCTGGGCGCATCTGTCTACTAGAGGCCCTGGCTTTGGGCTGCTCTG 557
QY 152 eTyRPhGlyAsnGlyTTPileProThrLeuIleThrAlaPheValLeuAlaThrSerG 172
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QY 172 nAlaGlnAlaGlyTTPLeuGlnHisAspTyRgIlyHisLeuSerValTyArgLysProLy 192
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312 oPheTyRgIlyLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHi 332
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1158 CCAGGACTGGCTCACCATGTCAGTTGAGTCTACTTGCACATTTGAACAGTTCGACCTTCAA 1217
372 nAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThrMetPr 392
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1278 CGGTATATACTACCACTGGTGGCTCTCTGTTGCTGTTGTTGTGAGAAACATGGACT 1337
412 eGluTyRgIleGlnLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLy 432
1338 TCCCTACCAAGGTCAGAGCTTTCAGAAAGCCATCATGATGTTTCGGGTCTACTGAGAA 1397
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RESULT 25
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LOCUS Salmo salar putative delta-6 fatty acyl desaturase (Fads6) mRNA,
DEFINITION complete cds.
ACCESSION AF478472
VERSION AF478472.1 GI:18959527
KEYWORDS Salmo salar (Atlantic salmon)
SOURCE Salmo salar
ORGANISM Salmo salar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 1365)
Hastings, N. Jr., Agaba, M.K., Tocher, D.R. and Teale, A.J.
The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
Freshwater Teleosts
Unpublished
2 (bases 1 to 1365)
Hastings, N. Jr., Agaba, M.K., Tocher, D.R. and Teale, A.J.
Direct Submission
Submitted (28-JAN-2002) Institute of Aquaculture, Pathfoot
Building, Stirling FK9 4LA, Scotland

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|   | 1..1365   | /codon_start=1   |               | 231   | ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250   |
|   | /product="putative delta-6 fatty acyl desaturase" | /protein_id="AAU82631.1"   |               | 721   | CCTGATATCAACTCAGTCCCTGCTTTCTGCTGGAGACACACAGCTGTAGAGTATGGT 780      |
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| Qy  | 19  | Pro-----ThrPheSerTrpGluGluIleGlnLysHisAsn 30   |               |       |  |
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| Qy  | 31  | LeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSer 50  |               |       |  |
| Db  | 121   | CACAGACGACACAGTGGTGGTTCATCGACGAGAGCTCTATATATATCCAGTGGGCA 180   |               |       |  |
| Qy  | 51  | IleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAsp 70  |               |       |  |
| Db  | 181   | AAGAGACACCCGGGTGGCATCAGGTCATCAGTCACTTTGCTGGAGAAGATGCCACGGAA 240  |               |       |  |
| Qy  | 71  | AlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeu 90  |               |       |  |
| Db  | 241   | GCAITTTCCGCATTCATCTTGATGCTAATTTGTCAGGAAGTTTCTGAGACCGCTTGCTG 300  |               |       |  |
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| Db  | 301   | ATTGAGAGCTGGCCACGACAGAGCCAGCCAGGACCATGGGAAAATGCAAGCTCTGGTG 360   |               |       |  |
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| Db  | 421   | CTGTCTTCAGCTCTACTGGGCACATCTGCTACTAGAGCGCTGGCTTTGGGCGCTG 480  |               |       |  |
| Qy  | 151   | ValPheTyrPheGlyAsnGlyTrpIleProThrIleThrAlaPheValLeuAlaThr 170  |               |       |  |
| Db  | 481   | CTCTGGGTGGGGGACGAGCTGGAGCGCTCACACTGCTCTCTCTCCATCGTGGCCACG 540  |               |       |  |
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## RESULT 26

AF309556

LOCUS

DEFINITION

AF309556

VERSION

AF309556.1

GI:10954034

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF309556 1590 bp mRNA linear VRT 05-DEC-2001  
 Danio rerio putative delta-6 fatty acyl desaturase (Fads6) mRNA,  
 complete cds.

AF309556  
 AF309556.1 GI:10954034  
 Danio rerio (zebrafish)

Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 1590)  
 Hastings, N., Agaba, M., Tocher, D.R., Leaver, M.J., Dick, J.R.,  
 Sargent, J.R. and Reale, A.J.

A vertebrate fatty acid desaturase with Delta 5 and Delta 6  
 activities

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)  
PUBMED 11724940  
REFERENCE 2 (bases 1 to 1590)  
AUTHORS Hastings.N., Agaba.M.K., Tocher.D.R., Teale.A.J. and Sargent.J.R.  
TITLE Direct Submission  
JOURNAL Submitted (28-SEP-2000) Genetics, Institute of Aquaculture,  
Stirling FK9 4LA, Scotland  
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DB: 5 Gaps: 0  
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QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
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QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
Db 661 CACGCTAAACCAACATCTTCAAGAGAGGACCGGACGTCACATCTGAACCCCTTTGTG 720  
QY 241 LeuGlyGluTrpGlnProIleGluTrpGlyLysLysLysLeuLysTrpLeuProTrpAsn 260  
Db 721 GTGGGAAACGTGACGCCGCTGGAGTATGGCTTAAAGATCAAGCATCTGCCCTACAAC 780  
QY 261 HisGlnHisGlyTrpPhePheLeuIleGlyProProLeuLeuIleProMetTrpPheGln 280  
Db 781 CATCAGACAAAGTACTTCTTCTTCTGCTGCTCCCTGCTCATCCCATGATTTCCAG 840  
QY 281 TyrGlnIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
Db 841 TTCCAAATCTTCACAATATGATCAGTCATGCGATGCGTGGTGACCTGCTGTGGTATC 900  
QY 301 SerTrpTrpIleArgPhePheIleThrTrpIleProPheTrpGlyLysLeuGlyAlaLeu 320  
Db 901 AGCTACTAGTCGATCTCTCTTCTTACAGCGCATCTTACGGCGTCTTTTGGGCTATT 960  
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340  
Db 961 ATCTCTTTAATTTCTGTCAGGTTTATGGAGGCCACTGTTGTTGTTGGTTCACACAGATG 1020  
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360  
Db 1021 AGCCACATCCCATGAACATGACTATGAGAAAAATCAGGACTGCTCAGCATGCAGCTG 1080  
QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380  
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QY 381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
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QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440  
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QY 441 TyrLeuHisLys 444  
Db 1321 TATCTCAACAA 1332  
RESULT 27  
AR221959 1943 bp DNA linear PAT 26-SEP-2002  
LOCUS Sequence 7 from patent US 6428990.  
DEFINITION AR221959  
ACCESSION AR221959  
VERSION AR221959.1 GI:23329262  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 1843)  
AUTHORS Mukerji,P., Leonard,A.E.Y., Huang,Y.-S. and Parker-Barnes,J.M.



TITLE Human desaturase gene and uses thereof  
JOURNAL Patent: US 6428990-A 7 06-AUG-2002;  
FEATURES Location/Qualifiers  
source 1..1843  
/organism="unknown"

BASE COUNT 356 a 598 c 466 g 423 t  
ORIGIN

Alignment Scores:

Pred. No.: 6,08e-149 Length: 1843  
Score: 1646.00 Matches: 294  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 67.51% Indels: 0  
DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x AR221959 (1-1843)

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Qy 171 SerGlnAlaGlnAlaGlyTrrPleGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
Db 61 TCTCAGGCCCAAGTGGTGGCTGCACATGATTATGGCCACCTGTCTGTACAGAAA 120  
Qy 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210  
Db 121 CCCAAGTGGACCAACCTTGTCCAAATTCGTATTGGCCACTTAAAGGGTGGCTCTGCC 180  
Qy 211 AsnTrpTrpAsnHisArgHisGlnHisAlaLysProAsnIlePheHisLysAsp 230  
Db 181 AACTGGTGGATATATCCCACTTCCAGACCAAGCCATCATCTTCCACAGGAT 240  
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Qy 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290  
Db 361 CCGCGCTGCTCATCCCATGATATTTCCAGTACCATCATCATGACCATGCTCCAT 420  
Qy 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
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Db 781 GGCATTGAATACACAGAGACCGCTACTGAGGCGCTGTGGATCATCATCAGGTCCCTG 840

Qy 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
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RESULT 28  
BD082639  
LOCUS

DEFINITION BD082639 1843 bp DNA linear PAT 27-AUG-2002  
Methods and compositions for synthesis of long chain  
poly-unsaturated fatty acids.

ACCESSION BD082639  
VERSION BD082639.1 GI:22628249  
KEYWORDS JP 2001523091-A/19.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1843)

AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and  
Leonard,A.E.Y.

TITLE Methods and compositions for synthesis of long chain

JOURNAL poly-unsaturated fatty acids

COMMENT Patent: JP 2001523091-A 19 20-NOV-2001;  
CALGENE LLC,ABBOTT LABORATORIES

PN JP 2001523091-A/19

PD 20-NOV-2001

PF 10-APR-1998 JP 1998544053

PR 11-APR-1997 US 08/834655

PI DEBORAH KNUZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI  
THURMOND,

PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD

PC C12N15/53, C12N15/81, C12N5/02, C12N5/10, C12N1/19, C12P7/64 PC

CC A23L1/30

CC Strandedness: Single;

CC topology: Linear;

CC Location/Qualifiers.

PH Key

Location/Qualifiers

1..1843

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/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

BASE COUNT 356 a 598 c 466 g 423 t

ORIGIN

Alignment Scores:

Pred. No.: 6,08e-149 Length: 1843  
Score: 1646.00 Matches: 294  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 67.51% Indels: 0  
DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x BD082639 (1-1843)

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Qy 171 SerGlnAlaGlnAlaGlyTrrPleGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190

Db 61 TCTCAGGCCCAAGTGGTGGCTGCACATGATTATGGCCACCTGTCTGTCTACAGAAA 120

Qy 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210

Db 121 CCCAAGTGGACCAACCTTGTCCAAATTCGTATTGGCCACTTAAAGGGTGGCTCTGCC 180

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 QY 271 ProProLeuLeuLeuProMetTyrPheGlnTyrGlnLeuLeuMetThrMetLeuValHis 290  
 Db 361 CCGCGCTGCTCATCCCATGATTTCCAGTACCATCATCATGACCATGATCTGCTCAT 420  
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheLeuThrTyr 310  
 Db 421 AAGAACCTGGGTGGACCTGGCGCTGGCGCTGAGTCTATCATCGGTCTTCTCATCCTAC 480  
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 Db 841 AAGAAGTCTGGAGCTGGTGGAGCGCTACCTTACAAA 882

RESULT 29  
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 LOCUS DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids.  
 ACCESSION BD082654  
 VERSION BD082654.1 GI:22628264  
 KEYWORDS JP 2001523092-A/14.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 1843)  
 AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.  
 TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids  
 JOURNAL Patent: JP 2001523092-A 14 20-NOV-2001;  
 COMMENT CALGENE LLC ABBOTT LABORATORIES  
 PN JP 2001523092-A/14  
 PD 20-NOV-2001  
 PF 10-APR-1998 JP 1998544176  
 PR 11-APR-1997 US 08/833610  
 PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,  
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD  
 PC  
 C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC  
 30, A23K1/00  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.  
 FEATURES Location/Qualifiers

source 1..1843  
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 BASE COUNT 356 a 598 c 466 g 423 t  
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 Pred. No.: 1646.00 Matches: 294  
 Score: 100.00% Conservativity: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 67.51% Gaps: 0  
 DB: 6  
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 QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170  
 Db 1 GTCCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCAGGCGCTTTGCTCTGTCTACC 60  
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 Db 61 TCTCAGCCCAAGCTGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120  
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210  
 Db 121 CCCAAGTGAACACCTTTGTCACAAATTCGTATGGCCACTTAAAGGGTGGCTCTGCC 180  
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAsp 230  
 Db 181 AACTGGTGAATCATCGCCACTTCCAGCACCCAGCCCAAGCTTACATCTTCCACAGGAT 240  
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 Db 241 CCGATGTGAACATGCTGCACGTGTTGTTCTGGCGGAATGCGACCCATCGRTACGGC 300  
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 Db 301 AAGAAGACTGAATACCTGCTTACATCACCAGCACGCAATACTTCTTCTCTGATTGGG 360  
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 Db 361 CCGCCCTCTCTCATCCCATGATTTCCAGTACACAGATCATCATGACCATGCTCCAT 420  
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
 Db 421 AAGAAGCTGGTGGACCTGCGCTGGCGCTGAGTACTACATCCGTTCTTCTCATCACCTAC 480  
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330  
 Db 481 ATCCCTTTTCTACGGCATCTGCGAGCCCTCTTTTCTCAACTTCATCAGGTTCTCTGGAG 540  
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 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430  
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QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 841 AAGAAGTCTGGAGAGCTGTGGCTGGACGCTACCTTCACAAA 882

RESULT 30
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LOCUS BD092933 1843 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION BD092933
VERSION BD092933.1 GI:22638544
KEYWORDS JP 2001527395-A/20
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1843)
AUTHORS Knutzen,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and
Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants
JOURNAL Patent: JP 2001527395-A 20 25-DEC-2001;
CALGENE LLC,ABBOTT LABORATORIES
COMMENT PN JP 2001527395-A/20
PD 25-DEC-2001
PF 10-APR-1998 JP 1998544175
PR 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR
11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI
DEBORAH KNUTZEN, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC
C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
30, A23K1/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source 1. 1843
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BASE COUNT 356 a 598 c 466 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 6.08e-149 Length: 1843
Score: 1646.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.51% Indels: 0
DB: 6 Gaps: 0

US-09-719-601-5 (1-444) x BD092933 (1-1843)

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Db 361 CCGCGCTGTCTCATCCCATGTATTTCCAGTACCATCATCATGACCATGATGTCATCAT 420

QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310
Db 421 AAGAACTGGGTGGACCTGGCGCTGGCGCTCAGCTACTACATCCGCTTCTTCTCATCACCTAC 480

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Db 841 AAGAAGTCTGGAGAGCTGTGGCTGGACGCTACCTTCACAAA 882

RESULT 31
AB070444 1692 bp mRNA linear VRT 23-AUG-2001
LOCUS Oncorhynchus masou FD6D mRNA for putative delata 6-desaturase,
DEFINITION complete cds.
ACCESSION AB070444
VERSION AB070444.1 GI:15281353
KEYWORDS Oncorhynchus masou (cherry salmon)
SOURCE Oncorhynchus masou
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1
AUTHORS Yoshizaki,G., Ishikawa,A., Takeuchi,T. and Gen,K.
TITLE delata6-desaturase-like cDNA in masou salmon
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1692)
AUTHORS Yoshizaki,G., Ishikawa,A., Takeuchi,T. and Gen,K.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-2001) Goto Yoshizaki, Tokyo University of
Fisheries; 4-5-7 Kounan, Minato-ku 108-8477, Japan
(E-mail:goto@tokyo-u-fish.ac.jp, Tel:81-3-5463-0558,
Fax:81-3-5463-0558)
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Gaps: 0
US-09-719-601-5 (1-444) x AB070444 (1-1692)
QY 8 GlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluLeuGln 27
Db 226 GGGTGGGCGCGGATGGAGGGGAGGTGGCAGTGCA-GTCTACCTGGGAGAGGTGCG 284
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 285 AGCACTGCCACAGAGCAGCAGGTGGTGGTATCGACAGAGAGGTCTATAATATTACC 344
QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 345 CAGTGGGGGAAGACACCCAGGGGGCATCAGGGTCATCAGTCATCTTGTCTGGAGAGAT 404
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 405 GCCACGAGAGCATTTGTCGATCTCCATCTCGAACCGAATTTTGTTCAGGAAGTTTCTGAAG 464
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 465 CCGTTGCTGATGGAGAGTGGCAGCAGAGAGCCAGCAGGACGAGGGGAGAAATGCA 524
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 525 GTACTGTGCGAGCATTCAGGCCCTCGTGCAGCGGTGGAGAGTGGAGTCTCTCCCT 584
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuLeuSerIleAla 147
Db 585 GCCCGCCCCCTCTCTCTAGCCCTTACCTGGGCGACATCTCTGCTAGAGGCCCTGGCT 644
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTyrIleProThrLeuIleThrAlaPheVal 167
Db 645 TTGGGCTGCTCTGGGTCTGGGAGCAGCAGTGGAGCTCAGCTGCTCTGTTCCCTCAG 704
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 705 CTGGCCACGCTCTAGGCCCGCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 764
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisValPheValIleGlyHisLeuLysGly 207
Db 765 TGCAGAAATCTGGCTGGAGAACCAACAAATGCAAGATTGCTATTGGACACCTTAAGGGT 824
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 825 GCCTCTGCTAACTGGTGGAGCACTCTGCTCCTTCCAGCAGCAGCAGCAGCAGCAGT 884
QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247

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Db 885 AGTAAGATCCTGATATCACTCACTCATGTCTTCTGCTGGGAGACAAACAGCCTGTA 944
QY 248 GluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 267
Db 945 GAGTATGATATTAAGAAGATTGAAGTATGATGATGATGATGATGATGATGATGATGATG 1004
QY 268 LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleLeuMetThrMet 287
Db 1005 CTCGTGGACCTCCACTCATGCTCCAGTGTCTTCAACATCCAGATATTCGGAGCATG 1064
QY 288 IleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePhe 307
Db 1065 TTTTCAACAGCAGACTGGTGGATCTGGCGTGGGAGTACTTCTTACCTTCGCTTCTTC 1124
QY 308 IleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArg 327
Db 1125 TGCTCTTACTATCCCTCTTCTTGGTGTCTTGGTGGTGGTGGTGGTGGTGGTGGTGG 1184
QY 328 PheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIle 347
Db 1185 TTTTGGAAAGCCACTGTTGTATGGGTGAGCCAGATGAGTACCTTCCGATGGAGATG 1244
QY 348 AspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGlu 367
Db 1245 GATCAGCAGAGACACGAGGACTGGCTCACCAGTGGTGGTGGTGGTGGTGGTGGTGG 1304
QY 368 GlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisIleu 387
Db 1305 CAGTCAACCTTCAACGACTGGTTCAGTGGACACCTTCACTTTCAGATTGAACCATCTG 1364
QY 388 PheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCys 407
Db 1365 TTTTCTTACCATGCCCCCTCATTAACCTACCATGGTGGTGGTGGTGGTGGTGGTGG 1424
QY 408 AlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIle 427
Db 1425 GAGAAACATGGAGTTCCTTACCAGGTCAGAGACTTTCGAGAAAGGAGGAGTACTGAT 1484
QY 428 ArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1485 AGTCACTGAAGAAGTACGGGGTCTGCTGGTGGATCGCTATCTCCATAAA 1535

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RESULT 32
BC049438 1708 bp mRNA linear VRT 01-APR-2003
LOCUS
DEFINITION
Danio rerio, clone MGC:56438 IMAGE:5612204, mRNA, complete cds.
ACCESSION
BC049438.1 GI:29436932
VERSION
MGC.
KEYWORDS
MGC.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (Bases 1 to 1708)
Strausberg, R.
Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NHL-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: csapbs-remail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

```

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smaluis, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 104 Row: e Column: 4.

#### FEATURES

Location/Qualifiers  
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/db\_xref="taxon:7955"  
/clone="MGC:56438 IMAGE:5612204"  
/tissue\_type="whole body, adult male"  
/clone\_lib="Sugano SJD adult male"  
/lab\_host="DH108"  
/notes="vector: pME18S-FL3"  
95..1429

#### CDS

/codon\_start=1  
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TLVAVLTAQQAQAGLQHDQFGLSVFKTSGMNLHVLKFPVIOHLKAGASGANNRRHF  
QHIAPNIFKDKDQNNMLAFVGVQVPEYGVKKIKHPLVHOKHYFFIIGPLLP  
YFQFQIFHNHISGHWMDLLWCI SYVRYFLCYQFVFWAIIIFNFVRFMESHF  
VYWTOMSRIPMNIDYEQNDLWQNLVATCNIBQSAFNDFWLSGHLNFQIEHLFPMP  
RHNRYRAAPRVRSICEKYGKVKOEKLYGAFADIIIRSLKSGELDLAYLNK"

BASE COUNT

466 a 417 c 426 g 399 t

#### ORIGIN

#### Alignment Scores:

Pred. No.: 2.6e-148 Length: 1708  
Score: 1639.00 Matches: 287  
Percent Similarity: 78.60% Conservatives: 62  
Best Local Similarity: 64.84% Mismatches: 95  
Query Match: 67.23% Indels: 0  
DB: 5 Gaps: 0

US-09-719-601-5 (1-444) x BC049438 (1-1708)

Qy 1 MetGlyLysGlyGlyAsnGlnGlyAlaAlaGluArgGluValSerValProThr 20  
Db 95 ATGGTGGCGGAGGACACAGACAGACGGAATCCAGCACCAACGCGCAGATTCCAGC 154  
Qy 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
Db 155 TACACCTGGGAGGAGATCGAGAAACACACACCAACATGAGATCAGTGGGTGGTGAG 214  
Qy 41 ArgLysValTyraAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
Db 215 AGGAGAGGTTTATAAGCTGAGCGAGTGGGTGAAGAGACACCCCGGAGGACTGAGATCTC 274  
Qy 61 GlyHisIleTyraAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeu 80  
Db 275 GGACACTATGCTGGAGAGAGAGCCACGCGAGGCGTTCACTGCGTTTCATCCAAACCTTCAG 334  
Qy 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100  
Db 335 CTGATGAGGAATACCTGAAGCGCTGCTATATCGAGAGCTGGAGCGGCTCTGAACCCAGT 394  
Qy 101 GlnAspHisGlyLysAsnSerIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
Db 395 CAGGACCGGACAGAAAACGCTCTCTCGTGGAGGATTTCCGAGCCCTCGGTGAGCGTCTG 454  
Qy 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
Db 455 GAGGCTGAGGCTGTTTAAACACGCGCGCTGTTTTCGCTCTGCTATTTGGGCCACATT 514

Qy 141 IleAlaLeuGluSerIleAlaIleTrpPheThrValPheTyrrPheGlyAsnGlyTrpIlePro 160  
Db 515 CTGCTCTGGAGGCGCATCGCTTTCGATGATGTTTTCGATTCGGCACCGGTTGGATCAAC 574  
Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlnAlaGlnHis 180  
Db 575 ACGTCTATCGTGGTGTATTCCTGGCTACTGCACAGTCACAGCTCAGAGCTGGTTCAGCAT 634  
Qy 181 AspTyrrGlyHisLeuSerValTyrrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
Db 635 CACTTCGGTCTATCTGCTCGTGTATAAACCTCTGGAATGAATCAATTTGGTGACAAATTT 694  
Qy 201 ValIleGlyHisLeuLysGlyValaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
Db 695 GTCATCGGACACCTGAGAGGAGCGCTTCGGGGCTGGTGGACCATCGGCATCTCCAGCAT 754  
Qy 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
Db 755 CACGCTAAACCAACATCTTCAAGAGAGGACCGGACGCTCAACATGCTGAACGCGCTTGTG 814  
Qy 241 LeuGlyGluTrpGlnProIleGluTyrrGlyLysLysLysLeuLysTyrrLeuProTyrrAsn 260  
Db 815 GTGGGAAACGTCGACCGCGTGGAGTACGGCGTTAAGAGATCAAGCATGCCCCATCAAC 874  
Qy 261 HisGlnHisGluTyrrPhePheLeuIleGlyProProLeuLeuIleProMetTyrrPheGln 280  
Db 875 CATCAGCAACAGTACTTCTTCTTATTTGGTCTCTCCCTGCTCATCCAGTGTATTTCAG 934  
Qy 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
Db 935 TTCCAAATCTTTCACATATGATCATGTCGATGTCGATGTCGGTGGACCTGCTGTGTATC 994  
Qy 301 SerTyrrIleArgPhePheIleThrTyrrIleProPheTyrrGlyIleLeuGlyAlaLeu 320  
Db 995 AGCTACTACGTCGATACTTCTTTTGTACACGCGAGTTCTACGCGCTCTCTTTGGGCTATT 1054  
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340  
Db 1055 ATCTCTCTTTAAATTCGTCAGGTTTATGAGAGCCACTGCTTGTGTGGGTTCACAGATG 1114  
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrrArgAspTrpPheSerSerGlnLeu 360  
Db 1115 AGCGCATCCCATGACATCGACTATGAGCAAAATCAGGACTGGCTCAGCATGCGAGTGT 1174  
Qy 361 ThrAlaThrCysAsnValGluIleSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380  
Db 1175 GTCGGACCTGTAAATCATGAGCAGTCTGCTTCAACGACTGGTTCAGCGGACACCTCAAC 1234  
Qy 381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
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Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrrGlnGluLysProLeuLeu 420  
Db 1295 CCACGGTTCGATCGTGTGTGAGAAATACGGAGTCAAAATACCAAGAGAGAACCTTGTATC 1354  
Qy 421 ArgAlaLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440  
Db 1355 GGAGCATTTGGGATATCATATTAGTCTTTGGAGAAATCTGGCAGCTCTGGCTGGATGG 1414  
Qy 441 TyrLeuHisLys 444  
Db 1415 TATCTCAACAAA 1426

#### RESULT 33

AF309557 1790 bp mRNA linear VMT 05-DEC-2001  
LOCUS  
DEFINITION  
Cyprinus carpio putative delta-6 fatty acyl desaturase (Fads6d6)  
mRNA, complete cds.  
AF309557  
AF309557.1 GI:10954036  
KEYWORDS  
Cyprinus carpio (common carp)

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ORGANISM  Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE  1 (bases 1 to 1790)
AUTHORS    Hastings,N., Acaba,M., Tocher,D.R., Leaver,M.J., Dick,J.R.,
            Sargent,J.R. and Teale,A.J.
TITLE      A vertebrate fatty acid desaturase with Delta 5 and Delta 6
            activities
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)
PUBMED     11724940
REFERENCE  2 (bases 1 to 1790)
AUTHORS    Hastings,N., Acaba,M.K., Tocher,D.R., Teale,A.J. and Sargent,J.R.
TITLE      Direct Submission
JOURNAL    Submitted (28-SEP-2000) Genetics, Institute of Aquaculture,
            Stirling FK9 4LA, Scotland
FEATURES   source
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            /genes="Fadsd5"
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BASE COUNT  466 a 410 c 458 g 456 t
ORIGIN
US-09-719-601-5 (1-444) x AF309557 (1-1790)
Alignment Scores:
Pred. No.: 2e-144 Length: 1790
Score: 1599.00 Matches: 278
Percent Similarity: 78.15% Conservative: 69
Best Local Similarity: 62.61% Mismatches: 97
Query Match: 65.59% Indels: 0
DB: Gaps: 0

1 MetGlyLysGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
Db 1 ATGGGTGGCGGAGGACAGCAGACGCGGATCCTCGGAGCAACCGGAGGTTCGGCACT 60
Qy 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
Db 61 TACACTGGGAGGAGGTTCGAGAACACACCAAGTTGGAGATCAGTGGATCGAGTTGAA 120
Qy 41 ArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGlnArgValIle 60
Db 121 AGGAAGGTTTATATGTGACCGAGTGGTGAGAGACACCCCGGAGGAGTGGAGTCTC 180
Qy 61 GlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 181 GGACACATATCTGGAGAGATGACCGAGGCGTTTACTGTCATTTCACGACCTTCG 240
Qy 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluLysProSer 100
Db 241 CTGTGTGAGAAATACATGAGCCGCTGTTAATCGGGGCGCTTGAGCGCTGTAACCCAGT 300
Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120

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RESULT 34  
AB069727  
LOCUS

AB069727 1576 bp mRNA linear VRT 11-AUG-2001



|   |  |
|---|--|
| DEFINITION                                  | Oreochromis niloticus Fad6 mRNA for putative delta-6 fatty acyl desaturase, complete cds.  |
| ACCESSION                                   | AB069727   |
| VERSION                                     | AB069727.1   |
| KEYWORDS                                    | GI:15147882  |
| SOURCE                                      | Oreochromis niloticus (Nile tilapia)   |
| ORGANISM                                    | Oreochromis niloticus  |
| REFERENCE                                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidae; Cichlidae; Oreochromis.  |
| REFERENCE                                   | 1 Sirisunay, S., Yoshizaki, G., Kiron, V., Takeuchi, T., Satoh, S. and Watanabe, T.  |
| AUTHORS                                     |  |
| TITLE                                       | Molecular cloning, Expression, and Activity of the Nile Tilapia (Oreochromis niloticus) Delta-6 Fatty Acyl Desaturase  |
| JOURNAL                                     | Unpublished  |
| REFERENCE                                   | 2 (bases 1 to 1576)  |
| AUTHORS                                     | Sirisunay, S., Yoshizaki, G., Kiron, V., Takeuchi, T., Satoh, S. and Watanabe, T.  |
| TITLE                                       | Direct Submission  |
| JOURNAL                                     | Submitted (09-AUG-2001) Soranuth Sirisunay, Tokyo University of Fisheries, Aquatic Biosciences, Konan 4-5-7, Minato, Tokyo 108-8477, Japan (E-mail: soranuth@yahoo.com, Tel:81-3-5463-0555, Fax:81-3-5463-0553)  |
| FEATURES                                    | Location/Qualifiers  |
| source                                      | 1..1576  |
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|   | 1..1576  |
|   | /gene="Fad6"   |
|   | 110..1447  |
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|   | /translation="MGGGQQTVPGEPSGKAGVYTWEEVQVHGRNDQWLVDRKV YNTQAKRHPGGQVTSFVAGEDATEAFTADHPDFVHKFLKPLGLLGLATPEPSQ DRDKNALVQDFELRAQVKEKGLPRAQPLFFELHSHILLLEALGWLTYWMAQTGWI QTLVCSFLATAQAGLQHDQFGLHSVFKKSNHLLAHFVGLHLCASSNNWNRH LRHAKNFIKQDINTLFLVLRTPQVEYKIKKMPYRQHRHYFLVGPPLII PVFNHVMQMSRRDWDIAWISFLRPFSCYLELYGLVGLSLVLIQVIRFLSHW FVWYTMHMDIDHEKHQDWTMQLOSTCNIEQSFNDWVSHLNFQIEHLVSDN AAOLPPGGPAVRALCEKHGPIGYOEKTLWRGFADIVTSLSKTSGLDLDAVLHK" |
| BASE COUNT                                  | 408 a 380 c 391 g 397 t  |
| ORIGIN                                      |  |
| Alignment Scores:                           |  |
| Pred. NO.:                                  | 2,946-144 Length: 1576   |
| Score:                                      | 1596.50 Matches: 283   |
| Percent Similarity:                         | 77.68% Conservative: 65  |
| Best Local Similarity:                      | 63.17% Mismatches: 94  |
| Query Match:                                | 85.48% Indels: 7   |
| DB:   | 5 Gaps: 2  |
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| Qy  | 1 VetGlyLysGlyGlyAsnGln-----GlyGluGlyAlaAlaGluArgGluValSer 17  |
| Db  | 110 ATGGAGGTGGNAGCCAGCAGCGTGGCGGAGAGCGGACGGGAGAAAGCTAAAGGT 169   |
| Qy  | 18 ValProThrPheSerTrpGluIuleGlnLysHisAsnLeuArgThrAspSerGlyLeu 37   |
| Db  | 170 GTT-----TACACCTGGGAGGAGGTGCAGAGCCACTGCAGCAGGAATGATCAATGGCTG 223  |
| Qy  | 38 ValIleAspActLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGln 57  |
| Db  | 224 GTCATCGATCGAAGAGTTTACACATCACTAGTGGCCAAAGGCATCCAGGAGGTTT 283  |
| Qy  | 58 ArgValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPhePro 77  |
| Db  | 1363 AACTTTGTGGCGAGGCTTCGCTGATATTGTCACTGCTCACTGAAACCTCTGGGACCTCTG 1422   |
| Db  | 1304 CCTGGTGGCCCGCA-GTCCGTGGCTCTGCGAGAAACACCGGATTCCTTACAGAGAA 1362   |
| Qy  | 397 slyIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGlu 417  |
| Db  | 1244 CACCTCACTTTCAATCGAGCACCACTTTGTTTCCATGATGCGCGGCACACACTACCA 1303  |
| Qy  | 378 HisLeuAsnPheGlnIleGluHis-LeuPheProThrMetProArgHisAsnLeuHi 397  |
| Db  | 1184 ATGCAGTTACAATCCACCTGTAATTCGAGCAGTCCCTTCTTCAACGACTGGGTGAGTGA 1243  |
| Qy  | 357 ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSer 357   |
| Db  | 1124 ACTCAGATGAATCACAATACCGATGCATCATGAAACACACAGAGCTGGGTGACC 1183   |
| Qy  | 317 TrpAlaValSerTrpTrpIleArgPhePheIleThrTrpIleProPheTrpGlyIleLeu 317   |
| Db  | 1004 TGGTTCATCTCATTTACCTTCGCTTCTTCTCTGTTATTTACCCCTGTATGGCTGGTT 1063  |
| Qy  | 337 GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal 337   |
| Db  | 1064 GGCTCATTTGGTGTGCATAGCATAGTACAGTTTTCGAGAGTCACTGGTTTGTGGGTG 1123  |
| Qy  | 297 TyrPheGlnTrpGlnIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297  |
| Db  | 944 TTCTTCAACATTTCATGATCAGACCATGATCCCGCGGAGTGGGTGATGATGGCT 1003  |
| Qy  | 277 ProTrpAsnHisGlnIleGluTrpPhePheLeuIleGlyProProLeuLeuIleProMet 277   |
| Db  | 884 CTTTCAATCGTCAGCACCATTTACTTCTTCGTGGGACACCCGCTGATCATTCAGTT 943   |
| Qy  | 883 CTTCTTCGACTTGGCGCACTCAACAGTGGATACGGGATACGGAATACAGAAATCAACACATG 883   |
| Db  | 257 ValPheValLeuGluTrpGlnProIleGluTrpGlyLysLysLysLysLysTrpLeu 257  |
| Qy  | 823 CTTAGGATACACCTTAAACCCCAACATTTTCAATTAAGGACCTTCCAACTGGTGAATCACCAGTGCAC 823   |
| Qy  | 237 PheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237   |
| Db  | 764 CTAGGATACACCTTAAACCCCAACATTTTCAATTAAGGACCTTCCAACTGGTGAATCACCAGTGCAC 823  |
| Qy  | 217 HisLysPheValIleGlyHisLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHis 217  |
| Db  | 704 CACAAATTGTTCATTTAAAGGAGCTTCTTCCAACTGGTGAATCACCAGTGCAC 763  |
| Qy  | 197 LeuGlnHisAspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsnHisLeuVal 197   |
| Db  | 644 CTGCAGCATGACTTTTGGTCACTGCTCTCTTTAAAAAGTCCAGCTCGAATCAGCTGCC 703   |
| Qy  | 177 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp 177   |
| Db  | 584 TGGATACAAACACTTGTGCTCTGCTTCTCGCAACCGCTCAGGCACAGCTGGATGG 643  |
| Qy  | 583 AGTCACTCTCTGCTAGAACCCCTCGATGGTGGTCCGCTCGATGGTGGGGCAGAGC 583  |
| Qy  | 157 AlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGly 157   |
| Db  | 524 AGTCACTCTCTGCTAGAACCCCTCGATGGTGGTCCGCTCGATGGTGGGGCAGAGC 583  |
| Qy  | 137 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137  |
| Db  | 464 GCTCAGGTGGAGAAAGGGGCTGTTTCAGCTCAGCTCAGCTGCTTCTTCTTCTCCACCTC 523  |
| Qy  | 117 GluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArg 117   |
| Db  | 344 GATCTAAGTTTGTGCATAAGTTTCTGAAGCCGCTGCTGATCGGAGAGTTGGCAACGACA 403  |
| Qy  | 97 AspLeuGluPheValGlyLysPheLeuLeuProLeuLeuIleGlyGluLeuAlaProGlu 97   |
| Db  | 284 CAAGTCATCAGCTTCTATGCTGGAGAGATGCCACGAGGAGCACTCACTGCTTTTCATCCT 343   |

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QY      437 pLeuAspAlaTyrIleuHisLys 444
Db      1423 GCTGGATGCATATCTCCATAAA 1444

RESULT 35
AF134404
LOCUS   AF134404
DEFINITION Homo sapiens delta-6 fatty acid desaturase (CY5SRP) mRNA, complete cds.
ACCESSION AF134404
VERSION   AF134404.1 GI:4868365
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE
  1. (bases 1 to 1705)
  Li, W., Metzker, M.L., Caskey, C.T. and Petrukhin, K.
  Human retina-specific delta 6 fatty acid desaturase
  Unpublished
  2. (bases 1 to 1705)
  Li, W., Metzker, M.L., Caskey, C.T. and Petrukhin, K.
  Direct Submission
  Submitted (11-MAR-1999) Human Genetics, Merck Research
  Laboratories, P.O. Box 4, West Point, PA 19486, USA
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ORIGIN

Alignment Scores:
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QY      19 ProThrPheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38
Db      131 CCCACCTTCTCTGGGAGCGATCCGCGCGCAGCAGCCCGCGCAGCAAGTGGTGTGTC 190
QY      39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58
Db      1268 GTGCCCCCGCTGGTCAAGTCGCTGTGTGCCAAGCAGCGCCCTCAGCTACGAAGTGAAGCCC 1327

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QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLeuLysLeuLysSerGlyLysLeuTrpLeu 438  
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QY 439 AspAlaTyrLeuHisLys 444  
Db 1388 GACGCTACCTCCATCAG 1405

RESULT 36  
AR264713  
LOCUS AR264713 1717 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 2 from patent US 6492108.  
ACCESSION AR264713  
VERSION AR264713.1 GI:29693075  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1717)  
AUTHORS Hillman,J.L., Guegler,K.J., Corley,N.C. and Shah,P.  
TITLE Delta-6 desaturase homologs  
JOURNAL Patent: US 6492108-A 2 10-DEC-2002;  
FEATURES Location/Qualifiers  
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source /organism="unknown"  
BASE COUNT 330 a 563 c 482 g 342 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9.82e-141 Length: 1717  
Score: 1560.50 Matches: 278  
Percent Similarity: 76.23% Conservative: 62  
Best Local Similarity: 62.33% Mismatches: 103  
Query Match: 64.01% Indels: 3  
DB: 6 Gaps: 2

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QY 19 ProThrPheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38  
Db 135 CCCACCTTCCTCGGGAGCGAGATCCGCGCGCACGACCGCGCGGCGGCGGCGGCGGCTG 194

QY 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58  
Db 195 ATCAGCGCGCGCTACGACATCAGCGCGCTGGGCGACGCGCGGCGGCGGCGGCGGCGG 254

QY 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78  
Db 255 CTATCGCGCCACCGCGGCTGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 314

QY 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98  
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QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118  
Db 375 CCCAGCGAGGATGACCGCCCTGAATGCGAGCTGGTGGAGACTTCGAGCGGCTGGCAGG 434

QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138  
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QY 139 HistIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp 158  
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QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178  
Db 1599 CACATCTCTGGCGATGAGGCTGCTGGCTGGCTCTTATCTACCTCTCGGCTCTGGCTGG 1788

Db 555 GTGCCAGTCCCTGGCGCGCTTCATCTCTGGCCATCTCTCAGGCTCAGTCTGGTGTCTG 614

QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198  
Db 615 CAGCATGACCTGGGCGATGCTCCATCTTCAAGAAGTCTGTGGTGAACACACGCTGGCCAG 674

QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218  
Db 675 AAGTTCGTATGGGCGAGCTTAAAGGGCTTCTCGCCACCTGGTGGAACTTCCGCCCATTC 734

QY 219 GlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238  
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QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuPro 258  
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QY 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278  
Db 852 TACAAACGACGACCGCTGTACTTCTCTGATCGGCGCGCGCTGCTCACCTGGTGAC 911

QY 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298  
Db 912 TTTCAAGTGGAAATCTGGCGTACATCTGTGTGTCATGCGTGGCGGAGTTTCTCTCG 971

QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly 318  
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QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338  
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QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358  
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QY 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378  
Db 1152 CAGCTGGGAGCGACCTGCAAGCTGGAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1211

QY 379 LeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLys 398  
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QY 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418  
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QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438  
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QY 439 AspAlaTyrLeuHisLys 444  
Db 1392 GACGCTACCTCCATCAG 1409

RESULT 37  
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LOCUS AX035942 1757 bp DNA linear PAT 15-NOV-2000  
DEFINITION Sequence 3 from Patent EP1035207.  
ACCESSION AX035942  
VERSION AX035942.1 GI:11191484  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Marquardt,A. and Weber,B.H.  
TITLE Cdna molecules of the members of gene family encoding human fatty acid desaturases and their use in diagnosis and therapy  
JOURNAL Patent: EP 1035207-A 3 13-SEP-2000;

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| QY         | 299  | AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly  | 318             |
| Db         | 1031   | GCCGCCAGCTTCTATGCGCGCTTCTTCTATCTCTACCTCCCTCTACGGGCTCCTGGG     | 1090            |
| QY         | 319  | AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTTPPheValTTPValThr  | 338             |
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| QY         | 399  | IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro  | 418             |
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| QY         | 419  | LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTTPLeu  | 438             |
| Db         | 1391   | TTCCTCCCGCGCTGGTGGACATCGTCAGTCCCTGAGAGAGTCTGGTGACATCTGGCTG    | 1450            |
| QY         | 439  | AspAlaTyrLeuHisLys 444  |                 |
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| DEFINITION | Homo sapiens fatty acid desaturase 3 (FADS3) mRNA, complete cds.   |   |                 |
| ACCESSION  | AF084560   |   |                 |
| VERSION    | AF084560.1   | GI:10798952   |                 |
| KEYWORDS   |  |   |                 |
| SOURCE     | Homo sapiens (human)   |   |                 |
| ORGANISM   | Homo sapiens   |   |                 |
| REFERENCE  | Ekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.      |   |                 |
| AUTHORS    | Marquardt, A., Stohr, H., White, K. and Weber, B.H.  |   |                 |
| TITLE      | CDNA cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family         |   |                 |
| JOURNAL    | Genomics 66 (2), 175-183 (2000)  |   |                 |
| MEDLINE    | 20318619   |   |                 |
| PUBMED     | 10860662   |   |                 |
| REFERENCE  | 2 (bases 1 to 1757)  |   |                 |
| AUTHORS    | Marquardt, A., Stohr, H., Passmore, L.A., Kraemer, F., Rivera, A. and Weber, B.H.F.  |   |                 |
| TITLE      | Direct Submission  |   |                 |
| JOURNAL    | Submitted (05-AUG-1998) Institute of Human Genetics, University of Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany |   |                 |
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Query Match: 64.01% Indels: 3
DB: 9 Gaps: 2

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DB 254 ATCGAGCGCGGCTGTACACATACAGCCGCTGGGCGACGGCCAGCCGCGGCGGCGGCGGCG 313
QY 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78
DB 314 CTCATCGGCCACACCGGCGCTGAGGAGCGCCAGCGATGCTTCCGTGCTTCCATCAAGAT 373
QY 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98
DB 374 CTCAAATTTTGTGGCAAGTCTCTACAGCCCTGTGATTGGAGAGCTGGCTCCCGAGAGA 433
QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
DB 434 CCCAGCCAGATGACCCCTGATGCGAGCTGGTGGAGCTTCCGAGCCCTGCAACAC 493
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QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
DB 614 GTGCCAGTCCCTGGCGGCTTCTATCTCTGGCCATCTCTCAGGCTCAGTCCCTGGTGTCTG 673
QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198

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QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyArgAsp 354  
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QY 395 AsnLeuHisIleAlaProLeuValLysSerLeuCysAlaIleHisGlyIleGluTyr 414  
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QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAlaLeuLeuIleArgSerLeuLysSerGly 434  
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QY 435 LysLeuTrpLeuAspAlaTyLeuHisLys 444  
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Search completed: December 10, 2003, 19:33:44  
Job time : 3474 secs



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| 2          | 1937.6 | 60.9  | 2257   | 4  | US-09-227-613-8    | Sequence 8, Appli |
| 3          | 1830.4 | 57.5  | 1843   | 4  | US-09-439-261-7    | Sequence 7, Appli |
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| 18         | 443.4  | 13.9  | 446    | 4  | US-09-433-836B-425 | Sequence 425, App |
| 19         | 443.4  | 13.9  | 446    | 4  | US-09-604-287A-425 | Sequence 425, App |
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| 21         | 421.6  | 13.2  | 864    | 4  | US-09-439-261-13   | Sequence 13, Appl |
| 22         | 370.4  | 11.6  | 960    | 4  | US-09-439-261-36   | Sequence 36, Appl |
| 23         | 370.4  | 11.5  | 960    | 4  | US-09-227-613-35   | Sequence 35, Appl |
| 24         | 367.4  | 11.5  | 948    | 4  | US-09-439-261-5    | Sequence 5, Appli |
| 25         | 367.4  | 11.5  | 948    | 4  | US-09-227-613-5    | Sequence 5, Appli |
| 26         | 351.8  | 11.0  | 990    | 4  | US-09-439-261-35   | Sequence 35, Appl |
| 27         | 351.8  | 11.0  | 990    | 4  | US-09-227-613-34   | Sequence 34, Appl |

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710 GCTGCAACATGATTAATGGCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 769  
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Db CGTGTGTGTCTGGGCGAATGGAGCCCATCGAGTACGGCAAGAGAGCTGAATACCT 734  
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## RESULT 2

US-09-227-613-8  
; Sequence 8, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Ananda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08



QY 2210 CCATTCCACCGCTCCCAACTTTGAGCTGTGACCTTGGACCAAAAGGGGAGTCCCTCG 2269  
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 Db 2235 GGCCCCA-GGGGAGTGGGCCCTG 2257

RESULT 3  
 US-09-439-261-7  
 ; Sequence 7, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pardeep  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P2  
 ; CURRENT APPLICATION NUMBER: US/09/439,261  
 ; PENDING FILING DATE: 1999-11-12  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1843  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-439-261-7

Query Match 57.5%; Score 1830.4; DB 4; Length 1843;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 QY 690 TCTCAGGCCAAGCTGGATGGTGCMAATGATTATGGCCACCTGTCTGTCTACGAAAA 749  
 Db 61 TCTCAGGCCAAGCTGGATGGTGCMAATGATTATGGCCACCTGTCTGTCTACGAAAA 120  
 QY 750 CCCAAGTGAACCAACCTTGTCCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCC 809  
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 QY 870 CCGCATGTGAACATGTGACGCTGTTTCTGGGGGAATGGCAGCCCAATCGAGTACGCG 929  
 Db 241 CCGCATGTGAACATGTGACGCTGTTTCTGGGGGAATGGCAGCCCAATCGAGTACGCG 300  
 QY 930 AAGAAGAAGCTGAAATACCTGCCCTACAATCACCAGCAGGAATATCTTCTTCTGATTGGG 989

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 Db 1081 CTGCGCT 1140  
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RESULT 4  
US-09-227-613-7  
; Sequence 7, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.PI  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 1843  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-7

Query Match 57.5%; Score 1830.4; DB 4; Length 1843;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
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Qy      2430  CAGCAATCTCTGGCAATTTGGCCCGCAGGGGAGCTGGGCGCTG 2473
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RESULT 5
US-09-439-261-6
; Sequence 6, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-6

Query Match      52.6%; Score 1675; DB 4; Length 1686;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db      1      GCCACTTAAAGGTGGCTTGCACCTGCTGGAATCATCGCCACTTCCAGCACCACGCCA 60
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Db      121  AATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTCAATCACCAGC 180
Qy      967  ACGAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCCCATATTTCCAGTACCAGA 1026
Db      181  ACGAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCCCATATTTCCAGTACCAGA 240
Qy      1027  TCATCATCAACCATGATCGTCCATTAAGACTGGGTGAGCTGGCTGGCGCTGAGCTACT 1086
Db      241  TCATCATCAACCATGATCGTCCATTAAGACTGGGTGAGCTGGCTGGCGCTGAGCTACT 300
Qy      1087  ACATCCGGTCTTTCATCACTACATCCCTTTCTACGCACTCCTGGGAGCCCTCCTTTTC 1146
Db      301  ACATCCGGTCTTTCATCACTACATCCCTTTCTACGCACTCCTGGGAGCCCTCCTTTTC 360
Qy      1147  TCACTTTTCATCAGTTCTCTGGAGAGCCACTGGTTGTGGGTGACAGATGAATCACA 1206
Db      361  TCACTTTTCATCAGTTCTCTGGAGAGCCACTGGTTGTGGGTGACAGATGAATCACA 420
Qy      1207  TCGTCATGAGATTCACAGAGAGGCTTACCGTGAAGTGGTTTCTAGTAGCCAGCTGACGCCA 1266
Db      421  TCGTCATGAGATTCACAGAGAGGCTTACCGTGAAGTGGTTTCTAGTAGCCAGCTGACGCCA 480
Qy      1267  CTGCAAGCTGAGAGAGCTCTTCTTCAACGACTGGTTTCTAGTAGGACCTTAACTTCCAGA 1326
Db      481  CTGCAAGCTGAGAGAGCTCTTCTTCAACGACTGGTTTCTAGTAGGACCTTAACTTCCAGA 540
Qy      1327  TTGAGCACCACTCTTCCCGCCACCATGCCCCCGGCACTTACACAAGATCCGCCCGCTGG 1386
Db      541  TTGAGCACCACTCTTCCCGCCACCATGCCCCCGGCACTTACACAAGATCCGCCCGCTGG 600
Qy      1387  TGAAGTCTCTATGTGCGCAAGCATGGCATTTGAATACAGGAGAGCCGCTACTGAGGGGCC 1446
Db      601  TGAAGTCTCTATGTGCGCAAGCATGGCATTTGAATACAGGAGAGCCGCTACTGAGGGGCC 660
Qy      1447  TCGTGACATCATCAGTCCCTTGAAGAGTCTGGGAAGCTGTGGTGGACGCTACCTTTC 1506
Db      661  TCGTGACATCATCAGTCCCTTGAAGAGTCTGGGAAGCTGTGGTGGACGCTACCTTTC 720
Qy      1507  ACAATGAAAGCCACAGCCCCCGGACACCTGTGGGGAAGGGTGCAGGTGGGGTGTATGCC 1566
Db      721  ACAATGAAAGCCACAGCCCCCGGACACCTGTGGGGAAGGGTGCAGGTGGGGTGTATGCC 780
Qy      1567  AGAGGATGATGGGCTTTTGTCTGAGGGTGTCCGAGAGGCTGTGTATGACACTGTCTCA 1626
Db      781  AGAGGATGATGGGCTTTTGTCTGAGGGTGTCCGAGAGGCTGTGTATGACACTGTCTCA 840
Qy      1627  CGGACCCCATGTTGGATCTTCTCCCTTCTCCTTCTCCTTTTCTCTTCTTCTTCTTCT 1686
Db      841  CGGACCCCATGTTGGATCTTCTCCCTTCTCCTTCTCCTTTTCTCTTCTTCTTCTTCT 900
Qy      1687  ATAGCACCCTGCCCTCATGGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGGGCC 1746
Db      901  ATAGCACCCTGCCCTCATGGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGGGCC 960
Qy      1747  TCCAGTGGCTCTCTAGCCCCCTTCTTCCAAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1806
Db      961  TCCAGTGGCTCTCTAGCCCCCTTCTTCCAAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1020
Qy      1807  TGTCTTACCTTCACTCTCTGCCCCCTTAAAGATGGGAGGAGACCGAGCTCCATGGGTCTGG 1866
Db      1021  TGTCTTACCTTCACTCTCTGCCCCCTTAAAGATGGGAGGAGACCGAGCTCCATGGGTCTGG 1080
Qy      1867  CTTGTGAGTCTCCCTTTGAGAGCTGTGTCTAGGATCACTAGGATCACTAGGATCACTAGG 1926
Db      1081  CTTGTGAGTCTCCCTTTGAGAGCTGTGTCTAGGATCACTAGGATCACTAGGATCACTAGG 1140
Qy      1927  TGTCTTTGGGTTTCAAGGGGAGGCTCTAGTGGGAGGAGGCGCTTACAGCTCCCGGCT 1986
Db      1141  TGTCTTTGGGTTTCAAGGGGAGGCTCTAGTGGGAGGAGGCGCTTACAGCTCCCGGCT 1200

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Qy 1987 GGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCCCTTTTCATAGAGAGCGCTGTTTGT 2046
Db 1201 GGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCCCTTTTCATAGAGAGCGCTGTTTGT 1260
Qy 2047 TACAAGCTGGGTCTCCCTCTCTGAGCTGGTTAAGTACCCGAGCGCTCTCTTAAGATG 2106
Db 1261 TACAAGCTGGGTCTCCCTCTCTGAGCTGGTTAAGTACCCGAGCGCTCTCTTAAGATG 1320
Qy 2107 TCCAGGGCCCCAGGGCGGGGACAGCCAGCCAAACCTTGGGCGCTCGAGAGCTCCTC 2166
Db 1321 TCCAGGGCCCCAGGGCGGGGACAGCCAGCCAAACCTTGGGCGCTCGAGAGCTCCTC 1380
Qy 2167 CACCCCACTACTAGAGTGTCTGACCTCTGGGCTTTCACGGGGCCCCATTCCACGGCTCC 2226
Db 1381 CACCCCACTACTAGAGTGTCTGACCTCTGGGCTTTCACGGGGCCCCATTCCACGGCTCC 1440
Qy 2227 CACTTGGAGCTGTGACCTTGGACCAAGAGGGGAGTCCCTGCTCTCTTGTGACTCAGCA 2286
Db 1441 CACTTGGAGCTGTGACCTTGGACCAAGAGGGGAGTCCCTGCTCTCTTGTGACTCAGCA 1500
Qy 2287 GAGCGATGGCCACGTTTCAGGAGGGGCGCGCTGGGCTGGAGGCTCAGCCCCACCTCCAG 2346
Db 1501 GAGCGATGGCCACGTTTCAGGAGGGGCGCGCTGGGCTGGAGGCTCAGCCCCACCTCCAG 1560
Qy 2347 CTTTCTCAGGCTGCTGAGTTCAGATTCAGATTCCTGGAGCATCTGACCTTCTCCHAAGG 2406
Db 1561 CTTTCTCAGGCTGCTGAGTTCAGATTCAGATTCCTGGAGCAATCTGACCTTCTCCHAAGG 1620
Qy 2407 CTCTGTTATCAGCTGGGAGTGCAGCCAACTCCTGGCCATTGGGCCCCAGGGGAGCTG 2466
Db 1621 CTCTGTTATCAGCTGGGAGTGCAGCCAACTCCTGGCCATTGGGCCCCAGGGGAGCTG 1679
Qy 2467 GGCCCTG 2473
Db 1680 GGCCCTG 1686

RESULT 6
US-09-227-613-6
; Sequence 6, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda B.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-6

Query Match 52.6%; Score 1675; DB 4; Length 1686;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 787 GCCACTTAAGGGTGCCTTGCCAACTGGTGGATCATCGCACTTCGACGACCAAGCCCA 846
Db 1 GCCACTTAAGGGTGCCTTGCCAACTGGTGGATCATCGCACTTCGACGACCAAGCCCA 60
Qy 847 AGCCTACATCTTCCACAAGATCCCGATGGAACATGCTGCAAGTGTGTTGTTGGCG 906
Db 61 AGCCTACATCTTCCACAAGATCCCGATGGAACATGCTGCAAGTGTGTTGTTGGCG 120
Qy 907 AATGCGACCCATCGAGTACGGCAAGAGAGCTGAAATACCTGCGCCCTACAATCACCAGC 966
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Db 121 AATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCGCTACAATCACCAGC 180
Qy 967 ACGAATACCTTCTTCCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGA 1026
Db 181 ACGAATACCTTCTTCCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGA 240
Qy 1027 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGAACCTGGGCTGGCGCTCAGCTACT 1086
Db 241 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGAACCTGGGCTGGCGCTCAGCTACT 300
Qy 1087 ACATCCGGTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCCTTTTC 1146
Db 301 ACATCCGGTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCCTTTTC 360
Qy 1147 TCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTCAACAGATGAATCACA 1206
Db 361 TCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTCAACAGATGAATCACA 420
Qy 1207 TCGTCATGGAGATTGACGAGAGCCCTACCGTGACTGGTTTCAGTAGGCACTGACAGCCA 1266
Db 421 TCGTCATGGAGATTGACGAGAGCCCTACCGTGACTGGTTTCAGTAGGCACTGACAGCCA 480
Qy 1267 CCTGCAACGTTGGAGCAGTCCCTTCTTCAACGACTGGTTTCAGTGAACACTTAACTTCCAGA 1326
Db 481 CCTGCAACGTTGGAGCAGTCCCTTCTTCAACGACTGGTTTCAGTGAACACTTAACTTCCAGA 540
Qy 1327 TTGAGCAGCACTCTTCCCAACCATGCCCGGCAACAATTACAAGATGCCCCGCTGG 1386
Db 541 TTGAGCAGCACTCTTCCCAACCATGCCCGGCAACAATTACAAGATGCCCCGCTGG 600
Qy 1387 TGAAGTCTCTATGTGCAAGCATGGCATTTGAATACCAAGGAGAGCCCTACTGAGGGCCC 1446
Db 601 TGAAGTCTCTATGTGCAAGCATGGCATTTGAATACCAAGGAGAGCCCTACTGAGGGCCC 660
Qy 1447 TCCTGGACATCATCAGTCCCTGAAGAGTGTGGAAAGCTGTGGCTGGACGCTACCTTC 1506
Db 661 TCCTGGACATCATCAGTCCCTGAAGAGTGTGGAAAGCTGTGGCTGGACGCTACCTTC 720
Qy 1507 ACAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGGTGAGGTGGGTGATGGCC 1566
Db 721 ACAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGGTGAGGTGGGTGATGGCC 780
Qy 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGGTGTATGCACTGTCTCA 1626
Db 781 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGGTGTATGCACTGTCTCA 840
Qy 1627 CGGACCCCATGTTGATCTTCTCCCTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686
Db 841 CGGACCCCATGTTGATCTTCTCCCTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Qy 1687 ATAGCACCCCTGCTCATGCGACCTGCCCTCCCTCAGCCGTCAGCCATCAGCCATGGGCC 1746
Db 901 ATAGCACCCCTGCTCATGCGACCTGCCCTCCCTCAGCCGTCAGCCATCAGCCATGGGCC 960
Qy 1747 TCCAGTGCCTCTAGAGCCCTTCTTCAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1806
Db 961 TCCAGTGCCTCTAGAGCCCTTCTTCAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1020
Qy 1807 TGTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1866
Db 1021 TGTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Qy 1867 CTTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1926
Db 1081 CTTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
Qy 1927 TGCTCTCTGGGTTCATAGGGCAGTCTCTAGTTCGGGAGGGGCCCTGACCTCCCGGCT 1986
Db 1141 TGCTCTCTGGGTTCATAGGGCAGTCTCTAGTTCGGGAGGGGCCCTGACCTCCCGGCT 1200
Qy 1987 GGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCTTTTCATAGAGAGGCTGCTTGT 2046
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QY 1098 TTCAATACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTCTTTCTCTCACTTCATC 1157  
Db 996 TTCTTATCTACCTACCTCCCTTTCTACGGCGTCCCTGGGTGCTGCTCTCTTTGTGTGTC 1055  
QY 1158 AGGTTCTCGAGAGCCACTCGGTTGTGTGGGTACACAGATGAATCACATCGTCATGGAG 1217  
Db 1056 AGGTTCTCGAAGCCACTGGTTGTGTGGATCACAGATGAACACATCCCAAGGAG 1115  
QY 1218 ATTACAGAGAGGCTACCTGATGCTTCTAGTAGCCAGCTGACAGCCACTCGCAAGTG 1277  
Db 1116 ATCGCCACAGAGAGCACCAGGATCGGTGCTGCTCTAGCTGCGAGCCACTCGCAAGTG 1175  
QY 1278 GAGCAGTCTCTTCTCAACGACTGGTTTCAGTGGACACCTTAATCTTCAGATTGACCAAC 1337  
Db 1176 GAGCCTCACTTTTCAACCACTGGTTTCAGCGGCACTCTCACTTCAGATCGAGCAAC 1235  
QY 1338 CTCTTCCCAACCTAGCCCGGCACTTACACAGATGATCCCGGCTGCTGGAATCTCTA 1397  
Db 1236 CTCTTCCCAAGATGCGGAGACAACTACAGCGGGTGGCCCGCTGGTCAAGTCGCTG 1295  
QY 1398 TGTCCCAAGCATGCTGATTAATACAGAGAGCCGCTACTGAGGCGCTGCTGGACATC 1457  
Db 1296 TGTCCCAAGCAGGCTCAGTACGAAGTGAAGCCCTTCTCACCGGCTGGTGGACATC 1355  
QY 1458 ATCAGGTCTCTGAAGAGTCTGGGAAGCTGTGGTGGACCCCTACCTTCAAAATGAAGC 1517  
Db 1356 GTCAAGTCTCTGAAGAGTCTGGTGACATCTGGTGGACCCCTACCTCCATCAGTGAAGG 1415  
QY 1518 CACAGCCCGGG 1530  
Db 1416 CACACCCAGGCG 1428

RESULT 8

US-09-048-888-4  
Sequence 4, Application US/0904888  
Patent No. 6492108  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/048,888  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0494 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1928 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BEPINOT01  
CLONE: 2056310  
US-09-048-888-4  
Query Match 19.1%; Score 608.2; DB 4; Length 1928;  
Best Local Similarity 66.0%; Pred. No. 4.7e-140; Indels 3; Gaps 1;  
Matches 896; Conservative 0; Mismatches 458;  
QY 200 GGGCGAGGGGGCGCGAGCGCGAGGTGTCTGGTCCCACTTCAGCTGGGAGGATTCATCA 259  
Db 101 GGGCGCGAGAGCGCGGTCTCAGGGACCTACCCCGGCTACTTCACCTGGGACGAGGTGGC 160  
QY 260 GAAGCATAACTTGGCCACCGGACAGTGGGTGGTCTATTGACCGCAAGTTTACACATCAC 319  
Db 161 CAGCGCTCAGGGTGCAGGAGCGGTGGCTAGTGTATGACCGTAAAGTGTACACATCAG 220  
QY 320 CAAATGGTCCATCCAGCACCCGGGGGGCGGAGCGGTTCATCGGGCACTACGCTGGAGAGA 379  
Db 221 CGAGTTCACCGCGCGGCTCCAGGGGGTCCCGGGTCTACAGCCACTACGCGCGGACGA 280  
QY 380 TGCACGATGCTTCCCGGCTTCCACCTGACCTGGAATTCGTGGCAAGTTCCTTGA 439  
Db 281 TGCCACGATCCCTTTGTGGGCTTCCACATCAACAAGGGCTTTGTGAAGAAAGTATATGA 340  
QY 440 ACCCTGCTGATTTGGTGAATCTGGGCGGAGAGCCAGCGGAGCCAGCCAGGCAAGAACTC 499  
Db 341 CTCCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCAGCTTTCAGCCCAACAGATAA 400  
QY 500 AAAGATCACTGAGGACTTCCGGGGCGCTGAGAGAGCGGCTGAGGACATGAACCTGTTCAA 559  
Db 401 AGAGCTGACAGATGAGTTCGCGGAGCTCGCGGCGCACAGTGGAGCGGATGGGGCTCATGA 460  
QY 560 GACCAACCAAGTGTCTTCT 619  
Db 461 GGCACCAAGTGTCTTCT 520  
QY 620 ATGGTTCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 679  
Db 521 CTGGCTCACCTTTTGGGTCTTTGGGACGCTCTTTTGGCCCTTCTCTCTCTCTCTCTCTCT 580  
QY 680 CTTGCTACCTCTCAGGCGCCAGCTGGATGGTGTGCAACATGATGATGATGATGATGATGAT 739  
Db 581 GCTCAGTGCAGTTCAGGCGCCAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 640  
QY 740 CTACAGAAAACCCAAAGTGGAAACCACTTGTTCACAAATTCGTCAATTCGTCACCTTAAAGG 799  
Db 641 CTTACAGACCTCAAAGTGGAAACCACTGTCTACATCATTTTGTGATTGGCCACCTGAAGG 700  
QY 800 TGCCTCTGCAACTGTTGGAATCATGCGCACTTCAGCAACCAAGCCAGCCATCATCTT 859  
Db 701 GGGCGCGCGAGTGTGGTGAACCACTGACATTCAGCACCACCATGCGCAAGCCCACTGCT 760  
QY 860 CCACAAAGGATCCCGATGTGAACATGCTGCAAGT---GTTTGTCTGGGCGAATGGCAGCC 916  
Db 761 CCGCAAGACCCAGACATCAACATGATCCCTTCTCTCTTGGCTTGGGGAAGATCCTCTC 820  
QY 917 CATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACATACACAGCAGGATATCTT 976  
Db 821 TGTGGAGCTTGGGAAACAGAGAAAATAATATGCGGTACAAACCCAGCAGCAAAATCTT 880  
QY 977 CTTCTGATTGGGCGCGCTGCTCTCATCCCATGATTTTCCAGTACCAGATCATCATGAC 1036  
Db 881 CTTCTTAATTGGCCCCCAGCCCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 940  
QY 1037 CATGATCGTCCATAAGAACTGGGTGGAACCTGGCCCTGGGCGGCTGAGCTACTACCTGG 1096  
Db 941 TGTATCCAGCAAGAAAGTGGGTGGAATCTGGCTGGATGATTACCTTCTTACCTCGCTT 1000



Db 1218 GTGTGCAAGCGTGGCATAGATACAGTCCAGAGCCCTGCTGTGAGCCCTTGGCGACAT 1277  
 Qy 1457 CATCAGTCCCTCAGAGTCTGGGAGCTGTGGCTGGAGCGCTACCTTCAACAATGA 1514  
 Db 1278 CATCCACTACTAAGAGTCCAGGAGCTCTGGCTAGATGCTTCTTCAACAAATA 1335

RESULT 10  
 US-09-227-613-1  
 ; Sequence 1, Application US/09227613A  
 ; Patent No. 6432684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKERJI, Pradip  
 ; APPLICANT: LEONARD, Amanda E.  
 ; APPLICANT: HUANG, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295, US, P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,613A  
 ; CURRENT FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1335  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-09-227-613-1

Query Match 18.9%; Score 602.8; DB 4; Length 1335;  
 Best Local Similarity 66.6%; Pred. No. 8.7e-139;  
 Matches 878; Conservative 0; Mismatches 437; Indels 3; Gaps 1;

Qy 200 GGGGAGGGGCGCCCGAGCGCGAGGTGTGGTGCCACCTTACAGCTGGAGAGATTCA 259  
 Db 18 GGGCGCGAGACCGCGCTCAGGACCTACCCGCGCTACTTACCTGGGACGAGTGGC 77  
 Qy 260 GAAGCATAACTGGCGACCGACAGTGGCTGCTATTGACCGCAAGTATTACACATCAC 319  
 Db 78 CCAGGCTCAGGTGGCGAGGCGGTGTAGTATCGACCGTAAAGTGTACACATCAG 137  
 Qy 320 CAATGCTCATCAGACACCGGGGCGAGCGGTGTATGGGCACTACCTGCGAGAGA 379  
 Db 138 CGAGTTACCGCGCGGATCCAGGGGCTCCCGGCTCATCAGCCACTACCGCGGCGAG 197  
 Qy 380 TGCAACGATGCTTCCGCGCTTCCACCTGACCTGGAATTCGTGGGCAAGTCTTTGAA 439  
 Db 198 TGCCACGATCCCTTTGTGGCTTCCATCAACAAGGCGCTTGTGAAGATATAGAA 257  
 Qy 440 ACCCTGCTGATGTTGTAACCTGGCCCGAGGAGCCCGAGGACCAACGCAAGAACTC 499  
 Db 258 CTCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCCGAGCTTTGAGCCCAAGATAA 317  
 Qy 500 AAGATCACTAGGACTCCGGGCGCTGAGAGAGCGCTGAGACATGAACCTGTTCAA 559  
 Db 318 AGAGCTGACATGATGTTCCGGGAGCTCGGGCCACAGTGGAGCGGATGGGCTCATGAA 377  
 Qy 560 GACCAACACATGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619  
 Db 378 GGGCAACCATGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437  
 Qy 620 ATGGTCTACTGCT 679  
 Db 438 CTGGCTACCCCTTTGGGCTTTGGGACGTCCTCTTTTGGCCCTCTCTCTCTCTCTCT 497  
 Qy 680 CTTTCT 739  
 Db 498 GCTCAGTGCAGTTGAGGCGGAGCTGGCTGGCTGAGCATGATCTTGGGCACTGTCGT 557  
 Qy 740 CTACAGAAAACCAAGTGAACCCCTTGTCCACAAATTCGTCATTTGGCCACTTAAAGGG 799  
 Db 558 CTTGACGACCTCAAGAGTGAACCATCTCTCTACATCATTTTGTGATTGGCCACTTGAAGG 617

Qy 800 TGCTCTGCAACCTGCTGGAAATCATGCCACTTCCAGCACACAGCCAGCCTTACATCTT 859  
 Db 618 GGGCCCGCCAGTGTGGTGAACACACATGCTACTTCCAGCACCATGCCAAGCCCACTT 677  
 Qy 860 CCACAGGATCCGATGTGAACATGCTGC--AGTGTGTGTGGCGCAATGGCAGCC 916  
 Db 678 CCGAAGACCCAGACATCAACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 737  
 Qy 917 CATCGAGTACGGCAAGAAAGCTGAAATACCTGCTTCCCTTACAATACACAGCAAGATCTT 976  
 Db 738 TGTGGAGCTTGGGAAACAGAAAGAAATATATGCCGTACAAACCCAGCACCAATACTT 797  
 Qy 977 CTTCTGATTTGGCGCGCGCTCTATCCCATGATTTTCCAGTACAGATCATCATGAC 1036  
 Db 798 CTTCTAATTTGGGCGCGCGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 857  
 Qy 1037 CATGATCTGTCATTAAGAACTGGGTGGACCTGGCTGGCGCGCTGAGCTACTACATCCGGT 1086  
 Db 858 TGTATCCAGCGAAAGAAAGTGGTGGACTTGGCGCTGATGATTACCTTCTACGTCGCTT 917  
 Qy 1097 CTTCTACCTACATCTCTCTTCTACGGCATCTCTGGAGCCCTCTCTCTCTCTCTCTCT 1156  
 Db 918 CTTCTCTCACTTATGTGCCACTATTGGGGCTGAAAGCCTTCTCTGGGCTTTTCTCTCATGT 977  
 Qy 1157 CAGGTTCTCTGAGAGCCCACTGCTTGTGTGGGTCAACAGATGAATCACTGCTCATGGA 1216  
 Db 978 CAGGTTCTCTGGAAGCACTGCTTGTGTGGGTGACACAGATGAACCATATTCCCATGCA 1037  
 Qy 1217 GATTACACAGGAGGCTTACCGTACTGCTTCACTAGCAGCAGCTGACAGCCTGCAAGT 1276  
 Db 1038 CATTGATCATGACCGGACATGAGTGGTGTTCACCCAGCTCTCTGGCCCATGCAATGT 1097  
 Qy 1277 GGAGCAGTCTCTTCTTCAACAGCTGCTTCACTGGGACACCTTAACTTCCAGATTGAGCACA 1336  
 Db 1098 CCAAGTCTGCTTCAATGACTGCTTCACTGGGACACCTCACTTCCAGATTGAGCACA 1157  
 Qy 1337 CTTCTTCCCAACATGCGCGGACACTTACACAGATGCGCGGCTGGTGAATCTCT 1396  
 Db 1158 TCTTTTCCAGATGCTCTGACACATTAACCAAAAGTGGCTCTCTCTGGTGGCTCTT 1217  
 Qy 1397 ATGTCGCAAGCATGCTTGAATACAGGAGAGCGCTACTGAGGGCCCTGCTGGACAT 1456  
 Db 1218 GTGTCCCAAGCGTGCATAGTACAGTACAGTCCAGCCCTGCTGTCAGCCTTCCGCGACAT 1277  
 Qy 1457 CATCAGGTCCTTGAAGAGTCTGGGAAGCTGTGGCTGGAGCCCTTACCTTCAAAATGA 1514  
 Db 1278 CATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCTCTATCTTCCCAATA 1335

RESULT 11  
 US-09-389-681-313  
 ; Sequence 313, Application US/09389681A  
 ; Patent No. 6518237  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YUQUI, Jiang  
 ; APPLICANT: DILLON, Davin C.  
 ; APPLICANT: MITCHELL, Jennifer L.  
 ; APPLICANT: XU, Jiangchun  
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
 ; FILE REFERENCE: 210121.470C3  
 ; CURRENT APPLICATION NUMBER: US/09/389,681A  
 ; CURRENT FILING DATE: 1999-09-02  
 ; NUMBER OF SEQ ID NOS: 463  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 313  
 ; LENGTH: 456  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-389-681-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;  
 Best Local Similarity 99.1%; Pred. No. 8.3e-100;

|    | Matches | 446;  | Conservative | 0; | Mismatches | 4; | Indels | 0; | Gaps | 0; |
|----|---------|---|--------------|----|------------|----|--------|----|------|----|
| Qy | 788     | CCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCACTTCCAGCACCAACGCCAA   | 847          |    |            |    |        |    |      |    |
| Db | 2       | CCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCACTTCCAGCACCAACGCCAA   | 61           |    |            |    |        |    |      |    |
| Qy | 848     | GCCTAACATCTTCCACAAAGATCCCGATGTGAACATGCTGCACGTGTTGTTCTGGGGCGA    | 907          |    |            |    |        |    |      |    |
| Db | 62      | GCCTAACATCTTCCACAAAGATCCCGATGTGAACATGCTGCACGTGTTGTTCTGGGGCGA    | 121          |    |            |    |        |    |      |    |
| Qy | 908     | ATGCGACCCCATCGAGTACGCGCAGAGAAGAGCTGAAATACCTCGCCCTACAAATCACCAGCA | 967          |    |            |    |        |    |      |    |
| Db | 122     | ATGCGACCCCATCGAGTACGCGCAGAGAAGAGCTGAAATACCTCGCCCTACAAATCACCAGCA | 181          |    |            |    |        |    |      |    |
| Qy | 968     | CGAATACCTCTTCTCGATTTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGAT      | 1027         |    |            |    |        |    |      |    |
| Db | 182     | CGAATACCTCTTCTCGATTTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGAT      | 241          |    |            |    |        |    |      |    |
| Qy | 1028    | CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGGCGCTGAGCTACTA     | 1087         |    |            |    |        |    |      |    |
| Db | 242     | CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGGCGCTGAGCTACTA     | 301          |    |            |    |        |    |      |    |
| Qy | 1088    | CATCCGGTTCTTCAATCACTACCTCCCTTTACGGCACTCTGGAGGCCCTCCTTTTCCT      | 1147         |    |            |    |        |    |      |    |
| Db | 302     | CATCCGGTTCTTCACTACCTACCTCCCTTTACGGCACTCTGGAGGCCCTCCTTTTCCT      | 361          |    |            |    |        |    |      |    |
| Qy | 1148    | CAACTTCATCAGGTTCTCGAGAGCCACTGGTGTGTGTGGGTACACAGATGAATCAAT       | 1207         |    |            |    |        |    |      |    |
| Db | 362     | CAACTTCATCAGGTTCTCGAGAGCCACTGGTGTGTGTGGGTACACAGATGAATCAAT       | 421          |    |            |    |        |    |      |    |
| Qy | 1208    | CGTCATGGAGATTGACGAGGCGCTACCG                                    | 1237         |    |            |    |        |    |      |    |
| Db | 422     | CGTCATGGAGATTGACGAGGAGGACTCGG                                   | 451          |    |            |    |        |    |      |    |

```

RESULT 12
US-09-620-405B-313
; Sequence 313, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepner, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-313

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122 ATGGCAGCCATCGAGTAGCGGCAAGAAAGCTGGAATACCTGCCTACAATCACCAGCA 181
968 CGAATACCTCTTCCTGATTGGCCCGCCCTCTCATCCCCATGTATTTCCAGTACCAGAT 1027
182 CGAATACCTCTTCCTGATTGGCCCGCCCTGCTCATCCCAATGATATTTCCAGTACCAGAT 241
1028 CATCATGACCATGATGTCCTCAATAAGAACTGGGTGGACCTGGCTGGGGCGCTCAGCTACTA 1087
242 CATCATGACCATGATGTCCTCAATAAGAACTGGGTGGACCTGGCTGGGGCGCTCAGCTACTA 301
1088 CATCCGGTTCCTTCATCACCTATACCTCCCTTTTACGGGCATCTCTGGAGAGCCCTCTTTTCCT 1147
302 CATCCGGTTCCTTCATCACTCACTACATCCCTTTTCAAGGCATCTCTGGAGAGCCCTCTTTTCCT 361
1148 CAATTCATCAGGTTCCCTGGAGAGCCACTGGTTGTGGGTGCACACAGATGAATCACAT 1207
362 CAATTCATCAGGTTCCCTGGAGAGCCACTGGTTGTGGGTGCACACAGATGAATCACAT 421
1208 CGTCATGGAGATTGACCAGAGGCCTACCG 1237
422 CGTCATGGAGATTGACCAGAGGCCTCGG 451

RESULT 13
US-09-339-338-313
; Sequence 313, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yudiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-313

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| Query Match           | 13.9%;          | Score 443.6;  | DB 4;     | Length 456; |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 99.1%;          | Pred. No. 8.3e-100;   |           |             |
| Matches 446;          | Conservative 0; | Mismatches 4;   | Indels 0; | Gaps 0;     |
| QY                    | 788             | CCACTTAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCACTTCAGCAACACACGCCAA  | 847       |             |
| DB                    | 2               | CCACTTAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCACTTCAGCAACACACGCCAA  | 61        |             |
| QY                    | 848             | GCTTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTTGGGCGA    | 907       |             |
| DB                    | 62              | GCTTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCACGTGTTTCTTGGGCGA    | 121       |             |
| QY                    | 908             | ATGGCAGCCCATCGAGTACGCGAAGAGAAGCTGAAATACCTGCCCTACAATCACCAGCA   | 967       |             |
| DB                    | 122             | ATGGCAGCCCATCGAGTACGCGAAGAGAAGCTGAAATACCTGCCCTACAATCACCAGCA   | 181       |             |
| QY                    | 968             | CGAATACTTCTTCTGTATTGGGCGCGCTGCTCATCCCATGTATTTCAGTACCAGAT      | 1027      |             |
| DB                    | 182             | CGAATACTTCTTCTGTATTGGGCGCGCTGCTCATCCCATGTATTTCAGTACCAGAT      | 241       |             |
| QY                    | 1028            | CATCATGACCATGATCGTCCATAGAAGCTGGGTGGAGCTGGCCCTGGGCCCTCAGCTACTA | 1087      |             |
| DB                    | 242             | CATCATGACCATGATCGTCCATAGAAGCTGGGTGGAGCTGGCCCTGGGCCCTCAGCTACTA | 301       |             |
| QY                    | 1088            | CATCCGGTTCATTCACTACCTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTTCCT   | 1147      |             |
| DB                    | 302             | CATCCGGTTCATTCACTACCTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTTCCT   | 361       |             |



QY 1148 CAACATCATCAGGTTCTCGAGAGCCACTGGTTGTGTGGTGCACACAGATGAATCAT 1207  
DB 362 CAACATCATCAGGTTCTCGAGAGCCACTGGTTGTGTGGTGCACACAGATGAATCAT 421  
QY 1208 CGTCATGAGATTGACACAGAGCCCTACCG 1237  
DB 422 CGTCATGAGATTGACACAGAGCCCTCGG 451

RESULT 14  
US-09-433-826B-313  
; Sequence 313, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433.826B  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;  
Best Local Similarity 99.1%; Pred. No. 8.3e-100;  
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTTAAGGGTGCCTCTGCAACTGCTGGAATCATCGCCACTTCACGACACACGCCAA 847  
DB 2 CCACCTTAAGGGTGCCTCTGCAACTGCTGGAATCATCGCCACTTCACGACACACGCCAA 61  
QY 848 GCCTAACATCTTCCACAGGATCCCGATGTGAACATCTGCACGTTGTTCTGGGGCA 907  
DB 62 GCCTAACATCTTCCACAGGATCCCGATGTGAACATCTGCACGTTGTTCTGGGGCA 121  
QY 908 ATGCGAGCCCATCGATACGACAGAGAGCTGAAATACCTGCCCTACATCACCAGCA 967  
DB 122 ATGCGAGCCCATCGATACGACAGAGAGCTGAAATACCTGCCCTACATCACCAGCA 181  
QY 968 CGAATACCTTCTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGAT 1027  
DB 182 CGAATACCTTCTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGAT 241  
QY 1028 CATCATGACATGATCGTCCATAGAACTGGGTGACCTGGCCCTGGGCGGTGAGTACTA 1087  
DB 242 CATCATGACATGATCGTCCATAGAACTGGGTGACCTGGCCCTGGGCGGTGAGTACTA 301  
QY 1088 CATCCGGTTCTTCATCACCCTTCTACGGCATCTCTGGGAGCCCTCTCTTTTCT 1147  
DB 302 CATCCGGTTCTTCATCACCCTTCTACGGCATCTCTGGGAGCCCTCTCTTTTCT 361  
QY 1148 CAACATCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGTGCACAGATGAATCAT 1207  
DB 362 CAACATCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGTGCACAGATGAATCAT 421  
QY 1208 CGTCATGAGATTGACACAGAGCCCTACCG 1237  
DB 422 CGTCATGAGATTGACACAGAGCCCTCGG 451

RESULT 15  
US-09-604-287A-313  
; Sequence 313, Application US/09604287A  
; Patent No. 6586572

; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604.287A  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-313

Query Match 13.9%; Score 443.6; DB 4; Length 456;  
Best Local Similarity 99.1%; Pred. No. 8.3e-100;  
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTTAAGGGTGCCTCTGCAACTGCTGGAATCATCGCCACTTCACGACACACGCCAA 847  
DB 2 CCACCTTAAGGGTGCCTCTGCAACTGCTGGAATCATCGCCACTTCACGACACACGCCAA 61  
QY 848 GCCTAACATCTTCCACAGGATCCCGATGTGAACATCTGCACGTTGTTCTGGGGCA 907  
DB 62 GCCTAACATCTTCCACAGGATCCCGATGTGAACATCTGCACGTTGTTCTGGGGCA 121  
QY 908 ATGCGAGCCCATCGATACGACAGAGAGCTGAAATACCTGCCCTACATCACCAGCA 967  
DB 122 ATGCGAGCCCATCGATACGACAGAGAGCTGAAATACCTGCCCTACATCACCAGCA 181  
QY 968 CGAATACCTTCTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGAT 1027  
DB 182 CGAATACCTTCTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGAT 241  
QY 1028 CATCATGACATGATCGTCCATAGAACTGGGTGACCTGGCCCTGGGCGGTGAGTACTA 1087  
DB 242 CATCATGACATGATCGTCCATAGAACTGGGTGACCTGGCCCTGGGCGGTGAGTACTA 301  
QY 1088 CATCCGGTTCTTCATCACCCTTCTACGGCATCTCTGGGAGCCCTCTCTTTTCT 1147  
DB 302 CATCCGGTTCTTCATCACCCTTCTACGGCATCTCTGGGAGCCCTCTCTTTTCT 361  
QY 1148 CAACATCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGTGCACAGATGAATCAT 1207  
DB 362 CAACATCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGTGCACAGATGAATCAT 421  
QY 1208 CGTCATGAGATTGACACAGAGCCCTACCG 1237  
DB 422 CGTCATGAGATTGACACAGAGCCCTCGG 451

RESULT 16  
US-09-389-681-425  
; Sequence 425, Application US/09389681A  
; Patent No. 6518237  
; GENERAL INFORMATION:  
; APPLICANT: Yugu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C3  
; CURRENT APPLICATION NUMBER: US/09/389.681A  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0

Thu Dec 11 15:18:13 2003

```

; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-425

Query Match      13.9%; Score 443.4; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 9.2e-100;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAA 847
D 1 CCACCTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAA 60

QY 848 GCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACATGCTGTTGTCTGGGCGA 907
D 61 GCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACATGCTGTTGTCTGGGCGA 120

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTTACATCAACACGCA 967
D 121 ATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTTACATCAACACGCA 180

QY 968 CGAATACCTTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1027
D 181 CGAATACCTTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 240

QY 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGCGCTCAGTACTA 1087
D 241 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGCGCTCAGTACTA 300

QY 1088 CATCCGGTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1147
D 301 CATCCGGTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 360

QY 1148 CAACTTCATCAGTTCCTCGAGAGCCACTGGTTTGTGGGTACACAGATGAATCAGAT 1207
D 361 CAACTTCATCAGTTCCTCGAGAGCCACTGGTTTGTGGGTACACAGATGAATCAGAT 420

QY 1208 CGTCATGGAGATGACGAGGAGGCC 1232
D 421 CGTCATGGAGATGACGAGGAGGCC 445

RESULT 17
US-09-620-405B-425
; Sequence 425, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-425

Query Match      13.9%; Score 443.4; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 9.2e-100;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAA 847
D 1 CCACCTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAA 60

QY 848 GCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACATGCTGTTGTCTGGGCGA 907
D 61 GCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACATGCTGTTGTCTGGGCGA 120

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTTACATCAACACGCA 967
D 121 ATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTTACATCAACACGCA 180

QY 968 CGAATACCTTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1027
D 181 CGAATACCTTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 240

QY 1028 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGCGCTCAGTACTA 1087
D 241 CATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGTGGCGCTCAGTACTA 300

QY 1088 CATCCGGTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1147
D 301 CATCCGGTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 360

QY 1148 CAACTTCATCAGTTCCTCGAGAGCCACTGGTTTGTGGGTACACAGATGAATCAGAT 1207
D 361 CAACTTCATCAGTTCCTCGAGAGCCACTGGTTTGTGGGTACACAGATGAATCAGAT 420

QY 1208 CGTCATGGAGATGACGAGGAGGCC 1232
D 421 CGTCATGGAGATGACGAGGAGGCC 445

RESULT 18
US-09-433-826B-425
; Sequence 425, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-425

Query Match      13.9%; Score 443.4; DB 4; Length 446;
Best Local Similarity 99.8%; Pred. No. 9.2e-100;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAA 847
D 1 CCACCTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAA 60

QY 848 GCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACATGCTGTTGTCTGGGCGA 907
D 61 GCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACATGCTGTTGTCTGGGCGA 120

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTTACATCAACACGCA 967
D 121 ATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCTGCCCTTACATCAACACGCA 180

QY 968 CGAATACCTTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 1027
D 181 CGAATACCTTCTTCATCAGTATGGGCGCCGCTGCTCATCCCCATGATTTTCCAGTACCAGAT 240

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QY 1028 CATCATGACCATGATCGTCCATTAAGAACTGGTGGAACTGGCTGGCCGCTCAGCTACTA 1087  
DB 241 CATCATGACCATGATCGTCCATTAAGAACTGGTGGAACTGGCTGGCCGCTCAGCTACTA 300  
QY 1088 CATCGGTTCTTCATACCTACCTACCTCTTCTACCGCATCTGGAGGCCCTCTCTTTTCCT 1147  
DB 301 CATCGGTTCTTCATACCTACCTCTTCTACCGCATCTGGAGGCCCTCTCTTTTCCT 360  
QY 1148 CAATTCATCAGGTTCTGGAGAGCACTGTTTGTGTGGGTACACAGATGAATCACAT 1207  
DB 361 CAATTCATCAGGTTCTGGAGAGCACTGTTTGTGTGGGTACACAGATGAATCACAT 420  
QY 1208 CGTCATGAGATTGACCAAGGAGGCC 1232  
DB 421 CGTCATGAGATTGACCAAGGAGGCC 445  
RESULT 19  
US-09-604-287A-425  
; Sequence 425, Application US/09604287A  
; Patent No. 6586572  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuxiu  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-425  
Query Match 13.9%; Score 443.4; DB 4; Length 446;  
Best Local Similarity 99.8%; Pred. No. 9.2e-100;  
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 788 CCACTTAAGGTTGCTCTGCCAACTGGTGGAACTCATCGCCACTCCAGCACCGCAA 847  
DB 1 CCACTTAAGGTTGCTCTGCCAACTGGTGGAACTCATCGCCACTCCAGCACCGCAA 60  
QY 848 GCCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACTGTTTGTCTGGCGA 907  
DB 61 GCCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACTGTTTGTCTGGCGA 120  
QY 908 ATGGAGGCCATCGAGTACGGCAAGAGAGCTGAAATACCTGCCCTACATCACCAGCA 967  
DB 121 ATGGAGGCCATCGAGTACGGCAAGAGAGCTGAAATACCTGCCCTACATCACCAGCA 180  
QY 968 CCAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATATTTCCAGTACCAGAT 1027  
DB 181 CCAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATATTTCCAGTACCAGAT 240  
QY 1028 CATCATGACCATGATCGTCCATTAAGAACTGGTGGAACTGGCTGGCCGCTCAGCTACTA 1087  
DB 241 CATCATGACCATGATCGTCCATTAAGAACTGGTGGAACTGGCTGGCCGCTCAGCTACTA 300  
QY 1088 CATCGGTTCTTCATACCTACCTCTTCTACCGCATCTGGAGGCCCTCTCTTTTCCT 1147  
DB 301 CATCGGTTCTTCATACCTACCTCTTCTACCGCATCTGGAGGCCCTCTCTTTTCCT 360  
QY 1148 CAATTCATCAGGTTCTGGAGAGCACTGTTTGTGTGGGTACACAGATGAATCACAT 1207  
DB 361 CAATTCATCAGGTTCTGGAGAGCACTGTTTGTGTGGGTACACAGATGAATCACAT 420

QY 1208 CGTCATGAGATTGACCAAGGAGGCC 1232  
DB 421 CGTCATGAGATTGACCAAGGAGGCC 445  
RESULT 20  
US-09-439-261-12  
; Sequence 12, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 864  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-439-261-12  
Query Match 13.2%; Score 421.6; DB 4; Length 864;  
Best Local Similarity 69.9%; Pred. No. 2.8e-94;  
Matches 584; Conservative 0; Mismatches 249; Indels 3; Gaps 1;  
QY 682 TTGCTACCTCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGCGCCACCTGTCTGTCT 741  
DB 29 TTCCGGCAGTTTCCAGGCCCAAGCTGGATGCTGCAACATGATTATGCGCCACCTGTCTGTCT 88  
QY 742 ACAGAAACCCAGTGGAGACCACTTGTCCCAAAATTCGTCATTCGCCCACTTAAAGGGG 801  
DB 89 TCAGCACCTCAAAGTGGAGACCACTTGTCTACATCATTTTGTGATTGGCCACCTGAAGGGG 148  
QY 802 CTTCTGCCAACTGGTGGAAATCATCGCCACTTTCAGCACCAACCCAGCCCAAGCTTAACATCTCC 861  
DB 149 CCCCCGCCAGTTGGTGGAAACCACTGCACTTCCAGCACCATGCAAGCCCACTGCTTCC 208  
QY 862 ACAAGATCCCGATGTAACATGCTGC---ACGTGTTTGTCTGGCGAATGGCAGCCCA 918  
DB 209 GCAAGACCCAGACATCAACATGCACTTCTTCTTCTGGGGAAGATCCTCTCTG 268  
QY 919 TCAGTACGGCAAGAAAGAGCTGAAATACCTGCCCTTACCAATCACCAAGCAGAACTACTTCT 978  
DB 269 TGAGGCTTGGGAAACAGAGAAATATATGCGGTACACCAACCAAGCAGAACTACTTCT 328  
QY 979 TCTGATTGGGCGCGCTGCTCATCCCATGATATTTCCAGTACCAAGATCATCATGACCA 1038  
DB 329 TCCTAATTGGGCGCGCGCTGCTGCTGCTTCTTCTTCTTCCAGTGGTATATTTCTATTTG 388  
QY 1039 TGATCGTCCATAAGAACTGGTGGAACTGGCTGGCCGCTCAGCTACTACTATCCCGTTCT 1098  
DB 389 TTATCCAGCAAGAAAGTGGTGGAACTTGGCTGGATGATACCTTCTAGCTCCGTTCT 448  
QY 1099 TCATCACTACATCCCTTTCTACGGCATCTGGGAGCCCTCTCTTTTCCTCAATTCATCA 1158  
DB 449 TCCTCACTTATGTGCCACTATTGGGCTGAAAGCCCTTCTCTGGGCTTTTCTTCTATAGTCA 508  
QY 1159 GGTTCCTGGAGAGCCACTGTTTGTGGGTACACAGATGAATCATGCTCATGAGCA 1218  
DB 509 GGTTCCTGGAAAGCACTGTTTGTGGGTGACACAGATGAATCATGCTCATGAGCA 568

QY 1219 TTGACAGAGGCTACCGTGACTGTTTCAGTACGACGATCAGACCACTGCAACGTTG 1278  
 DB 569 TTGATCATGACCGGAAATGAGACTGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCC 628  
 QY 1279 AGCAGTCTCTTCAACGAGCTGGTTTCAGTGGACACCTTAACTTCCAGATTGACACCAAC 1338  
 DB 629 ARAAGTCTGCTTCAATGACTGGTTTCAGTGGACACCTTAACTTCCAGATTGACACCAATC 688  
 QY 1339 TCCTTCCCAACATCCCGGCGGACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTAT 1398  
 DB 689 TTTTCCCAACATCCCGGCGGACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTAT 748  
 QY 1399 GTGCCAAGCTGGATTTGAATACACAGAGAGAGCGCTACTGAGGCGCTGCTGGACATCA 1458  
 DB 749 GTGCCAAGCTGGATTTGAATACACAGAGAGAGCGCTACTGAGGCGCTGCTGGACATCA 808  
 QY 1459 TCAGTCTGCTGAGAGTCTGGAGCTGGTGGTGGAGCGCTACTTCCAAATGA 1514  
 DB 809 TCCACTACTAAAGAGTCAGGCGAGCTCTGGCTAGATGCTATCTTCCAAATGA 864

RESULT 21  
 US-09-227-613-13  
 ; Sequence 13, Application US/09227613A  
 ; Patent No. 6432684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKERJI, Pradip  
 ; APPLICANT: LEONARD, Amanda E.  
 ; APPLICANT: HUANG, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,613A  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 13  
 ; LENGTH: 864  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-09-227-613-13

Query Match 13.2%; Score 421.6; DB 4; Length 864;  
 Best Local Similarity 69.9%; Pred. No. 2.8e-94;  
 Matches 584; Conservative 0; Mismatches 249; Indels 3; Gaps 1;

QY 682 TTGCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATATGCGCACTGTCTGTCT 741  
 DB 29 TTCCGGCAGTTTCAGGCCCAAGCTGGATGGCTGCAACATGATATGCGCACTGTCTGTCT 88  
 QY 742 ACAGAAACCCAGTGGACCACTTGTCCACAAATTTGCTATTTGCTATTTGCTATTTGCT 801  
 DB 89 TCAGCACTCTCAAGTGGACCACTTGTCTATTTGCTATTTGCTATTTGCTATTTGCT 148  
 QY 802 CTCTCTCCCACTGGTGGATCTATGCGCACTTCCAGCACCAACCGCAAGCTTAACATCTTCC 861  
 DB 149 CCCCCCGAGTTGGTGGACCACTATGCTTCCAGCACCAACCGCAAGCTTAACATCTTCC 208  
 QY 862 ACAGGATCCGATGTGAATCTCTG---AGTGTGTTGTTGTTGGCGAATGGCAGCCA 918  
 DB 209 GCAAGACCCAGACATCAACATGATCCCTTCTTTGCTTGGGGAAGATCTCTCTG 268  
 QY 919 TCAGTACGGCAAGAGAGAGCTGAAATACCTGCGCTTACAACTCACCAGACGAAATCTTCT 978  
 DB 269 TGGAGCTTGGAAACAG 328  
 QY 979 TCTGATTTGGGCGCGCTGCTCATCCCATGATTTTCCAGTACGAGATCATCATGACCA 1038  
 DB 329 TCCTAATTTGGGCGCGCGCTGCTCATCCCATGATTTTCCAGTACGAGATCATCATGACCA 388  
 QY 1039 TGATCGCTCAATAGAACTGGTGTGACCTGGCTGGCGCTGAGTACTACTACATCCGGTCT 1098

DB 389 TTATCCAGGAAAGAGTGGGTGGACTTGGCTTGGATGATTACCTTTAGCTCCGCTTCT 448  
 QY 1039 TCATCACCTACATCCCTTTTACGGCATCTGGAGCGCTCTCTTTTCTCAACTTTCATCA 1158  
 DB 449 TCTCCTATTTGTGGCACTATTTGGGCTGAAAGCTTCTCTGGGCTTTTCTTTCATAGTCA 508  
 QY 1159 GGTTCCTGGAGGACCACTGGTTTGTGGTTCACAGATGAATCAATCTGTCATGGAGA 1218  
 DB 509 GGTTCCTGGAAAGCAACTGGTTTGTGGTTCACAGATGAATCAATCTTCCCATGACCA 568  
 QY 1219 TTGACCAAGGCGCTTACCGTGGCTTGTTCAGTGGATGACAGCCAGCTTGCACACGTTG 1278  
 DB 569 TTGATCATGACCGGAACATGAGTGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCC 628  
 QY 1279 AGCAGTCTCTTCAACGACTGGTTTCAGTGGACACTTAACTTCCAGATTGAGCAACACC 1338  
 DB 629 ACAAGTCTGCTTCAATGACTGGTTTCAGTGGACACTTCAACTTCCAGATTGAGCAACACC 688  
 QY 1339 TCTTCCCAACCACTCCCGGCGGACAACTTACCAAGATCGCCCGCTGGTGAAGTCTCTAT 1398  
 DB 689 TTTTCCCAACCACTCCCGGCGGACAACTTACCAAGATCGCCCGCTGGTGAAGTCTCTAT 748  
 QY 1399 GTGCCAAGCATGGCTTGAATACACAGAGAGAGCGCTACTGAGGCGCTGCTGGACATCA 1458  
 DB 749 GTGCCAAGCATGGCTTGAATACACAGAGAGAGCGCTACTGAGGCGCTGCTGGACATCA 808  
 QY 1459 TCAGTCTGCTGAGAGTCTGGAGCTGGTGGTGGAGCGCTACTTCCAAATGA 1514  
 DB 809 TCCACTACTAAAGAGTCAGGCGAGCTCTGGCTAGATGCTATCTTCCAAATGA 864

RESULT 22  
 US-09-439-261-36  
 ; Sequence 36, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P2  
 ; CURRENT APPLICATION NUMBER: US/09/439,261  
 ; CURRENT FILING DATE: 1999-11-12  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 36  
 ; LENGTH: 960  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-439-261-36

Query Match 11.6%; Score 370.4; DB 4; Length 960;  
 Best Local Similarity 64.5%; Pred. No. 1.2e-81;  
 Matches 570; Conservative 0; Mismatches 311; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGCGCGCGAGCGGAGGTGTGGTGGCGCCACCTTCCAGTGGGAGGAGATTC 259  
 DB 48 GGGCGCGAGACCGCGGCTCAGGACCTACCCGCGTACTTCCCTGGAGCGAGGTGGC 107  
 QY 260 GAACGATAAATCTGCGCACCGACAGTGGGTGTTGATTCGCGCAAGGTTTACAACTCAC 319  
 DB 108 CCACGCTCAGGTGCGAGGAGCGGTGGCTAGTATCGACCGCTAAGGTGTACAACTCAG 167  
 QY 320 CAATGTGCTCATCAGACACCGGGGCGGAGGCTCATCGGCACTACCGCTGAGAGGA 379  
 DB 168 CGAGTTACCGCGCGGATCCAGGGGCTCCCGGCTCATCAGCCACTACCGCGGCGAGA 227

380 TGCAACGAGTGCCTTCGCGCCCTTCCACCTGACCTGGAATTCGTGGCAAGTTCTTGAA 439  
 Db TGCACGAGTCCCTTTGTGSCCTTCCACATCAACAAGGCTTTGTGAAGAGTATATGAA 287  
 Qy 440 ACCCTGCTGATTTGGTGAATTCGCGGAGGAGCCAGCAGGACCAAGGCAAGACTC 499  
 Db 288 CTCTCTCTGATTTGGAGAACTGCTCCAGAGCAGCCCGCTTTGAGCCCAACCAAGAA 347  
 Qy 500 AAGATCACTGAGACTTCCGCGCCCTGAGAGAGAGGCTGAGGACATGAACCTGTTCAA 559  
 Db 348 AGAGTCACAGATGAGTTCCGAGAGCTGCGGCGCAAGTGGGCTCATGAA 407  
 Qy 560 GACCAACCAAGTTCCT 619  
 Db 408 GGCAACCACTGCT 467  
 Qy 620 ATGCTTCACTGCT 679  
 Db 468 CTGCTCACT 527  
 Qy 680 CTTGCTACCTCTCAGCCCAAGCTGGATGGTGAACATGATATGAGCACTGCTCTGT 739  
 Db 528 GCTCAGTGCAGTTTCCGCGCCAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 587  
 Qy 740 CTACAGAAACCCCAAGTGGAGCACTGTTGCCAATTCGTACATCATTTTGTATGGCC 799  
 Db 588 CTTGAGCACTCAAAGTGGAGCACTGTTGCCAATTCGTACATCATTTTGTATGGCC 647  
 Qy 800 TGCCTCTGCCAATCTGAGTGAATCATCGCCACTTCCAGCACCAGCCAGCCAGCTAAC 859  
 Db 648 GGCCCCCGCAGTTTGGTGAACCAATGATGATGATGATGATGATGATGATGATGAT 707  
 Qy 860 CCACAGGATCCCATGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916  
 Db 708 TGTATCCAGCAAGAGTGGTGGAGCTTGGCTGGAGCTTGGCTGGAGTCA 931

RESULT 23  
 US-09-227-613-35  
 ; Sequence 35, Application US/09227613A  
 ; Patent No. 6432684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKERJI, Pradip  
 ; APPLICANT: LEONARD, Amanda E.  
 ; APPLICANT: HUANG, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,613A  
 ; CURRENT FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 35  
 ; LENGTH: 960  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-09-227-613-35  
 Query Match 11.6%; Score 370.4; DB 4; Length 960;

Best Local Similarity 64.5%; Pred. No. 1.2e-81;  
 Matches 570; Conservative 0; Mismatches 311; Indels 3; Gaps 1;  
 Qy 200 GGGGAGGGGGCCCGAGCGAGGTGTGGGTCCACCTTACGCTGGGAGGATTCATCA 259  
 Db 48 GGCGCGAGAGCCCGGGCTCAGGACCTACCCCGCTACTTCACTGGGACGAGGTGGC 107  
 Qy 260 GAAGATTAACCTGCGCAGCAGTGGGTGCTCATTTAGCCGCAAGTTTACACATCAC 319  
 Db 108 CCAGCGCTCAGGGTCCGAGGAGCGGTAGTGTATGATGACCGTAAGGTGTACACATCAG 167  
 Qy 320 CAATATGCTCCATCCAGACACCCGCGGGCCAGCGGCTCATCGGGCACTACGCTGAGAGA 379  
 Db 168 CGAGTTCAACCCCGCGGATCCAGGGGCTCCCGGCTCATCAGCCACTAGCGCGGCGAG 227  
 Qy 380 TGCAACGAGTGCCTTCGCGGCTTCCACCTGACCTGGAATTCGTGGGCAAGTTTCTTGA 439  
 Db 228 TGCCACGATCCCTTTGTGGGCTTCCACATCAAAGGGGCTTGTGAAGAGTATATGAA 287  
 Qy 440 ACCCTGCTGATTTGTGAATTCGCGGAGAGCCAGCCAGGACCAAGCAAGAACTC 499  
 Db 288 CTCTCTCTCTGATTTGGAGAACTGTCTCCAGAGCAGCCAGCTTTCAGCCACCAAGATAA 347  
 Qy 500 AAGATCACTGAGGACTTCCGCGCCCTGAGAGAGCGCTGAGGACATGAACCTGTTCAA 559  
 Db 348 AGAGCTGACAGATGAGTTCCGCGAGCTGCGGCGCCACAGTGGAGGAGTGGGCTCATGAA 407  
 Qy 560 GACCAACCAAGTTCCT 619  
 Db 408 GGCAACCACTGCT 467  
 Qy 620 ATGCTTCACTGCT 679  
 Db 468 CTGCTCACT 527  
 Qy 680 CTTGCTACCTCTCAGCCCAAGCTGGATGGTGAACATGATATGAGCACTGCTCTGT 739  
 Db 528 GCTCAGTGCAGTTTCCGCGCCAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 587  
 Qy 740 CTACAGAAACCCCAAGTGGAGCACTGTTGCCAATTCGTACATCATTTTGTATGGCC 799  
 Db 588 CTTGAGCACTCAAAGTGGAGCACTGTTGCCAATTCGTACATCATTTTGTATGGCC 647  
 Qy 800 TGCCTCTGCCAATCTGAGTGAATCATCGCCACTTCCAGCACCAGCCAGCCAGCTAAC 859  
 Db 648 GGCCCCCGCAGTTTGGTGAACCAATGATGATGATGATGATGATGATGATGATGAT 707  
 Qy 860 CCACAGGATCCCATGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916  
 Db 708 TGTATCCAGCAAGAGTGGTGGAGCTTGGCTGGAGCTTGGCTGGAGTCA 931

RESULT 24  
 US-09-439-261-5  
 ; Sequence 5, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng

;/ TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;/ FILE REFERENCE: 6295.US.P2  
;/ CURRENT APPLICATION NUMBER: US/09/439,261  
;/ CURRENT FILING DATE: 1999-11-12  
;/ PRIOR APPLICATION NUMBER: US 08/833,610  
;/ PRIOR FILING DATE: 1997-04-11  
;/ PRIOR APPLICATION NUMBER: PCT/US98/07422  
;/ PRIOR FILING DATE: 1998-04-10  
;/ PRIOR APPLICATION NUMBER: US 09/227,613  
;/ PRIOR FILING DATE: 1999-01-08  
;/ NUMBER OF SEQ ID NOS: 60  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 5  
;/ LENGTH: 918  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
;/ FEATURE:  
;/ NAME/KEY: misc feature  
;/ LOCATION: (755)...(755)  
;/ OTHER INFORMATION: r = g or a at position 755  
US-09-439-261-5

Query Match 11.5%; Score 367.4; DB 4; Length 918;  
Best Local Similarity 65.2%; Pred. No. 6.2e-81;  
Matches 555; Conservative 1; Mismatches 292; Indels 3; Gaps 1;  
QY 233 GCCACCTTCAGCTGGAGAGATTGAGAGATACCTGCGACCGACGAGTGGCTGGT 292  
Db 15 GCCTACTTCACCTGGGACGAGTGGCCCGCTCAGGGTGGAGAGCGTGGCTAGT 74  
QY 293 CATTCACCGCAGGTTTACAACTACCAATGCTTCATCCAGACCCCGGGGCGACGC 352  
Db 75 GATCGACCGTAAGTGTACAACTACGCGAGTTCAACCGCGGCATCCAGGGGCTCCCG 134  
QY 353 GGTCTATCGGCACTACCTGGAGAGATGCAAGATCACTGAGGACTTCCCGGCTTCCACCTGA 412  
Db 135 GGTCTATCGGCACTACCTGGAGAGATGCAAGATCACTGAGGACTTCCCGGCTTCCACCTGA 194  
QY 413 CTTGGAATTCGTGGGCAAGTTCTTGAACCCCTGCTGATGTTGTAACCTGCGGAGGA 472  
Db 195 CAAGGGCTTTGTGAAGAGTATATGAACCTCTCTCTGATTTGGAAGACTGCTCCAGAGCA 254  
QY 473 GCCAGCCAGGACCGACGCAAGAACTCAAGATCACTGAGGACTTCCCGGCTTCCAGGAA 532  
Db 255 GCCAGCTTTGAGCCCAAGAACTAAAGAGTGAAGATGATGTTCCCGGAGCTGCGGGC 314  
QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACCAAGTGTCTTCTCTCTCTCTCTGCT 592  
Db 315 CACAGTGGAGCGGATGGGCTCATGAAGCGCAACCACTGCTCTCTCTCTCTCTCTCTGCT 374  
QY 593 CCACATCATCGCCCTGGAGAGCAATTCAGATGCTTCTCTCTCTCTCTCTCTCTCTCTCT 652  
Db 375 GCACATCTTGTCTGAGTGTGTGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 434  
QY 653 GATTCCTACCTCCATCAGCGCTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 712  
Db 435 TTTGCCCTTCT 494  
QY 713 GCACATGATATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 772  
Db 495 GCAGATGATATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 554  
QY 773 CAATTCGTCAATGGGCACTTAAAGGGTGCCTCTGCAACTGGTGGAAATCATCGCACTT 832  
Db 555 TCAATTTGTGATTTGGCCACCTGAAGGGGGCCCGCGCAGTTGTGTGGAACCATGCACTT 614  
QY 833 CCAGCACCAGCGCAAGCTTAACATCTTCCAGCAAGATCCGATGTGAATGCTGCTGCTGCT 889  
Db 615 CCAGCACCAGCGCAAGCTTAACATCTTCCAGCAAGATCCGATGTGAATGCTGCTGCTGCT 674  
QY 890 CGTGTGTTGTTCTGGGCGAATGGCAGCCCATCGAGTACGGCAAGAAAGAGCTGAATACCT 949  
Db 675 CTTCCTTTGCTGGGAGAGATCTCTCTCTGAGCTTGGGAAACAGAGAAATAATAT 734

QY 950 GCCCTACAATCACCAGCAGCAATATCTTCTCTGATTTGGGCGCGCTGCTCATCCCAT 1009  
Db 735 GCGGTACAACACCAGCAGCAATATCTTCTCTGATTTGGGCGCGCTGCTCATCCCAT 794  
QY 1010 GTATTTCAGTACAGATCATCATGATGATGATGATGATGATGATGATGATGATGATG 1069  
Db 795 CTACTTCAGTGTGATATTTTCTATTTTGTATTCAGGAAAGAGTGGGTGGACTGGC 854  
QY 1070 CTGGGCGCTCA 1080  
Db 855 CTGGATCAGCA 865

RESULT 25  
US-09-227-613-5  
;/ Sequence S, Application US/09227613A  
;/ Patent No. 6432684  
;/ GENERAL INFORMATION:  
;/ APPLICANT: MUKERJI, Pradip  
;/ APPLICANT: LEONARD, Amanda E.  
;/ APPLICANT: HUANG, Yung-Sheng  
;/ TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;/ FILE REFERENCE: 6295.US.P1  
;/ CURRENT APPLICATION NUMBER: US/09/227,613A  
;/ CURRENT FILING DATE: 1999-01-08  
;/ PRIOR APPLICATION NUMBER: 08/833,610  
;/ PRIOR FILING DATE: 1997-04-11  
;/ NUMBER OF SEQ ID NOS: 42  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 5  
;/ LENGTH: 918  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapien  
US-09-227-613-5

Query Match 11.5%; Score 367.4; DB 4; Length 918;  
Best Local Similarity 65.2%; Pred. No. 6.2e-81;  
Matches 555; Conservative 1; Mismatches 292; Indels 3; Gaps 1;  
QY 233 GCCACCTTCAGCTGGAGAGATTGAGAGATACCTGCGACCGACGAGTGGCTGGT 292  
Db 15 GCCTACTTCACCTGGGACGAGTGGCCCGCTCAGGGTGGAGAGCGTGGCTAGT 74  
QY 293 CATTCACCGCAGGTTTACAACTACCAATGCTTCATCCAGACCCCGGGGCGACGC 352  
Db 75 GATCGACCGTAAGTGTACAACTACGCGAGTTCAACCGCGGCATCCAGGGGCTCCCG 134  
QY 353 GGTCTATCGGCACTACCTGGAGAGATGCAAGATCACTGAGGACTTCCCGGCTTCCACCTGA 412  
Db 135 GGTCTATCGGCACTACCTGGAGAGATGCAAGATCACTGAGGACTTCCCGGCTTCCACCTGA 194  
QY 413 CTTGGAATTCGTGGGCAAGTTCTTGAACCCCTGCTGATTTGGTGAATGCGCGCGGAGGA 472  
Db 195 CAAGGGCTTTGTGAAGAGTATATGAACCTCTCTCTGATTTGGAAGACTGCTCCAGAGCA 254  
QY 473 GCCAGCCAGGACCGACGCAAGAACTCAAGATCACTGAGGACTTCCCGGCTTCCAGGAA 532  
Db 255 GCCAGCTTTGAGCCCAAGAACTAAAGAGTGAAGATGATGTTCCCGGAGCTGCGGGC 314  
QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACCAAGTGTCTTCTCTCTCTCTCTCT 592  
Db 315 CACAGTGGAGCGGATGGGCTCATGAAGCGCAACCACTGCTCTCTCTCTCTCTCTCTCT 374  
QY 593 CCACATCATCGCCCTGGAGAGCAATTCAGATGCTTCTCTCTCTCTCTCTCTCTCTCTCT 652  
Db 375 GCACATCTTGTCTGAGTGTGTGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 434  
QY 653 GATTCCTACCTCCATCAGCGCTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 712  
Db 435 TTTGCCCTTCT 494  
QY 713 GCACATGATATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 772



Db 495 GCAGCATGACTTTGGGACCTCTCGGTTCTGACACCTCAAGTGGAAACCACTGCTACA 554  
QY 773 CAAATTCGTCAATGAGGCTTAAAGGCTGCTCTCCCAACTGGTGAATCAATCGCACTT 832  
Db 555 TCATTTTGTGATTTGGCCACCTGAAGGGGCCCCCGCCAGTTGGTGGAAACCACTGCACTT 614  
QY 833 CCAGCACCACGACGACCTTAACATCTTCCACAGGATCCGATGGAACATGCTGC--A 889  
Db 615 CCAGCACCACGACGACCTTAACATCTTCCACAGGATCCGATGGAACATGCTGC--A 889  
QY 890 CGTGTGTTGTTCTGGGCGAATGACGCCATCGATGACGACGACGACGACGACGACGAC 674  
Db 675 CTTCTTTGCTTTGGGAGATCCTCTCTGTGAGCTTGGGAAACAGAAAGAAATATAT 734  
QY 950 GGCCTACATCCACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1009  
Db 735 GCGGTACACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 794  
QY 1010 GTATTTCCAGTACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1069  
Db 795 CTACTTCCAGTGTATTTTCTATTTTGTATCCAGGAAAGAGTGGGTGGCTTGGC 854  
QY 1070 CTGGGCGGTCA 1080  
Db 855 CTGGATCAGCA 865

RESULT 26  
US-09-439-261-35  
; Sequence 35, Application US/09439251  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-439-261-35

Query Match 11.0%; Score 351.8; DB 4; Length 990;  
Best Local Similarity 64.7%; Pred. No. 4.4e-77;  
Matches 540; Conservative 0; Mismatches 292; Indels 3; Gaps 1;  
QY 200 GGGGAGGGGGCGCGGAGCGGAGGTGTCGGTCCCACTTCACTGGGAGGATTC 259  
Db 18 GGGCGGAGAGCGGCGGTCTAGGACCTTACCCCGGTCTACCTGGGACGAGGTGGC 77  
QY 260 GAAGCATAACTGCGCACCGCAGTGGGCTGGTCAATGACCGCAAGTTTACACATCAC 319  
Db 78 CCAGCGCTCAGGTGCGGAGGCGGTGCTAGTGTGACCGTGAAGGTGTACACATCAG 137  
QY 320 CAAATGGTCCATCCAGACCGCGGGGGCGGACGGGTCTATCGGGCTATCGGTGAGAGA 379  
Db 138 CGAGTTACCCCGCGGCTCCAGGGGCTCCCGGGTCTATCAGCCACTACGCGGGCAGGA 197  
QY 380 TCAACGATGCTTCCCGGCTTCCACCTGACCTGGAATCTGTGGGAGAGTTCTTGAA 439

Db 198 TGCCACGATCCCTTTGTGGCCTTCCACATCAACAAGGCGCTTGTGAAGATATATGAA 257  
QY 440 ACCCTGCTGATTTGGTGAACCTGGCCCCGAGAGCGCCAGGACCAAGCAAGATTC 499  
Db 258 CTCTCTCTGATTTGGAACTGTCTCCAGAGCAGCCAGCTTTGAGCCCAACCAAGATAA 317  
QY 500 AAAGATCACTGAGGACTTTCGGGCGCTTGAAGAGCGGCTGAGGACATGAACCTGTTCAA 559  
Db 318 AGAGCTGACAGATGAGTTTCGGGAGCTGGGGCCACAGTGGAGCGGATGGGGCTCATGAA 377  
QY 560 GACCAACCACTGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619  
Db 378 GGCACACCATGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437  
QY 620 ATGTTTCACTGTTCTTCT 679  
Db 438 CTGGCTCACCTTTGGGTCTTTTGGGACGTCCTTTTGGCCCTTCTCTCTCTCTCTCTCT 497  
QY 580 CTTTGTCT 739  
Db 498 GCTCAGTGCAGTTTCAGGCCCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 557  
QY 740 CTACAGAAAAACCAAGTGAACCACTTGTCCCAAAATTCGTTCATTTGGTGGCCACTTAAAGG 799  
Db 558 CTTTCAAGCACTTCAAGTGAACCACTTGTCTACATCATTTTGTGATTGGCCACCTGAAGG 617  
QY 800 TGCTCTGCGCACTGTTGGTGAATCATCGCCACTTCCAGCACCAGCCAGCCTTAACATCTT 859  
Db 618 GGGCGGCGGAGTTGGTGGAAACCACTGTCATCTCCAGCACCAGCCAGCCTTAACATCTT 677  
QY 860 CCACAAGGATCCCGATGTGAACATGTGTC---AGTGTGTTGTTCTGGGCGAATGGGAGCC 916  
Db 678 CCGCAAGACCCAGACATCAACATGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737  
QY 917 CATGAGTACGCGAAGAGAGTGAATACCTGCTCCCTTACATCAATCAACAGCAGCAATCTT 976  
Db 738 TGTGAGCTTTGGGAAACAGAAATAATATATCCCTGATACCAACCAAGCAGCAATCTT 797  
QY 977 CTTCTGATTTGGGCGGCGCTGCTCATCCCCCATGATTTCCAGTACCAGATCATC 1031  
Db 798 CTTCTTAATTTGGGCGGCGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852

RESULT 27  
US-09-227-613-34  
; Sequence 34, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Paridip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 34  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-34

Query Match 11.0%; Score 351.8; DB 4; Length 990;  
Best Local Similarity 64.7%; Pred. No. 4.4e-77;  
Matches 540; Conservative 0; Mismatches 292; Indels 3; Gaps 1;  
QY 200 GGGGAGGGGGCGCGGAGCGGAGGTGTCGGTGGCCCACTTCACTGGGAGGATTC 259  
Db 18 GGGCGGAGAGCGGCGGTCTAGGACCTTACCCCGGTCTACCTGGGACGAGGTGGC 77

|     |   |      |
|-----|---|------|
| 260 | GAAGCATAACTGCGCAGCGACAGTGGCGCTGGTCATTGACGCCGAAGTTTACAACTACAC    | 319  |
| 78  | CCAGCGCTCAGGGTGCAGGACGCGTGGCTAGTGATCGACCGCTAAAGGTGTACAACTACAG   | 137  |
| 320 | CAAAATGGTCCATTCAGCACCCCGGGGGGCCAGCGGTTCATCGGCACTACGCTGGAGAAGA   | 379  |
| 138 | CGAGTTCAACCGCCGGCATCCAGGGGGCTCCCGGGTTCATCAGCCACTACGCCGGGACGA    | 197  |
| 380 | TGCACCGGATGCGTTCCGGGCTTCCACCTCGACCTCGGAATTCGTGGGCAAGTTCTTGAA    | 439  |
| 198 | TGCCACGGATCCCTTTGTGGCTTCCCATCAACAAGGGCTTTGTGAAGAAGTATATGAA      | 257  |
| 440 | ACCCCTGCTGATTTGGTGAACCTGGCCCGGAGAGCCACGACGACGACCCAGCGAAGAACTC   | 499  |
| 258 | CTCTCTCTGATTGGAGAACCTGTCTCAGAGCAGCCACGAGCTTTGAGCCCAACCAAGATAA   | 317  |
| 500 | AAAGATCACTGAGGACTTCGGGGCCCTGAGGAAGACGGCTGAGGACATGAACCTGTTCAA    | 559  |
| 318 | AGAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGGAGCGATGGGCTCATGAA      | 377  |
| 560 | GACCAACACAGTGTTCCTTCCTCTCTCTGGCCCCACATCATGGCCCTGGAGAGCATTC      | 619  |
| 378 | GGCCAAACCATGCTTCCTCTGCTGCTACCTGCTGCACATCTTGCTGCTGATGGTCACG      | 437  |
| 620 | ATGGTTCACTGCTTCTACTTTTGGCAATGGCTGGGATTCCTAACCCCTCATCAGGCCCTTGT  | 679  |
| 438 | CTGGCTCAACCTTTGGGCTCTTTGGAGCGTCCTTTTGGCCCTTCTCTCTGTGCGGTGCT     | 497  |
| 680 | CCTTGTACTCTCTCAGGCCCAAGCTGGATGGCTGCACATGATATGTCGCCACCTGTCGT     | 739  |
| 498 | GCTCAGTGCAGTTTCAGGCCCCAGGCTGGCTGGCTGCAGCATGACTTTGGGGCACTGTCGT   | 557  |
| 740 | CTACAGAAACCCAAAGTGGAAACCACTTGTGCCACAAATTCGTCAATTTGGGCCACTTAAAGG | 799  |
| 558 | CTTCAGCACCTCAAAAGTGGAAACCATCTGCTACATCATTTGTGATTTGGCCACCTGAAGG   | 617  |
| 800 | TGCCTCTGCAACTGGTGGATCATCGGCACCTCCAGCACACCGCAAGCCTTAACACTTT      | 859  |
| 618 | GGCCCCCGCGAGTTGGTGGAACCAATGCATTTCCAGCACCAATGCCNAGCCCAACTGCTTT   | 677  |
| 860 | CCACAAGGATCCCGATGTGAACATGCTGC---AGCTGTTTGTCTGGGGGAATGGCAGCC     | 916  |
| 678 | CCGCAAAAGACCCAGACATCAACATGCATCCCTCTTCTTTGCTTTGGGGAAGATCCCTCTC   | 737  |
| 917 | CATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCCACGACGACGAATACCTT    | 976  |
| 738 | TGTGGAGCTTGGAAACAGAGAAATAATATATGCCGTACAAACCAACGACCAATACTTT      | 797  |
| 977 | CTTCTCTGATTTGGGCCCGCTGCTCATCCCATGTATTTCCAGTACCATCATC            | 1031 |
| 798 | CTTCTCTAAATGGGCCCCAGCCCTTCTGCTCTCTACTTGCAGTGGTATATTTTC          | 852  |

RESULT 28  
US-09-439-261-4  
; Sequence 4, Application US/09439261

```

PATENT NO. 6428990
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Faridip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.P2
CURRENT APPLICATION NUMBER: US/09/439,261
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 60

```

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-4
```

```

Query Match          9.5%; Score 302.4; DB 4; Length 304;
Best Local Similarity 99.7%; Pred. No. 3.9e-65;
Matches 303; Conservative 0; Mismatches 1; Indels 0

```

|    |     |  |     |
|----|-----|--|-----|
| QY | 630 | GTCTTCTACTTTTGGCAATGGCTGGATTCCTACCCCTGATCAACGGCCCTTTGTCTTGTCTACG | 689 |
| DB | 1   | GTCTTTTACTTTTGGCAATGGCTGGATTCCTACCCCTGATCAACGGCCCTTTGTCTTGTCTACG | 60  |
| QY | 690 | TTTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCCCACCTGTCTGTCTACAGAAA     | 749 |
| DB | 61  | TTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCCCACCTGTCTGTCTACAGAAA    | 120 |
| QY | 750 | CCCAGTGGAAACACACTTTGTCCACAAATTGTCGATATTGGCCACCTTAAGGGTGGCTCTGGC  | 809 |
| DB | 121 | CCCAGTGGAAACACACTTTGTCCACAAATTGTCGATATTGGCCACCTTAAGGGTGGCTCTGGC  | 180 |
| QY | 810 | AACCTGTGGAAATCATCGCCACTTCACGACCAACGCCAAGCCTAACATCTTCCACAAAGAT    | 869 |
| DB | 181 | AACCTGTGGAAATCATCGCCACTTCACGACCAACGCCAAGCCTAACATCTTCCACAAAGAT    | 240 |
| QY | 870 | CCCGATGTCAACATCGTCGACGCTTTTGTCTTGGCGGAATGGCAGCCCATCGATACGGC      | 929 |
| DB | 241 | CCCGATGTCAACATCGTCGACGCTTTTGTCTTGGCGGAATGGCAGCCCATCGATACGGC      | 300 |
| QY | 930 | AAGA 933   |     |
| DB | 301 | AAGA 304   |     |

RESULT 29  
US-09-227-613-4  
; Sequence 4, Application US/09227613A

Patent No. 6432684  
GENERAL INFORMATION:  
APPLICANT: MUKERJI, Pradip  
APPLICANT: LEONARD, Amanda E.  
APPLICANT: HUANG, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295-US.P1  
CURRENT APPLICATION NUMBER: US/09/227,613A  
CURRENT FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FASTSEQ for Windows Version 3.0

Query Match 9.5%; Score 302.4; DB 4; Length 304;  
Best Local Similarity 99.7%; Pred. No. 3.9e-65;  
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 630 | GTCTTCTCACTTTTGGCAATGGGTGGATTCTACCTCTANTCAGCGCCTTTGTCTTGTCTACC  | 689 |
| DB | 1   | GTCTTTTCACTTTTGGCAATGGGTGGATTCTACCTCTANTCAGCGCCTTTGTCTTGTCTACC  | 60  |
| QY | 690 | TCTCAGGCCCAAGCTGGATGCTGCTCAACATGATTATGCGCCACTGTCTGTCTACAGAAAA   | 749 |
| DB | 61  | TCTCAGGCCCAAGCTGGATGCTGCTCAACATGATTATGCGCCACTGTCTGTCTACAGAAAA   | 120 |
| QY | 750 | CCCAAGTGGAAACAACCTTGTGCACAAATTTGTCATTATGGCCACTTAAAGGGTGTCTCTGCC | 809 |
| DB | 121 | CCCAAGTGGAAACAACCTTGTGCACAAATTTGTCATTATGGCCACTTAAAGGGTGTCTCTGCC | 180 |

QY 810 AACTGTGGATATCCGACCTCCAGACACAGCCAGGCTTACATCTTCCACAGGAT 869  
 DB 181 AACTGTGGATATCCGACCTCCAGACACAGCCAGGCTTACATCTTCCACAGGAT 240  
 QY 870 CCCGATGTGAACATGCTGACGCTGTTTGTCTGGGCGAATGGAGCCCATCGAGTACGGC 929  
 DB 241 CCCGATGTGAACATGCTGACGCTGTTTGTCTGGGCGAATGGAGCCCATCGAGTACGGC 300  
 QY 930 AAGA 933  
 DB 301 AAGA 304

RESULT 30  
 US-09-439-261-37  
 ; Sequence 37, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295-US.P2  
 ; CURRENT APPLICATION NUMBER: US/09/439,261  
 ; CURRENT FILING DATE: 1999-11-12  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 37  
 ; LENGTH: 473  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-439-261-37

Query Match 8.0%; Score 253.8; DB 4; Length 473;  
 Best Local Similarity 71.6%; Pred. No. 4.2e-53;  
 Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAACTGGGTGGACCTGGCGCTGAGTACTACATCCGGTCTTCACTACCTAC 1109  
 DB 9 AAGAACTGGGTGGACCTGGCGCTGAGTACTACATCCGGTCTTCACTACCTAT 68  
 QY 1110 ATCCCTTTCTACGGCATCTGGGACCTCTTCTTCTCACTTCACTAGCTTCTGGAG 1169  
 DB 69 GTGCCACTATTGGGCTGAAAGCCTTCTCTTCACTAGTCAAGTTCCTGGAA 128  
 QY 1170 AGCCACTGGTGTGGTGCACAGATGAATACATCGTCACTAGTCAAGTTCCTGGAG 1229  
 DB 129 AGCAACTGGTGTGGTGCACAGATGAATACATCGTCACTAGTCAAGTTCCTGGAG 188  
 QY 1230 GCTTACCGTGTGCTTCACTAGTCACTAGTCACTAGTCACTAGTCACTAGTCACT 1289  
 DB 189 CGGAACATGCTGGTGTCCACCGCTTCTTCCACCGCTTCTTCCACCGCTTCTTCC 248  
 QY 1290 TTCAACGACTGGTGTGAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1349  
 DB 249 TTCAATGACTGGTGTGAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 308  
 QY 1350 ATGCCCCGGCACAATTCACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 1409  
 DB 309 ATGCTCTGACACAATTCACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 368  
 QY 1410 GGCATTGAATACAGAGAACCGCTTACCTGAGGGCCCTGCTGAGATCATCAGTCCCTG 1469  
 DB 369 GGCATAGATGAGTCAAGTCAAGCCCTGCTGTGAGCCCTTGGCCGACATCATCCACTCA 428

QY 1470 AAGAGTCTGGGAAGCTGTGCTGGAGCCCTACCTTACCAATGA 1514  
 DB 429 AAGAGTCTGGGAAGCTGTGCTGGAGCCCTTACCTTACCAATGA 473

RESULT 31  
 US-09-227-613-36  
 ; Sequence 36, Application US/09227613A  
 ; Patent No. 6432684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKERJI, Pradip  
 ; APPLICANT: LEONARD, Amanda E.  
 ; APPLICANT: HUANG, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295-US.P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,613A  
 ; CURRENT FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 36  
 ; LENGTH: 473  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-09-227-613-36

Query Match 8.0%; Score 253.8; DB 4; Length 473;  
 Best Local Similarity 71.6%; Pred. No. 4.2e-53;  
 Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAACTGGGTGGACCTGGCGCTGAGTACTACATCCGGTCTTCACTACCTAC 1109  
 DB 9 AAGAACTGGGTGGACCTGGCGCTGAGTACTACATCCGGTCTTCACTACCTAT 68  
 QY 1110 ATCCCTTTCTACGGCATCTGGGACCTCTTCTTCTCACTTCACTAGTCAAGTTCCTGGAG 1169  
 DB 69 GTGCCACTATTGGGCTGAAAGCCTTCTCTTCACTAGTCAAGTTCCTGGAA 128  
 QY 1170 AGCCACTGGTGTGGTGCACAGATGAATACATCGTCACTAGTCAAGTTCCTGGAG 1229  
 DB 129 AGCAACTGGTGTGGTGCACAGATGAATACATCGTCACTAGTCAAGTTCCTGGAG 188  
 QY 1230 GCTTACCGTGTGCTTCACTAGTCACTAGTCACTAGTCACTAGTCACTAGTCACT 1289  
 DB 189 CGGAACATGCTGGTGTCCACCGCTTCTTCCACCGCTTCTTCCACCGCTTCTTCC 248  
 QY 1290 TTCAACGACTGGTGTGAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1349  
 DB 249 TTCAATGACTGGTGTGAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 308  
 QY 1350 ATGCCCCGGCACAATTCACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 1409  
 DB 309 ATGCTCTGACACAATTCACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 368  
 QY 1410 GGCATTGAATACAGAGAACCGCTTACCTGAGGGCCCTGCTGAGATCATCAGTCCCTG 1469  
 DB 369 GGCATAGATGAGTCAAGTCAAGCCCTGCTGTGAGCCCTTGGCCGACATCATCCACTCA 428

RESULT 32  
 US-09-439-261-3  
 ; Sequence 3, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng

```
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-439-261-3
```

Query Match      7.2%; Score 230.4; DB 4; Length 655;  
Best Local Similarity 69.1%; Pred.No. 2.8e-47; Indels 1; Gaps 1;  
Matches 329; Conservative 0; Mismatches 146;

```
QY      1078 TCAGTACTACATCCGGTTTCATTCACTCATCACCCTACATCCCTTTTACCGGCATCTGCGGCC 1137  
DB      1 TTACCTTTACGTCCGGTTCCTCTCACTTAITGTGCCACTATTGGGGCT -GAAGA GTTCC 59  
  
QY      1138 TCCCTTTTCCCTCAACTTCATCAGGTTCCCTGGAGAGCCACTGGTTTGTTGTGGGTGACACACA 1197  
DB      60 TGGGCTTTTCTTTCATAGTAGGTTCCTGGAAAGCACTGCTGTTGTGTGGGTGACACACA 119  
  
QY      1198 TGAATCACATCGTCATGAGGATTGACCAGGAGGCGCTACCGTGACTGTTTCACTAGCCAGC 1257  
DB      120 TGAACCATATTCCCATGACATTGATCATGACCGAATCATGGACTGGTTTCCACCCAGC 179  
  
QY      1258 TGACAGCCACCTCGAACGTGGAGCAGTCTCTTTCAACGACTGGTTTCACTGGGACACCTTA 1317  
DB      180 TCCAGGCCACATGANAATGTCACAGTCTGCTTCAATGACTGTTTCACTGGGACACCTCA 239  
  
QY      1318 ACTTCCAGATTGAGCACCACTCTTCCCCACCATGCCCGGCCACAACTTACAGAAGATCG 1377  
DB      240 ACTTCCAGATTGAGCACCACTCTTCCCCACCATGCCCGGCCACAACTTACAGAAGATCG 299  
  
QY      1378 CCCCCTGGTGAAGTCTCTATGTCGAAGCATGGCATTGAATACAGGAGAACGCCGTAC 1437  
DB      300 CTCCTTGGTGCAGTCTCTATGTCGAAGCATGGCATTGAATACAGGAGAACGCCGTAC 359  
  
QY      1438 TGAGGGCCCTGCTGGACATCATCAGTCTCTGGAAGATCTGGAAGCTGTGGTGGAGC 1497  
DB      360 TGTGAGCCCTTCCGCCACATCATCCACTCACTAAAAGGAGTCAGGCGAGCTTGGCTAGATG 419  
  
QY      1498 CCTACTTTCACAAATGAAAGCCACAGCCCGCCGAGCACCGTGGGAGAGGGGTGACG 1553  
DB      420 CCTATCTTCCAAATAACACAGCCACCTGCCAGTCTGGAAGAGAGGAGGAAG 475
```

RESULT 33  
US-09-439-261-3  
Sequence 3, Application US/09227613A  
Patent No. 6432684  
GENERAL INFORMATION:  
APPLICANT: Mukerji, Pradip  
APPLICANT: LEONARD, Amanda E.  
APPLICANT: HUANG, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.P1  
CURRENT APPLICATION NUMBER: US/09/227,613A  
CURRENT FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 655

```
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-439-261-3
```

Query Match      7.2%; Score 230.4; DB 4; Length 655;  
Best Local Similarity 69.1%; Pred.No. 2.8e-47; Indels 1; Gaps 1;  
Matches 329; Conservative 0; Mismatches 146;

```
QY      1078 TCAGTACTACATCCGGTTTCATTCACTCATCACCCTACATCCCTTTTACCGGCATCTGCGGCC 1137  
DB      1 TTACCTTTACGTCCGGTTCCTCTCACTTAITGTGCCACTATTGGGGCT -GAAGA GTTCC 59  
  
QY      1138 TCCCTTTTCCCTCAACTTCATCAGGTTCCCTGGAGAGCCACTGGTTTGTTGTGGGTGACACACA 1197  
DB      60 TGGGCTTTTCTTTCATAGTAGGTTCCTGGAAAGCACTGCTGTTGTGTGGGTGACACACA 119  
  
QY      1198 TGAATCACATCGTCATGAGGATTGACCAGGAGGCGCTACCGTGACTGTTTCACTAGCCAGC 1257  
DB      120 TGAACCATATTCCCATGACATTGATCATGACCGAATCATGGACTGGTTTCCACCCAGC 179  
  
QY      1258 TGACAGCCACCTCGAACGTGGAGCAGTCTCTTTCAACGACTGGTTTCACTGGGACACCTTA 1317  
DB      180 TCCAGGCCACATGANAATGTCACAGTCTGCTTCAATGACTGTTTCACTGGGACACCTCA 239  
  
QY      1318 ACTTCCAGATTGAGCACCACTCTTCCCCACCATGCCCGGCCACAACTTACAGAAGATCG 1377  
DB      240 ACTTCCAGATTGAGCACCACTCTTCCCCACCATGCCCGGCCACAACTTACAGAAGATCG 299  
  
QY      1378 CCCCCTGGTGAAGTCTCTATGTCGAAGCATGGCATTGAATACAGGAGAACGCCGTAC 1437  
DB      300 CTCCTTGGTGCAGTCTCTATGTCGAAGCATGGCATTGAATACAGGAGAACGCCGTAC 359  
  
QY      1438 TGAGGGCCCTGCTGGACATCATCAGTCTCTGGAAGATCTGGAAGCTGTGGTGGAGC 1497  
DB      360 TGTGAGCCCTTCCGCCACATCATCCACTCACTAAAAGGAGTCAGGCGAGCTTGGCTAGATG 419  
  
QY      1498 CCTACTTTCACAAATGAAAGCCACAGCCCGCCGAGCACCGTGGGAGAGGGGTGACG 1553  
DB      420 CCTATCTTCCAAATAACACAGCCACCTGCCAGTCTGGAAGAGAGGAGGAAG 475
```

RESULT 33  
US-09-439-261-3  
Sequence 3, Application US/09227613A  
Patent No. 6432684  
GENERAL INFORMATION:  
APPLICANT: Mukerji, Pradip  
APPLICANT: LEONARD, Amanda E.  
APPLICANT: HUANG, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.P1  
CURRENT APPLICATION NUMBER: US/09/227,613A  
CURRENT FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 655

|   |      |   |                                      |  |
|---|------|---|--------------------------------------|--|
| US-09-439-261-38  |      | Query Match   | 7.1%; Score 226.8; DB 4; Length 449; |  |
|   |      | Best Local Similarity   | 71.0%; Pred. No. 1.8e-46;            |  |
|   |      | Matches 314; Conservative                                       | 0; Mismatches 127; Indels 1; Gaps 1; |  |
| QY  | 1078 | TGAGTACTACATCCGGTCTTTCATACCTTACATCCCTTTCACGGCATCTCGGAGCCC       | 1137                                 |  |
| DB  | 7    | TTACCTTCTAGTCCGGCTTCTCTCATATATGCGCACTATTGGGGCT-GAAAGCTTCC       | 65                                   |  |
| QY  | 1138 | TCCTTTTCCCTCAACTTCATCAGGTTCTGGAGAGCCACTGGTTTGTGGGTACACAGA       | 1197                                 |  |
| DB  | 66   | TGGGCCCTTTTCTTCATAGTCAGGTTCTGGAAGCAACTGGTTTGTGGGTACACAGA        | 125                                  |  |
| QY  | 1198 | TGAATCACAATCGTCATCGGATGACAGGAGGCTACCGTGACTGGTTCAGTAGCCAGC       | 1257                                 |  |
| DB  | 126  | TGAACCATATTCCTATGCACTTATGATCATGCCGACATGGACTGGTTTCCACCCAGC       | 185                                  |  |
| QY  | 1258 | TGACAGCCACTGCAACGTGGAGCAGTCCTTCTTAACGACTGGTTCAGTGGACACTTA       | 1317                                 |  |
| DB  | 186  | TCCAGGCCACATGCAATGTCCAAAGTCTGCTTCAATGACTGGTTCAGTGGACACTCA       | 245                                  |  |
| QY  | 1318 | ACTTCCAGATTGAGCACCACCTCTTCCCCACCATGTCCTCCCGSCACAACTTACACAAGATCG | 1377                                 |  |
| DB  | 246  | ACTTCCAGATTGAGCACCACCTCTTTCACGATGCTCGACACAATTACCACAAAGTGG       | 305                                  |  |
| QY  | 1378 | CCCGCTGGTGAAGTCTCTATGTGCGAAGCATGGCATGTGATACAGAGAGAGCCGCTAC      | 1437                                 |  |
| DB  | 306  | CTCCCTGGTGCAGTCCCTGTGTGCCAAGCATGGCATAGTACCATGTCGAAGCCCTGC       | 365                                  |  |
| QY  | 1438 | TGAGGGCCCTGCTGCATCATCATCAGGTCCCTGAAAGAGTCTGGGAAGCTGTGGTGGACG    | 1497                                 |  |
| DB  | 366  | TGTCAGCCTTCGCGGACATCATCCACTCATAAAGGAGTCAGGCGAGCTCTGGCTAGATG     | 425                                  |  |
| QY  | 1498 | CCTACCTTCACAATGAAGCCA   | 1519                                 |  |
| DB  | 426  | CCTATCTTCAACAATAACAACA  | 447                                  |  |
| RESULT 36   |      |   |                                      |  |
| US-09-172-108-35  |      |   |                                      |  |
| ; Sequence 35, Application US/09172108                        |      |   |                                      |  |
| ; Patent No. 6160104  |      |   |                                      |  |
| ; GENERAL INFORMATION:  |      |   |                                      |  |
| ; APPLICANT: Cunningham, Mary Jane                            |      |   |                                      |  |
| ; APPLICANT: Zweiger, Gary B.                                 |      |   |                                      |  |
| ; APPLICANT: Panzer, Scott R.                                 |      |   |                                      |  |
| ; APPLICANT: Seilhammer, Jeffrey J.                           |      |   |                                      |  |
| ; TITLE OF INVENTION: MARKERS FOR PEROXISOMAL PROLIFERATORS   |      |   |                                      |  |
| ; FILE REFERENCE: PA-0012 US                                  |      |   |                                      |  |
| ; CURRENT APPLICATION NUMBER: US/09/172,108                   |      |   |                                      |  |
| ; CURRENT FILING DATE: 1998-10-13                             |      |   |                                      |  |
| ; NUMBER OF SEQ ID NOS: 56                                    |      |   |                                      |  |
| ; SOFTWARE: PERL Program                                      |      |   |                                      |  |
| ; SEQ ID NO 35  |      |   |                                      |  |
| ; LENGTH: 259   |      |   |                                      |  |
| ; TYPE: DNA   |      |   |                                      |  |
| ; ORGANISM: Homo sapiens                                      |      |   |                                      |  |
| ; FEATURE:  |      |   |                                      |  |
| ; NAME/KEY: unsure  |      |   |                                      |  |
| ; LOCATION: 219   |      |   |                                      |  |
| ; OTHER INFORMATION: a o r g o r c o r t, unknown, or other   |      |   |                                      |  |
| ; FEATURE:  |      |   |                                      |  |
| ; OTHER INFORMATION: 700483475H1                              |      |   |                                      |  |
| ; US-09-172-108-35  |      |   |                                      |  |
| Query Match 6.2%; Score 198; DB 3; Length 259;                |      |   |                                      |  |
| Best Local Similarity 87.6%; Pred. No. 1.8e-39;               |      |   |                                      |  |
| Matches 227; Conservative 0; Mismatches 31; Indels 1; Gaps 1; |      |   |                                      |  |
| QY  | 631  | TCCTTACTTTGGCAATGGCTGATTCCTACCTCATACGGCCTTGTCTTGTACCT           | 690                                  |  |
| DB  | 2    | TCCTGACTTTCGGCAATGGCTGATTCCTACCTCATACGGCCTTGTCTTGTACCT          | 61                                   |  |
| QY  | 691  | CTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAAC       | 750                                  |  |
| DB  | 62   | CCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTTCTGTCTATAAGAAAT      | 121                                  |  |
| QY  | 751  | CCAAGTGGAAACCACTTGTCCCAAAATTCGTATTTGGCCACTTAAGGGTGTCTGCCA       | 810                                  |  |
| DB  | 122  | CCATATGGAACCACTTGTCCCAAAATTCGTATTTGGCCACTTAAGGGTGTCTGCCA        | 181                                  |  |
| QY  | 811  | ACTGGTGGATCATCGCATCTTCCAGCACCCAGCCAGCTTAACATCTTCCCAAGGATC       | 870                                  |  |
| DB  | 182  | ACTGGTGGAAACCACTTGTCCCAAAATTCGTATTTGGCCACTTAAGGGTGTCTGCCA       | 240                                  |  |
| QY  | 871  | CCGATGTGAACATGCTGCA   | 889                                  |  |

Db 241 CCGACATAAAGAGCGCTGCA 259  
|||||

## RESULT 37

US-09-172-711-33

; Sequence 33, Application US/09127211

; Patent No. 6160105

; GENERAL INFORMATION:

; APPLICANT: Cunningham, Mary Jane

; APPLICANT: Zweiger, Gary B.

; APPLICANT: Panzer, Scott R.

; APPLICANT: Seilhamer, Jeffrey J.

; TITLE OF INVENTION: MONITORING TOXICOLOGICAL RESPONSES

; FILE REFERENCE: PA-0011 US

; CURRENT APPLICATION NUMBER: US/09/172,711

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PERL Program

; SEQ ID NO 33

; LENGTH: 259

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 219

; OTHER INFORMATION: a or g or c or t, unknown, or other

; FEATURE:

; OTHER INFORMATION: 700483475H1

US-09-172-711-33

## Query Match

Best Local Similarity 6.2%; Score 198; DB 3; Length 259;

Mismatches 227; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

Qy 631 TCTTCTACTTGGCAATGGCTGATTCCTACCTCATACAGGCTTTGCTGCTACT 690

Db 2 TCTCGTACTTCGGCAATGGCTGATTCCTACCTCATACAGGCTTTGCTGCTACT 61

Qy 691 CTCAGGCCCCAGCTGGATGCTCAACATGATTTATGGCCACTGCTGCTACACAAAC 750

Db 62 CCCAGGCCCCAGCTGGATGCTCAACATGATTTATGGCCACTTCTGCTATAAGAAAT 121

Qy 751 CCAAGTGGAAACCACTTGTCCACAAATTCGTATTGGCCCACTTAAAGGTGCTCTGCCA 810

Db 122 CCATATGGAACCACTTGTCCACAAATTCGTATTGGCCCACTTAAAGGTGCTCTGCCA 181

Qy 811 ACTGGTGAATCATCGCCACTTCCAGCACACCGCCAAAGCTTAACATCTCCACAGGATC 870

Db 182 ACTGGTGAATCATCGCCACTTCCAGCACACCGCCAAAGCTTAACATCTCCACAGGATC 240

## RESULT 38

US-09-702-705-355/c

; Sequence 355, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705  
; CURRENT FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 1833  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 355  
; LENGTH: 347  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-09-702-705-355

Query Match 5.4%; Score 173.2; DB 4; Length 347;  
Best Local Similarity 77.0%; Pred. No. 2.5e-33;  
Matches 211; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 1257 CTGACAGCCACCTGCAACGTGGAGCAGTCTTCTTCAACGACTGTTTCAAGTGGACACTT 1316

Db 347 CTGGCAGCCACCTGCAACGTGGAGCAGTCTTCTTCAACGACTGTTTCAAGTGGACACTT 288

Qy 1317 AACTTCCAGATTGAGCACCACTCTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTT 1376

Db 287 AACTTCCAGATTGAGCACCACTCTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTT 228

Qy 1377 GCGCCGCTGCTGAAGTCTTATGTCGCAAGCATGCTTGAATACCAAGGAGAACCCCTA 1436

Db 227 GCGCCGCTGCTGAAGTCTTATGTCGCAAGCATGCTTGAATACCAAGGAGAACCCCTC 168

Qy 1437 CTGAGGGCCCTGCTGGACATCATCAGTCCCTGGAAGTCTGGGAAGTCTGGCTGGAC 1496

Db 167 CTCACCGGCTGCTGGACATCATCAGTCCCTGGAAGTCTGGGAAGTCTGGCTGGAC 108

Qy 1497 GCGTACCTTCACAAATGAAGCCACAGCCCGCCGG 1530

Db 107 GCGTACCTTCACAAATGAAGCCACAGCCCGCCGG 74

## RESULT 39

US-09-736-457-355/c

; Sequence 355, Application US/09736457

; Patent No. 6509448

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; APPLICANT: Wang, Aijun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736,457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1884

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 355

; LENGTH: 347

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-736-457-355

Query Match 5.4%; Score 173.2; DB 4; Length 347;  
Best Local Similarity 77.0%; Pred. No. 2.5e-33;  
Matches 211; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 1257 CTGACAGCCACCTGCAACGTGGAGCAGTCTTCTTCAACGACTGTTTCAAGTGGACACTT 1316

Db 347 CTGGCAGCCACCTGCAACGTGGAGCAGTCTTCTTCAACGACTGTTTCAAGTGGACACTT 288

Qy 1317 AACTTCCAGATTGAGCACCACTCTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTT 1376

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Db      287  AACTTCAGATCGAGCACCACTCTTCCGAGGATCCGAGACACAACTACAGCGGGTG 228
Qy      1377  GCGCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCAATTGAATACCAGGAGCGGCTA 1436
Db      227  GCGCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCAATTGAATACCAGGAGCGGCTT 168
Qy      1437  CTGAGGCGCTTCTGAGCATCATCAGGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGAC 1496
Db      167  CTCACCGCGTGGTGGACATCGTCAGTCCCGAAGAAGTCTGGTGACATCTGGCTGGAC 108
Qy      1497  GCCTACCTTCACAAATGAAGCCACAGCCCCCGG 1530
Db      107  GCCTACCTTCATCAGTGAAGGCAACACCCAGGCG 74
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## RESULT 40

```
US-09-440-315A-3/C
; Sequence 3, Application US/09440315A
; Patent No. 6551812
; GENERAL INFORMATION:
; APPLICANT: Gould-Rothberg, Bonnie
; TITLE OF INVENTION: Compositions and Methods Relating to the
; TITLE OF INVENTION: Peroxisomal Proliferator Activated Receptor-Alpha
; TITLE OF INVENTION: Mediated Pathway
; FILE REFERENCE: 15966-333
; CURRENT APPLICATION NUMBER: US/09/440,315A
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/108,293
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/126,465
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: g0m0_173.1
; NAME/KEY: misc_feature
; LOCATION: (11)..(204)
; OTHER INFORMATION: wherein n may be a or t or g or c
US-09-440-315A-3
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Query Match      3.2%; Score 102; DB 4; Length 253;
Best Local Similarity 65.3%; Pred. No. 7.4e-16;
Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
Qy      334  AGCACCGGGGGGCGAGCGGCTCATCGGGCACTACGCTGGAGAGATGCAACGGATGCCT 393
Db      225  ACCACCGGGAGGCTCCCGGTGATCAGCCACTACGCTGGTGGATGCCAGGATCCTT 166
Qy      394  TCCGCGCTTCCACCTGACCTGGAATTCGTGGGCAAGTCTTGAACCCCTGCTGATTG 453
Db      165  TTGTGGCATTCACATTAAACAAGGCGCTTGTGAGAAAGTATATGAACCTCTCTTCTGATTG 106
Qy      454  GTGACTGCGCCCGGAGAGCGCCAGGAGGACCGGCAAGCAACTCAAGATCACTGAGG 513
Db      105  GAGAGCTAGCTCCGGAGAGCGCCAGCTTTGAACCCACCAAGATAGCGGCTNACTGATG 46
Qy      514  ACTTCCGGGCGCTGAGGAGAGCGCTGAGGACATGAACCTGTTCA 558
Db      45  AATTCGGGGGCTGGGGGCCACAGTGGAGGGAATNGSCCTCATGA 1
```

Search completed: December 10, 2003, 16:24:53  
Job time : 157 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 10, 2003, 18:18:30 ; Search time 73 Seconds  
(without alignments)

2684.577 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

Sequence: 1 MGXGNGQGAERVSVP.....DIIRSLKSGKMLDAYLHK 444

Scoring table: BLOSUM62

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Xgapop 10.0, Xgapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US09719601/runat 09122003 094909 21199/app query.fasta\_1.583  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:  
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2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq:  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Match | Length | ID | Description      |
|------------|--------|-------|--------|----|------------------|
| 1          | 1935   | 79.4  | 2257   | 4  | US-09-439-261-8  |
| 2          | 1935   | 79.4  | 2257   | 4  | US-09-227-613-8  |
| 3          | 1646   | 67.5  | 1843   | 4  | US-09-439-261-7  |
| 4          | 1646   | 67.5  | 1843   | 4  | US-09-227-613-7  |
| 5          | 1560.5 | 64.0  | 1717   | 4  | US-09-048-888-2  |
| 6          | 1515   | 62.1  | 1928   | 4  | US-09-048-888-4  |
| 7          | 1508   | 61.9  | 1335   | 4  | US-09-439-261-1  |
| 8          | 1508   | 61.9  | 1335   | 4  | US-09-227-613-1  |
| 9          | 1348   | 55.3  | 1686   | 4  | US-09-439-261-6  |
| 10         | 1348   | 55.3  | 1686   | 4  | US-09-227-613-6  |
| 11         | 1103   | 45.2  | 864    | 4  | US-09-439-261-12 |
| 12         | 1103   | 45.2  | 864    | 4  | US-09-227-613-13 |

|    |       |      |      |   |                    |
|----|-------|------|------|---|--------------------|
| 13 | 960   | 39.4 | 990  | 4 | US-09-439-261-35   |
| 14 | 960   | 39.4 | 990  | 4 | US-09-227-613-34   |
| 15 | 933   | 38.3 | 960  | 4 | US-09-439-261-36   |
| 16 | 933   | 38.3 | 960  | 4 | US-09-227-613-35   |
| 17 | 923   | 37.9 | 918  | 4 | US-09-439-261-5    |
| 18 | 923   | 37.9 | 918  | 4 | US-09-227-613-5    |
| 19 | 934   | 34.2 | 446  | 4 | US-09-389-681-425  |
| 20 | 934   | 34.2 | 446  | 4 | US-09-620-405B-425 |
| 21 | 834   | 34.2 | 446  | 4 | US-09-433-826B-425 |
| 22 | 834   | 34.2 | 446  | 4 | US-09-604-287A-425 |
| 23 | 834   | 34.2 | 456  | 4 | US-09-389-681-313  |
| 24 | 834   | 34.2 | 456  | 4 | US-09-620-405B-313 |
| 25 | 834   | 34.2 | 456  | 4 | US-09-339-338-313  |
| 26 | 834   | 34.2 | 456  | 4 | US-09-433-826B-313 |
| 27 | 834   | 34.2 | 456  | 4 | US-09-604-287A-313 |
| 28 | 620   | 25.4 | 473  | 4 | US-09-439-261-37   |
| 29 | 620   | 25.4 | 473  | 4 | US-09-227-613-36   |
| 30 | 585   | 24.0 | 304  | 4 | US-09-439-261-4    |
| 31 | 585   | 24.0 | 304  | 4 | US-09-227-613-4    |
| 32 | 566   | 23.2 | 449  | 4 | US-09-439-261-38   |
| 33 | 566   | 23.2 | 449  | 4 | US-09-227-613-37   |
| 34 | 566   | 23.2 | 655  | 4 | US-09-439-261-3    |
| 35 | 566   | 23.2 | 655  | 4 | US-09-227-613-3    |
| 36 | 459   | 18.8 | 1617 | 2 | US-08-834-655-1    |
| 37 | 459   | 18.8 | 1617 | 3 | US-08-834-033A-1   |
| 38 | 459   | 18.8 | 1617 | 3 | US-09-363-574-1    |
| 39 | 459   | 18.8 | 1617 | 4 | US-09-363-526-1    |
| 40 | 459   | 18.8 | 1617 | 4 | US-09-330-235-17   |
| 41 | 435.5 | 17.9 | 1684 | 2 | US-08-831-570-1    |
| 42 | 435.5 | 17.9 | 1684 | 2 | US-08-831-575-1    |
| 43 | 435.5 | 17.9 | 1685 | 1 | US-08-366-779-4    |
| 44 | 435.5 | 17.9 | 1685 | 1 | US-08-789-936-4    |
| 45 | 435.5 | 17.9 | 1685 | 4 | US-08-934-254-4    |

ALIGNMENTS

RESULT 1

US-09-439-261-8  
; Sequence 8, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2257  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-439-261-8

Alignment Scores:  
Pred. No.: 1.96e-215 Length: 2257  
Score: 1935.00 Matches: 352  
Percent Similarity: 88.84% Conservative: 30  
Best Local Similarity: 81.86% Mismatches: 44  
Query Match: 79.37% Indels: 4  
DB: 4 Gaps: 2

US-09-719-601-5 (1-444) x US-09-439-261-8 (1-2257)

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|----|------|---|------|
| QY | 19   | ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer        | 35   |
| DB | 7    | CTACCCCGCGGTACTTCACTCCGCGACGAGGTGCCACGCGCTCAAGGTCCGAGGACGGG     | 66   |
| QY | 36   | GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly    | 55   |
| DB | 67   | TGGCTAGTGATCGACGTAAGGTGTACAACATCAGCGAGTTCACCCGCGGCATCCAGG       | 126  |
| QY | 56   | GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe    | 75   |
| DB | 127  | GGTCCCGGTATCAGCCRCATCAGCCCGGCGAGATGCCACGATCCCTTTGTGGCCCTC       | 186  |
| QY | 76   | HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla    | 95   |
| DB | 187  | CACATCAACAAGGGCGTTGTGAAGAAGTATATGAACATCTCTCTGTATGGAGAACTGTCT    | 246  |
| QY | 96   | ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla    | 115  |
| DB | 247  | CCAGACAGCCCGCTTTGAGCCACCAAGAAATAAGAGCTGACAGATGAGTTCCGGGAG       | 306  |
| QY | 116  | LeuArgLysThrAlaGluAspValAsnLeuPheLysThrAsnHisValPhePheLeuLeu    | 135  |
| DB | 307  | CTCGGGCCACAGTGTGAGCGGATGGGGCTCATGAAGCCCAACATGTCTCTCTCGTGTG      | 366  |
| QY | 136  | LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly    | 155  |
| DB | 367  | TACCTGCTGCACATCTTGCTGTGGATGGTGCAGCCCTGGCTCACCTTTGGGTCTTGGG      | 426  |
| QY | 156  | AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln    | 174  |
| DB | 427  | ACGTCTTTTTCGCCCTTCCTCTGTGCGGTGTGCTCAGTGCATTCAGCAGGCCCAAA        | 486  |
| QY | 175  | AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn    | 194  |
| DB | 487  | GCTGGAGTGCCTGCACATGATTATGGCCACCTGTCTGTCTACAGAAAACCAAGTGAAC      | 546  |
| QY | 195  | HisLeuValHisLysPheValIleGlyHisLeuLysGlyValAsnAlaSerAlaSerTrpAsn | 214  |
| DB | 547  | CACCTTGTCTCAAAATTTGTCATTTGGCCACTTAAGGGTGCCTCTGCCAACTGTGTGAAT    | 606  |
| QY | 215  | HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn    | 234  |
| DB | 607  | CATCGGCATCTTCAGCACACGCGCAAGCTAAATCTTCCACAAGGATCCCGATGTGAAC      | 666  |
| QY | 235  | MetLeuHisValPheValLeuGlyLurGlnProIleGlnTyrGlyLysLysLysLeu       | 254  |
| DB | 667  | ATGCTGCACGTGTGTTCTGGCGGATGGCAGCCCATCGAGTACGGCAGAAGAAGCTG        | 726  |
| QY | 255  | LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu    | 274  |
| DB | 727  | AAATACCTGCCCTACAATCACACGACAGAACTACTTCTTCGTGATTGGGCGCGGTGTC      | 786  |
| QY | 275  | IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal    | 294  |
| DB | 787  | ATCCCCATGCTATTTCCAGTACAGATCATGACCATGATCGTCCATAAGAACCTGGGTG      | 846  |
| QY | 295  | AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr    | 314  |
| DB | 847  | GACCTGGCTGGCGCGTCAAGTACTACATCCGGTTCCTCATCACTTACATCCCTTTCAC      | 906  |
| QY | 315  | GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe    | 334  |
| DB | 907  | GGCATCTCGGGAGCCCTCTTTCTCAACTTTCATCAGGTTCTCTGGAGAGCCACTGGTTT     | 966  |
| QY | 335  | ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp    | 354  |
| DB | 967  | GTGTGGGTCAACAGATGATACATCGTCAATGGAGATTGACCACGAGGCGCTACCGTGAC     | 1026 |
| QY | 355  | TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp    | 374  |
| DB | 1027 | TGTTTCAGTAGCAGCTGACAGCCACTGCAACGTGGAGCAGTTCCTTCTTCAACACTGG      | 1086 |

|  |      |  |      |
|--|------|--|------|
| Qy   | 375  | PhSerGlyHisLeuAsnProGlnleGluHisLeuPheProThrWetProArgHis        | 394  |
| Db   | 1087 | TTCAATGAGACACCTTAACCTTCCAGATGTAGCACCACCTCTCCCCACCATCCCGCGCAC   | 1146 |
| Qy   | 395  | AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr   | 414  |
| Db   | 1147 | AACTTACACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTGAATAC    | 1206 |
| Qy   | 415  | GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly      | 434  |
| Db   | 1207 | CAGGAGAAGCGCTACTGTAGGCGCCCTCTGGACATCATCAGGTCCCTGAAGAAGTCTGGG   | 1266 |
| Qy   | 435  | LysLeuTyrLeuAspAlaTyrLeuHisLys                                 | 444  |
| Db   | 1267 | AACTGTGGCTGGAGCGCTACCTTCACAAA                                  | 1296 |
| RESULT 2   |      |  |      |
| US-09-227-613-8  |      |  |      |
| ; Sequence 8, Application US/09227613A                       |      |  |      |
| ; Patent No. 6432684   |      |  |      |
| ; GENERAL INFORMATION:                                       |      |  |      |
| ; APPLICANT: NUKERJTI, Pradip                                |      |  |      |
| ; APPLICANT: LEONARD, Amanda E.                              |      |  |      |
| ; APPLICANT: HUANG, Yung-Sheng                               |      |  |      |
| ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF |      |  |      |
| ; FILE REFERENCE: 6295-US.P1                                 |      |  |      |
| ; CURRENT APPLICATION NUMBER: US/09/227,613A                 |      |  |      |
| ; CURRENT FILING DATE: 1999-01-08                            |      |  |      |
| ; PRIOR APPLICATION NUMBER: 08/833,610                       |      |  |      |
| ; PRIOR FILING DATE: 1997-04-11                              |      |  |      |
| ; NUMBER OF SEQ ID NOS: 42                                   |      |  |      |
| ; SOFTWARE: FastSeq for Windows Version 3.0                  |      |  |      |
| ; SEQ ID NO 8  |      |  |      |
| ; LENGTH: 2257   |      |  |      |
| ; TYPE: DNA  |      |  |      |
| ; ORGANISM: Homo Sapien                                      |      |  |      |
| US-09-227-613-8  |      |  |      |
| Alignment Scores:  |      |  |      |
| Pred. No.: 1.96e-215 Length: 2257                            |      |  |      |
| Score: 1935.00 Matches: 352                                  |      |  |      |
| Percent Similarity: 88.84% Conservative: 30                  |      |  |      |
| Best Local Similarity: 81.86% Mismatches: 44                 |      |  |      |
| Query Match: 79.37% Indels: 4                                |      |  |      |
| DB: 4 Gaps: 2  |      |  |      |
| US-09-719-601-5 (1-444) x US-09-227-613-8 (1-2257)           |      |  |      |
| Qy   | 19   | ProThr-----PheSerTyrGluGluIleGlnLysHisAsnLeuArgThrAspSer       | 35   |
| Db   | 7    | CTATCCCGCGCTACTTCACTCGGACGAGGTGGCCGACGCTCAGGTGGCAGAGCGG        | 66   |
| Qy   | 36   | GlyLeuValIleAspArgLysValTyrAsnIleThrLysTyrSerIleGlnHisProGly   | 55   |
| Db   | 67   | TGGCTAGTAGTATCGACCGTAGGTGTACAAATCATCGAGGTTCACCGCGCGCATCCAGGG   | 126  |
| Qy   | 56   | GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe   | 75   |
| Db   | 127  | GGCTCCGGGTCAACCCACTACGCGCGGCGAGGATGCCAGGATCCCTTTGTGCGCTTC      | 186  |
| Qy   | 76   | HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla   | 95   |
| Db   | 187  | CACATTCACAAGCGCCCTTGTGAAGAAGTATATGAATCTCTCTCTGATTGGAGAATCTGTCT | 246  |
| Qy   | 96   | ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla   | 115  |
| Db   | 247  | CCAGACGAGCCGCTTTGAGCCCAACGAATAAAGAGCTGACAGATGAGTTCGCGGAG       | 306  |
| Qy   | 116  | LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu   | 135  |
| Db   | 307  | CTGCGGGCCACAGTGGAGCGGATGGGGCTCATGAAGGCCCAACCATGTCTCTTCTCTGCTG  | 366  |
| Qy   | 136  | LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTyrPheThrValPheTyrPheGly   | 155  |



Db 661 TTCAACGACTGGTTCACTGGACACCTTAATCTCCAGATTGAGCACACCTCTTCCCCACC 720  
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCGGACAACTTACACAGATCGCCCGCTGGTGAATCTCTATGTCGAAGCAT 780  
 Qy 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuAspIleIleArgSerLeu 430  
 Db 781 GGCAATTGAATACAGGAGAGCCGCTACTGAGGGCCCTGCTGGACATCATCAGTCCCTG 840  
 Qy 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrLeuHisLys 444  
 Db 841 AAGAGTCTGGGAGCTGTGGCTGGAGCGCTACTTCCACAAA 882

## RESULT 4

US-09-227-613-7  
 ; Sequence 7, Application US/09227613A  
 ; Patent No. 6432684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKERJI, Pradip  
 ; APPLICANT: LEONARD, Amanda E.  
 ; APPLICANT: HUANG, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295-US.P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,613A  
 ; CURRENT FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1843  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-09-227-613-7

## Alignment Scores:

Pred. No.: 7,16e-182 Length: 1843  
 Scores: 1645.00 Matches: 294  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 67.51% Indels: 0  
 DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-227-613-7 (1-1843)

Qy 151 ValPheTyrPheGlyAsnGlyTyrIleProThrLeuIleThrAlaPheValLeuAlaThr 170  
 Db 1 GTCTTTACTTTGGCAATGGCTGGATGCTCAACATGATTATGCCACCTGTCTGTACAGAAA 60  
 Qy 171 SerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 Db 61 TCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGCCACCTGTCTGTACAGAAA 120  
 Qy 191 ProLysTyrAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210  
 Db 121 CCCAAGTAGAACACCTTTGCCACAAATTTGTCTATGGCCACCTTAAGGTCCTCTGCC 180  
 Qy 211 AsnTyrPheAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230  
 Db 181 AACTGGTGAATCATCTGCCATCTCCAGCACCAAGCCCTAACATCTTCCACAGGAT 240  
 Qy 231 ProAspValAsnMetLeuHisValPheValLeuGlyGlnTyrPheGlnProIleGlyTyrGly 250  
 Db 241 CCCGATGTGAACATGCTCCAGCTGTTTGTCTGGCGAATGGCAGCCCATCGATAGGC 300  
 Qy 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270  
 Db 301 AAGAGAGAGCTGAATACCTGCCCTACAATCACAGCACCAAGCAATCTCTCTCTGATGGG 360  
 Qy 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290  
 Db 361 CCGCGCTGCTCTACCCCATGATTTTCCAGTACCAAGATCATCATGACCAATGATCGTCCAT 420

Qy 291 LysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
 Db 421 AAGAACTGGGTGGACCTGGCCCTGGCTGAGTACTACATCCGGTTCTTTCATCACCTAC 480  
 Qy 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330  
 Db 481 ATCCCTTTCTACGGGATCCTGGAGCCCTCTCTTCTCAACTTCATCAGGTTCTCTGGAG 540  
 Qy 331 SerHisTyrPheValTyrValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350  
 Db 541 AGCCACTGGTTGTGGTGCACACAGATGAATCACAATCGTCATGGAGATTGACAGGAG 600  
 Qy 351 AlaTyrArgAspTyrPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370  
 Db 601 GCCTACCGTGACTGGTTCACTAGTAGCCAGCTGACAGCACCTGCAACGTGAGCAGTCTTC 660  
 Qy 371 PheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390  
 Db 661 TTCAACGACTGGTTTCACTGGACACCTTAATCTCCAGATTGAGCACCACTCTTCCCCACC 720  
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCGGACAACTTACACAGATCGCCCGCTGGTGAATCTCTATGTCGAAGCAT 780  
 Qy 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430  
 Db 781 GGCAATTGAATACAGGAGAGCCGCTACTGAGGGCCCTGCTGGACATCATCAGTCCCTG 840  
 Qy 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrLeuHisLys 444  
 Db 841 AAGAGTCTGGGAGCTGTGGCTGGAGCGCTACTTCCACAAA 882

## RESULT 5

US-09-048-888-2  
 ; Sequence 2, Application US/09048888  
 ; Patent No. 6492108  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Shah, Purvi  
 ; TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/048,888  
 ; FILING DATE: Filed Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Carrone, Michael C.  
 ; REGISTRATION NUMBER: 39,132  
 ; REFERENCE/DOCKET NUMBER: PF-0494 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1717 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: ENDANOT01  
CLONE: 2451043  
US-09-048-888-2

Alignment Scores:

Pred. No.: 5,986-172 Length: 1717  
Score: 1560.50 Matches: 278  
Percent Similarity: 76.23% Conservatives: 62  
Best Local Similarity: 62.33% Mismatches: 103  
Query Match: 64.01% Indels: 3  
DB: 4 Gaps: 2

US-09-719-601-5 (1-444) x US-09-048-888-2 (1-1717)

QY 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluAArgGluValSerVal 18  
DB 75 ATGGCGCGGTCGGGAGCGCGGAGCGCGGAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 134  
QY 19 ProThrPheSerTrpGluGluGlnGlyHisAsnLeuAArgThrAspSerGlyLeuVal 38  
DB 135 CCCACCTTCTGCTGGAGGAGATCCGCGCGACGACCGCGCGCGCGCGCGCGCGCGCGCGCG 194  
QY 39 IleAspArgLysValTyAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58  
DB 195 ATCGAGCGCGGCTACGACATCAGCGCTGGCGCACGACGCCACCGCGCGCGCGCGCGCG 254  
QY 59 ValIleGlyHisTyAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78  
DB 255 CTCATCGCGCACCGCGCGCTGAGGACCGCGCGGATGCTTCCGTCGCTTCCATCAAGAT 314  
QY 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98  
DB 315 CTCATTTTGTGGCAAGTTCCTACAGCCCTGTGATGGAGACTGGCTCCGGAAGA 374  
QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118  
DB 375 CCAGCGAGGATGAGCCCGCTGAATGCGAGCTGGTGGAGGACTCCGAGCGCTCGCAGCAG 434  
QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138  
DB 435 GCAGCGGAGGATGAGGCTGTTGATGCGAGTCCACCTTCTTGTCTTCTTCTTCTTCTG 494  
QY 139 HisIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrp 158  
DB 495 CACATCCTGCGCATGGAGGCTGCTGGCTGCTGCTTATCTATCTATCTATCTATCTATCT 554  
QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178  
DB 555 GTCCCGAGTGGCTGGCGCGCTTATCTTCCCTGGCATCTCTCAGCTCAGCTCAGCTCAG 614  
QY 179 GlnHisAspTrpGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHis 198  
DB 615 CAGCATGACCTGGCCATGCTCCATCTTCAAGAGTCTGTGGAGAACCAACGTCGGCGCAG 674  
QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218  
DB 675 AAGTTCGTGATGGGCGAGCTTAAGGGCTTCTCGCGCCACTGGTGGAACTTCGCGCACCTC 734  
QY 219 GlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238  
DB 735 CAGCACACCGCCAGCCACATCTTCCACAGAGCCAGAGCTGAGCGGTGGCGCGCGCTG 794  
QY 239 PheValLeuGlyGluTrpGlnProIleGluTyGlyLysLysLeuLysTrpLeuPro 258  
DB 795 TTCCTCTCTGGGGAG---TCATCCGTGAGTATGGCAAGAGAACCGAGATACCTTACCC 851  
QY 259 TyrAsnHisGlnHisGlyTrpPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278  
DB 852 TACACACGAGGACCTGTACTTCTTCTGATCGGCGCGCGCTGCTCACCCTGGTGAGAC 911

QY 279 PheGlnTyGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298  
DB 912 TTGGAAGTGAATAATCTGGCGTACATGCTGGTGTGCATGTCAGTGGCGGATTTGCTCGG 971  
QY 299 AlaValSerTyTrpIleArgPhePheIleThrTyIleProPheTyTrpGlyLeuGly 318  
DB 972 GCGCCAGCTTCTATGCGCGCTTCTTATCTACCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1031  
QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338  
DB 1032 GTGCTCTCTTCTTCTTCTCTCTGAGGTCCTGGAAAGCCATGCTTCTGTTGGATCACA 1091  
QY 339 GlnMetAsnHisIleValMetGluLeuAspGlnGluAlaTyArgAspTrpPheSerSer 358  
DB 1092 CAGATGAACCATCTCCCAAGGAGATCGCGCCAGGAGCACCGGAGCTGGGTCTAGCTCT 1151  
QY 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378  
DB 1152 CAGCTGGCGGACCATCTGCAACGTCGAGCCCTTCTTCCAGGATCCGAGACACAACTACAGCCG 1211  
QY 379 LeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLys 398  
DB 1212 CTCAACTTCCAGATCGAGCACCACTTCTTCCAGGATCCGAGACACAACTACAGCCG 1271  
QY 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyGlnGluLysPro 418  
DB 1272 GTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1331  
QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysTrpLeu 438  
DB 1332 TTCTTCCAGCGCTGCTGGACATCGTCAGTCCCTGCAAGAGTCTGTCATCTGCTGCTG 1391  
QY 439 AspAlaTrpLeuHisLys 444  
DB 1392 GAGCGCTTACCTCCATCAG 1409  
RESULT 6  
US-09-048-888-4  
; Sequence 4, Application US/09048888  
; Patent NO. 6492108  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/048,888  
; FILING DATE: Filed Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0494 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555

```

TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BEPNOT01
CLONE: 2056310
US-09-048-888-4

Alignment Scores:
Pred. No.: 1,45e-166 Length: 1928
Score: 1515.00 Matches: 272
Percent Similarity: 76.08% Conservative: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.14% Indels: 6
DB: 3

US-09-719-601-5 (1-444) x US-09-048-888-4 (1-1928)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluLutIleGln 27
Db 102 GCGCCGAGACCGCGCTCAGGACCTACCCGCGTACTTCCCTGGGACGAGTGCC 161
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTrzAsnIleThr 47
Db 162 CAGCGCTCAGGTCGCGAGCGGTGGTGTAGTCGACCGTAAGGTGTACAACTCAGC 221
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrzAlaGlyLysAsp 67
Db 222 GAGTTCACCGCGCGGATCCAGGGGCTCCCGGGTCTATCAGGCATACCGCGGCGAGAT 281
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 282 GCCACGGATCCCTTTGTGGCTTCACATCAACAGGCGCTTGTGAAGAAGTATATGAC 341
QY 88 ProIleuLeuGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
Db 342 TCTCTCTGATGGAGAACTGTCTCCAGAGACAGCCGAGCTTTGAGCCCAAGAAATAAA 401
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 402 GAGCTGACATGAGTTCGCGAGCTCGCGCCACAGTGGAGCGGTGGGCTCATGAG 461
QY 128 ThrAsnHisValPhePheLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 462 GCCAACCATGCTCTCTCTGCTGTACTCTGTCACATCTTGTCTGTGATGCTGCAGCC 521
QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 522 TGGCTCACCTTTGGGCTTTGGAGCGCTCTTTTGGCCCTCTCTCTCTGCGGTGCTG 581
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
Db 582 CTCAGTCAGTTCAGGCCCGAGCTGGCTGCTGCGAGCATGACTTTGGCCACCTGTGCTC 641
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 642 TTCAGCACCTCAAAAGTGAAACATCTGCTACATCATTTGTGATGGCCACCTGAGAGGG 701
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 702 GCCCCCGCCAGTTGGTGAACCAACATGCTCCAGCACCATGCGCAAGCCCACTGCTTC 761
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValIleGlyGluTrpGln 245
Db 762 CGCAAGACCCAGACATCAACATG---CATCCCTTCTCTCTTGTGCTGGGAGATCCTC 818
QY 246 ProIleGluTrpGlyLysLysLeuLysTrpLeuProTrpAsnHisGlnHisGluTrp 265
Db 819 TCTGTGGAGCTTGGAAACAGAGAAATAATATGCGGTACACCAACCAGCACAAATAC 878

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QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTrpGlnIleIleMet 285
Db 879 TTTCTTCTAAATGGGCCCCCAGCCCTGCTCTCTACTTCCAGTGGTATATTTCTAT 938
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTrpTrzIleAsp 305
Db 939 TTTGTTATCCAGCGAAAGAGTGGTGGACTTGGCTGGATGATTACCTTACGTCGCC 998
QY 306 PhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 999 TTTTCTCTACATTATGTGCACCTATTGGGGCTGAAAGCCCTTCTGGGCCCTTTCTTCA 1058
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 1059 GTCAGGTTCCTGGAAGCAACTGGTTGTGTGGGTGACACAGATGAACCATATTCCTATG 1118
QY 346 GluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1119 CACATTGATCATGACCGGACATGGACTGGTTCACCCAGCTCCAGGCCACATGCAAT 1178
QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1179 GTCCACAGAGTCTGCTTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTGAGCAC 1238
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1239 CATCTTTTCCACGATGCTCCTCGACACATATACCAAAAGTGGCTCCCTGGTGCAGTCC 1298
QY 406 LeuCysAlaLysHisGlyIleGluTrpGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1299 TTGTGTCCCAAGCATGCGATAGAGTACCAAGCCCTGCTGTCAGCCCTTCGCCGAC 1358
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTrpLeuHisLys 444
Db 1359 ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCTTCTTCCACCA 1415

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## RESULT 7

```

US-09-439-261-1
Sequence 1, Application US/09439261
Patent No. 6428990
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295 US P2
CURRENT APPLICATION NUMBER: US/09/439,261
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1335
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-261-1

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Alignment Scores:
Pred. No.: 5,34e-166 Length: 1335
Score: 1508.00 Matches: 271
Percent Similarity: 75.85% Conservative: 62
Best Local Similarity: 61.73% Mismatches: 100
Query Match: 61.85% Indels: 6
DB: 3

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US-09-719-601-5 (1-444) x US-09-439-261-1 (1-1335)

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```
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCACCTGGGACGAGGTGGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTrpAsnIleThr 47
Db 79 CAGCGCTCAGGTGGCGAGCGGTGGCTAGTGTACACCGTAAAGGTGTACAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlyClnArgValIleGlyHisTrpAlaGlyGluAsp 67
Db 139 GAGTTTACCCCGCGCATCCAGGGGCTCCCGGGTTCATCAGCCACTACCGCGGCGAGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCACGGATCCCTTGTGCGCTTCCACATCAACAGAGCGCTTGTGAAGAGTATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluLupProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCTGATTGGAGAACTGTCTCCAGAGAGCCCGACCTTTGAGCCGCCACCAAGATAAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACAGATGAGTTCGGGAGCTGGCGCCACAGTGGAGCGGATGGGCTCATGAAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 379 GCCAACCATGCTTCTCTGCTGTACCTGTGTCACATCTTGTCTGTGATGGTGGCGAGCC 438
QY 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 439 TGCTCTACCCCTTGGGTCTTGGGAGCTCTTTTGGCCCTTCTCTCTGCTGGTGGCTG 498
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 499 CTGAGTGCAGTTCAGGCCCGAGCTGGCTGGCTGCAGCATGACTTTGGGCACCTGTGCTC 558
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 559 TTCAGACCTCAAGTGGAAACCATCTGTACATCATTTTGTGATTTGGCCACTGAAGGG 618
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 619 GCGCCGCGAGTGTGTGGAAACACATGCATCTCCAGCACCATGCGCAAGCCCAACTGCTTC 678
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTTCTTCTTTCCTTGGGGAAGATCTCTC 735
QY 246 ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
Db 735 TCTGTGGAGCTTGGGAAACAGAGAAATAATATATGCGGTACACACCCAGCACACAAATAC 795
QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285
Db 796 TTCTTCTTAATTTGGGCGCCCGAGCTTGTGCTCTCTACTTCCAGTGTATATTTCTAT 855
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
Db 856 TTGTGTATCAGCGAAAGAGTGGGTGGACTTGGCTGGATGATTAACCTTCTACCTCCGCG 915
QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 916 TTCTTCTCTACTTATGTGCACTATTGGGGCTGAAAGCGCTTCTCTGGCGCTTTTCTTCATA 975
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 976 GTCAGGTTCCTGAAAGCAACTGTTTGTGTGGTGACACATGACATGACCATATTCCTCATG 1035
QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1036 CACATTGATCATGACCCGGAACATGGACTGGGTTTCCACCCAGCTCTCTGCGCACATGCAAT 1095
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QY 366 ValGluGlnSerPheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1096 GTCCACAAGTCTGCTTCAATGACTGGTTCAGTGACACCTCACTTCCAGATTGAGCAC 1155
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1156 CATCTTTTCCACCATGCTCGACACAATTACCAAGTGGCTCCCTTGTGTGAGTCC 1215
QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1216 TTGTGTGCCAAGCGTGGCATAGTACCATCAAGCCCTCTGTGACGCTTCGCCGAC 1275
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1276 ATCATCTCACTCTAAAGAGTCAGGCGAGCTCTGGCTAGATGCTATCTTCCACAA 1332
RESULT 8
US-09-227-613-1
; Sequence 1, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.PI
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-1
Alignment Scores:
Pred. No.: 5 34e-166 Length: 1335
Score: 1508.00 Matches: 271
Percent Similarity: 75.85% Conservative: 62
Best Local Similarity: 61.73% Mismatches: 100
Query Match: 61.85% Indels: 6
DB: 4 Gaps: 3
US-09-719-601-5 (1-444) x US-09-227-613-1 (1-1335)
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCACCTGGGACGAGGTGGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTrpAsnIleThr 47
Db 79 CAGCGCTCAGGTGGCGAGCGGTGGCTAGTGTACACCGTAAAGGTGTACAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrpAlaGlyGluAsp 67
Db 139 GAGTTTACCCCGCGCATCCAGGGGCTCCCGGGTTCATCAGCCACTACCGCGGCGAGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCACGGATCCCTTGTGCGCTTCCACATCAACAGAGCGCTTGTGAAGAGTATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluLupProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCTGATTGGAGAACTGTCTCCAGAGAGCCCGACCTTTGAGCCGCCACCAAGATAAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACATGAGTTCGGGAGCTGGCGCCACAGTGGAGCGGATGGGCTCATGAAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
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Db 663 CTGGACATCATCAGTCCCTCGAAGAGTCTGGGAAGCTGTGGTGGAGCGCTACCTTCAC 722
QY 444 Lys 444
Db 723 AAA 725
RESULT 10
US-09-227-613-6
; Sequence 6, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-6
Alignment Scores:
Pred. No.: 3.5e-147 Length: 1686
Score: 1348.00 Matches: 241
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.29% Indels: 0
DB: 4 Gaps: 0
US-09-719-601-5 (1-444) x US-09-227-613-6 (1-1686)
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpAsnHisArgHisPheGlnHisAlaLys 223
Db 3 CACTTAAGGGTGCTCTGCCACCTGTGGGAATCATGCCACTCCACGACCAAG 62
QY 224 ProAsnIlePheHisGlyAspProaspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCACAAAGATCCGATGTGAACATGTCACATGTTTGTCTGGGCGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLys 263
Db 123 TGGCAGCCCATCGATGACGCGAAGAGCTGAATACCTGCCCTCAATCACCAGCAC 182
QY 264 GluTyrPhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACTCTTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
Db 243 ATCATGACCATGATGTCATAGAACTGGGTGGACCTGGCTGGCGCTGAGCTACTAC 302
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTTCTACGGCATCCTGGGAGCCCTCTTTTCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTCATCAGGTTCTCGAGAGCCACTCGTGGTTGTGTGGTGCACACATGAATCACA 422
QY 344 ValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThr 363
Db 423 GTCATGGAGATTGACACAGAGGCTTACCTGACTGGTTGAGTACGAGCTGACGCCACC 482
QY 364 CysAsnValGluGlnSerPheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIle 383
Db 483 TGCACGTGGAGCAGTCTTCTTCAACGACTGGTTCAAGTGGACACCTTAACCTTCCAGATT 542
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QY 384 GluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuVal 403
Db 543 GAGCACCACTCTTCCCAACCATGCCCGGCACAACTTACACAAGATGCCCGCGGTGGTG 602
QY 404 LysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeu 423
Db 603 AAGTCTCTATGTGCCAAGCATGGCATTGAATACCAAGGAGAACCGCTACTGAGGGCCCTG 662
QY 424 LeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHis 443
Db 663 CTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGTGGACGCTACCTTCAC 722
QY 444 Lys 444
Db 723 AAA 725
RESULT 11
US-09-439-261-12
; Sequence 12, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-12
Alignment Scores:
Pred. No.: 4.55e-119 Length: 864
Score: 1103.00 Matches: 194
Percent Similarity: 77.93% Conservative: 32
Best Local Similarity: 66.90% Mismatches: 52
Query Match: 45.24% Indels: 12
DB: 4 Gaps: 3
US-09-719-601-5 (1-444) x US-09-439-261-12 (1-864)
QY 157 GlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGly 176
Db 22 GGGGAATTCGGCAGTT-----CAGGCCAAGGTGGC 54
QY 177 TrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeu 196
Db 55 TGGCTGCAGCATGACATTGGGCACCTGTGGTCTTCAGCACCTTCAAAAGTGAACCATCTG 114
QY 197 ValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArg 216
Db 115 CTACATCATTTTGTGATTGGCCACCTGGAAGGGGGCCCCCGCCAGTTGGTGGAAACCATG 174
QY 217 HisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProPheValAsnMetLeu 236
Db 175 CACTTCCAGCACCATGCCAAGCCCACTGCTTCCGCAAGAGCCAGACATCAACATG--- 231
QY 237 His-----ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254
Db 232 CATCCCTCTCTTTTGGCTTGGGGAAGATCCTCTCTGTGGAGCTTGGGAACAGAA 291
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255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGlyProProLeuLeu 274  
 292 AAATATATCCCGTACACACACACACAAATACTTCTCTTAATTTGGGCCCCAGCCTTG 351  
 275 IleProMetTyrPheGlnTyrGlnIleleMetThrMetIleValHisLysAsnTyrVal 294  
 352 CTGCTCTCTACTTCCAGTGGTATATTTCTATTTTGTATCCACGCAAGAAAGTGGGTG 411  
 295 AspLeuAlaTyrAlaValSerTyrIleArgPhePheIleThrTyrIleProPheTyr 314  
 412 GACTTGGCTGGATGATTAACCTTCTACGTCGCTCTCTCTCTCTCTCTCTCTCTCTCT 471  
 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlnSerHisTyrPhe 334  
 472 GGCTCAAAAGCCTTCTGCGGCTCTTCTCTCATAGTCAGGCTCTCTGAAAGCAACTGGTT 531  
 335 ValTyrValThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAlaTyrArgAsp 354  
 532 GTGTGGGTGACACAGATGAACCAATATCCATGACATGATGATGACCGGACATGGAC 591  
 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGlnSerPhePheAsnAspTyr 374  
 592 TGGGTTTCCACCCAGCTCCAGGACACATGCAATGTCCACAAAGTCTGCTTCAATGACTGG 651  
 375 PheSerGlyHisLeuAsnGlnIleGluHisHisLeuPheProThrMetProArgHis 394  
 652 TTCAGTGGACACCTCACTTCCAGATGAGACCACTTTTCCACGATGCTCGACAC 711  
 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414  
 712 AATTACCAAAAGTGGCTCCCTGCTGAGTCTCTGTCGCAAGCATGCGCATAGAGTAC 771  
 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434  
 772 CAGTCCAAAGCCCTGCTGTCAGCTTCCAGCTTCCGCGCATCATCTCACTAAAGGAGTCAGG 831

435 LysLeuTyrLeuAspAlaTyrLeuHisLys 444  
 832 CAGCTCTGGTAGTATGCTATCTTCACCAA 861  
 RESULT 12  
 US-09-719-613-13  
 ; Sequence 13, Application US/092276:3A  
 ; Patent No. 6432684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKERJI, Pradip  
 ; APPLICANT: LEONARD, Amanda E.  
 ; APPLICANT: HUANG, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,613A  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 13  
 ; LENGTH: 864  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-09-719-613-13  
 Alignment Scores:  
 Pred. No.: 4,55e-119 Length: 864  
 Score: 1103.00 Matches: 194  
 Percent Similarity: 77.93% Conservative: 32  
 Best Local Similarity: 66.90% Mismatches: 52  
 Query Match: 45.24% Indels: 12  
 Gaps: 3  
 DB: 4  
 US-09-719-601-5 (1-444) x US-09-227-613-13 (1-864)

157 GlyTyrIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGly 176  
 22 GGCGGAATTCGCGCAGTT-----CAGCCCGAGGCTGGC 54  
 177 TrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTyrPheHisLeu 196  
 55 TGCTCGACGATGACCTTGGGACCTGTCGGTCTTCAGCACCTCAAGTGAACCATCTG 114  
 197 ValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTyrPheHisAsp 216  
 115 CTACATCATTTTGTATGTCACCTGAAGGGGGCCCCCGCCAGTGGTGGGAACCAATG 174  
 217 HisPheGlnHisLysAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeu 236  
 175 CACTTCAGACCATGCGAAGCCCACTGCTTCGCAAGAGCCGACATCAACATG--- 231  
 237 His-----ValPheValLeuGlyGluTyrGlnProIleGluTyrGlyLysLysLysLeu 254  
 232 CATCCCTCTCTTCTTGGGGAAGATCTCTCTGTGGAGCTTGGGAAACAGAAAGAA 291  
 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274  
 292 AAATATATGCGTACACACACAGCAATACTTCTTCTTAATTTGGGCCCCAGCCTTG 351  
 275 IleProMetTyrPheGlnTyrGlnIleleMetThrMetIleValHisLysAsnTyrVal 294  
 352 CTGCTCTCTACTTCCAGTGGTATATTTCTATTTTGTATCCAGCGAAAGAGTGGGTG 411  
 295 AspLeuAlaTyrAlaValSerTyrIleArgPhePheIleThrTyrIleProPheTyr 314  
 412 GACTTGGCTGGATGATTAACCTTCTACGTCGCTTCTCTCTCTCTCTCTCTCTCTCT 471  
 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlnSerHisTyrPhe 334  
 472 GGCTCAAAAGCCTTCTGCGGCTCTTCTCTCATAGTCAGGTCCTGGAAGCAACTGGTT 531  
 335 ValTyrValThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAlaTyrArgAsp 354  
 532 GTGTGGGTGACACAGATGAACCAATATCCATGACATGATGATGACCGGACATGGAC 591  
 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGlnSerPhePheAsnAspTyr 374  
 592 TGGGTTTCCACCCAGCTCCAGGACACATGCAATGTCCACAAAGTCTGCTTCAATGACTGG 651  
 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394  
 652 TTCAGTGGACACCTCAACTTCCAGATGAGACCACTTTTCCACGATGCTCGACAC 711  
 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414  
 712 AATTACCAAAAGTGGCTCCCTGCTGAGTCTCTGTCGCAAGCATGCGCATAGAGTAC 771  
 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly 434  
 772 CAGTCCAAAGCCCTGCTGTCAGCTTCCGCGCATCATCTCACTAAAGGAGTCAGG 831  
 435 LysLeuTyrLeuAspAlaTyrLeuHisLys 444  
 832 CAGCTCTGGTAGATGCTATCTTCACCAA 861  
 RESULT 13  
 US-09-439-261-35  
 ; Sequence 35, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P2  
 ; CURRENT APPLICATION NUMBER: US/09/439,261  
 ; CURRENT FILING DATE: 1999-11-12

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; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-35

Alignment Scores:
Pred. No.: 2,67e-102 Length: 990
Score: 960.00 Matches: 176
Percent Similarity: 69.54% Conservative: 50
Best Local Similarity: 54.15% Mismatches: 73
Query Match: 39.38% Indels: 26
DB: 4 Gaps: 4

US-09-719-601-5 (1-444) x US-09-439-261-35 (1-990)

Qy 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCGCGCTACTTCACTTGGAGAGGTGGCC 78
Qy 28 LysHisAsnLeuArgThrAspSerGlyLeuValleAspArgLysValTrAsnIleThr 47
Db 79 CAGCGCTCAGGCTGCGAGCGGTGGCTAGTATGATGACCGCTAAGGTGATCAACATCAGC 138
Qy 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrAlaGlyGluAsp 67
Db 139 GAGTTCAACCGCGGATCCAGGGGCTCCCGGGTCATCAGCCACTACCGCGGCGAGAT 198
Qy 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCAGGATCCCTTTGTGGCTTCCATCATCAACAGAGGCGCTTGTGAAGATATATGAAC 258
Qy 88 ProLeuLeuIleGlyLeuLeuAlaPheHisProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCCTGATGGAGACTGCTCCAGAGACCGGCTTGGAGCCACCAAGAAATAAA 318
Qy 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACAGATGAGTTCCGGAGCTGGGGCCACAGTGGAGCGGATGGGCTCATGAAG 378
Qy 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 379 GCCAACCATGCTCTTCTGCTGTACCTGTGACATCTTGTCTGTGATGGTGGTGCAGCC 438
Qy 148 TrpPheThrValPheTrpPheGlyAsnGlyTTPileProThrLeuIleThrAlaPheVal 167
Db 439 TGCTCACCCTTTGGGCTTTGGAGGCTTTTGGCGCTTCTCTCTCTGCGGTGCTG 498
Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
Db 499 CTCAGTGCAATTCAGGCCCGGCTGGCTGCGCATGACTTTGGGCGCATCTGTCGGTC 558
Qy 188 TrpArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 559 TTCAGCACTCAAGTGGGAACCATTTGCTACATCATTTTGTGATTTGGCACTGAGGGG 618
Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 619 GCGCCCGCAGTGGTGGGAACACATGCTTCCAGCACCATGCGCAAGCCCAACTGCTTC 678
Qy 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 679 CGCAAGAGCCGACATCAACATG---CATCCCTTCTTCTTCTTGGGGAAGATCCTC 735
Qy 246 ProIleGluTrpGlyLysLysLysLeuLysTrpLeuProTyrAsnHisGlnHisGluTrp 265
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Db 736 TCTGTGGAGCTTGGGAAACAGAGAGAAATATATGCGGTACCAACACGACCAATAC 795
Qy 266 PhePheLeuIleGly----- 270
Db 796 TTCTTCTTAATTTGGGCCCCCAGCCCTGTGCTCTCTACTTCCAGTGGTATATTTCTAT 855
Qy 271 -----ProProLeuLeuLeuProMetTyrPheGlnTrpGlnIleleMet 285
Db 856 TTTGTATATCCAGCGACCCCGCCAGCCCTTGTGCTCTCTACTTCCAGTGGTATATTTCTAT 915
Qy 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIleArg 305
Db 916 TTTGTATATCCAGGAAGAGTGGTGGACTTGGCTGGATGATTACCTTCTACGTCGCG 975
Qy 306 PhePheIleThrTyr 310
Db 976 TTCTTCTCATTAT 990

RESULT 14
US-09-227-613-34
; Sequence 34, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.PI
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-227-613-34

Alignment Scores:
Pred. No.: 2,67e-102 Length: 990
Score: 960.00 Matches: 176
Percent Similarity: 69.54% Conservative: 50
Best Local Similarity: 54.15% Mismatches: 73
Query Match: 39.38% Indels: 26
DB: 4 Gaps: 4

US-09-719-601-5 (1-444) x US-09-227-613-34 (1-990)

Qy 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
Db 19 GCGCGGAGACCGCGGCTCAGGACCTACCGCGCTACTTCACTTGGAGAGGTGGCC 78
Qy 28 LysHisAsnLeuArgThrAspSerGlyLeuValleAspArgLysValTrAsnIleThr 47
Db 79 CAGCGCTCAGGCTGCGAGGCGGTGGCTAGTATGATCAGCGTAAAGTGTACACATCAGC 138
Qy 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrAlaGlyGluAsp 67
Db 139 GAGTTCAACCGCGGATCCAGGGGCTCCCGGGTCATCAGCCACTACCGCGGCGAGAT 198
Qy 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCAGGATCCCTTTGTGGCTTCCATCATCAACAGAGGCGCTTGTGAAGATATATGAAC 258
Qy 88 ProLeuLeuIleGlyLeuLeuAlaPheHisProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCCTGATGGAGACTGCTCCAGAGACCGGCTTGGAGCCACCAAGAAATAAA 318
Qy 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACAGATGAGTTCCGGAGCTGGGGCCACAGTGGAGCGGATGGGCTCATGAAG 378
Qy 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 379 GCCAACCATGCTCTTCTGCTGTACCTGTGACATCTTGTCTGTGATGGTGGTGCAGCC 438
Qy 148 TrpPheThrValPheTrpPheGlyAsnGlyTTPileProThrLeuIleThrAlaPheVal 167
Db 439 TGCTCACCCTTTGGGCTTTGGAGGCTTTTGGCGCTTCTCTCTCTGCGGTGCTG 498
Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
Db 499 CTCAGTGCAATTCAGGCCCGGCTGGCTGCGCATGACTTTGGGCGCATCTGTCGGTC 558
Qy 188 TrpArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 559 TTCAGCACTCAAGTGGGAACCATTTGCTACATCATTTTGTGATTTGGCACTGAGGGG 618
Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 619 GCGCCCGCAGTGGTGGGAACACATGCTTCCAGCACCATGCGCAAGCCCAACTGCTTC 678
Qy 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 679 CGCAAGAGCCGACATCAACATG---CATCCCTTCTTCTTCTTGGGGAAGATCCTC 735
Qy 246 ProIleGluTrpGlyLysLysLysLeuLysTrpLeuProTyrAsnHisGlnHisGluTrp 265
```

Db 319 GAGCTGACAGATGCTCCGGAGCTCGGGCCACAGTGGAGCGGATGGGGCTCATGAAG 378  
 Qy 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 Db 379 GCCAACCATGCTTCTCTGCTGACCTGCTGCACATCTTGTGCTGGATGGTGCAGCC 438  
 Qy 148 TTPPheThrValPheTyrPheGlyAsnGlyTTPileProThrLeuIleThrAlaPheVal 167  
 Db 439 TGGCTCACCTTGGGTCTTGGGAGCTCCCTTTGGCCCTCTCTGCGGTGCTG 498  
 Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187  
 Db 499 CTAGTGCAGTTCAGGCCAGCTGGCTGGCAGCATGATTTGGGCACTGTGCGTTC 558  
 Qy 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 Db 559 TTCAGCACCTCAAGTGGGAACCATCTGTCATCATTTTGTGATTTGGCCACTGAGGGG 618  
 Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysPheAsnIlePhe 227  
 Db 619 GCGCCGCCAGTGTGGTGAACACATGCACTTCCAGCACCATGTCACCAAGCCCACTGCTTC 678  
 Qy 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValIleGlyLutrpGln 245  
 Db 679 CGCAAGAGCCAGACATCAACATG---CATCCCTTCTCTTTGGCTTGGGGAAGATCCTC 735  
 Qy 246 ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265  
 Db 736 TCTGTGGAGCTTGGGAAACAGAGAAATAATATATGCGCTCAACACCAAGCAGCAATAAC 795  
 Qy 266 PhePheIleGly----- 270  
 Db 796 TTCTTCTTAATTTGGGCCCCCAGCCTTGTGCTCTCTACTTCCAGTGGATATATTTCTAT 855  
 Qy 271 -----ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285  
 Db 856 TTGTGTTATCCAGCGACCCCGAGCTTGTGCTCTCTACTTCCAGTGGATATATTTCTAT 915  
 Qy 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrileArg 305  
 Db 916 TTTGTTATCCAGCGAAGAGTGGTGGTGGCTTGGCTGGATGATTAACCTTACGTCGCG 975  
 Qy 306 PhePheIleThrTyr 310  
 Db 976 TTCTTCTCACTTAT 990

RESULT 15  
 US-09-439-261-36  
 ; Sequence 36, Application US/09439261  
 ; Patent No. 6428990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pardip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.P2  
 ; CURRENT APPLICATION NUMBER: US/09/439,261  
 ; CURRENT FILING DATE: 1999-11-12  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 36  
 ; LENGTH: 960  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-439-261-36

Alignment Scores: 3.58e-99 Length: 960  
 Pred. No.: 933.00 Matches: 170  
 Score: 73.38% Conservative: 45  
 Percent Similarity: 73.38% Mismatches: 72  
 Best Local Similarity: 58.02% Indels: 6  
 Query Match: 38.27% Gaps: 3  
 DB: 4  
 US-09-719-601-5 (1-444) x US-09-439-261-36 (1-960)  
 Qy 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27  
 Db 49 GCGCCGAGACCCGCGCTCAGGACTACCCGCGCTACTTCACTGGAGCAGGTGGCC 108  
 Qy 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47  
 Db 109 CAGCGCTCAGGGTGGCAGGAGCGGTGGCTAGTGTAGTCAGCGTAAGGTGTACACATCAG 168  
 Qy 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67  
 Db 169 GAGTTCACCGCGCGCATCCAGGGGCTCCCGGTGTCATGAGCCTACGCCGGGAGGAT 228  
 Qy 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 Db 229 GGCACGGATCCCTTTGTGGCTTCCACATCAACAGGGGCTTGTGAAGAAGTATATGAAC 288  
 Qy 88 ProLeuLeuIleGlyLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107  
 Db 289 TCTCTCTGATGGAGACTGTCTCCAGAGCAGCCAGCTTTGAGCCCAAGATATAA 348  
 Qy 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 Db 349 GAGCTGACAGATGAGTCCGGAGCTGGGGCCACAGTGGAGCGATGGGCTCATGAAG 408  
 Qy 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 Db 409 GCCAACCATGCTTCTCTGCTGTACCTGCTGCATCTTGTCTGTGATGGTGGAGCC 488  
 Qy 148 TrpPheThrValPheTyrPheGlyAsnGlyTTPileProThrLeuIleThrAlaPheVal 167  
 Db 469 TGGTCTACCTTTGGGTCTTGGGAGCTCTTTTGGCTCTCTCTCTCTCTCTCTCTG 528  
 Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187  
 Db 529 CTCAGTGCAGTTCAGGCCAGCTGGCTGGCTGCTGAGCATCTTGGGCACTTGGGCACTG 588  
 Qy 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 Db 589 TTCAGCACCTCAAGTGGAGCCATCTGTCATCATTTTGTGATTTGGCCACTGAGGGG 648  
 Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysPheAsnIlePhe 227  
 Db 649 GCGCCGCGCATGTTGGTGAACACATGCACTTCCAGCACCATGTCACCAAGCCCACTGCTTC 708  
 Qy 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245  
 Db 709 CGCAAGAGCCAGACATCAACATG---CATCCCTTCTCTCTTGGCTTGGGGAAGATCCTC 765  
 Qy 246 ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265  
 Db 766 TCTGTGGAGCTTGGGAAACAGAGAAATAATATATGCGTACACCAAGCAGCAATAAC 825  
 Qy 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285  
 Db 826 TTTCTTCTTAATTTGGGCCCCCAGCCTTGTGCTCTCTCTCTCTCTCTCTCTCTAT 885  
 Qy 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298  
 Db 886 TTTGTTATCCAGCGAAGAGTGGGTGGATGCTGGCTGG 924  
 RESULT 16  
 US-09-227-613-35  
 ; Sequence 35, Application US/09227613A

Patent No. 6432694  
GENERAL INFORMATION:  
APPLICANT: MUKERJI, Pradiip  
APPLICANT: LEONARD, Amanda E.  
APPLICANT: HUANG, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.P1  
CURRENT APPLICATION NUMBER: US/09/227,613A  
PRIOR FILING DATE: 1999-01-08  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 35  
LENGTH: 960  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-09-227-613-35

Alignment Scores:  
Pred. No.: 3.58e-99 Length: 960  
Score: 933.00 Matches: 170  
Percent Similarity: 73.38% Conservative: 45  
Best Local Similarity: 58.02% Mismatches: 72  
Query Match: 38.27% Indels: 6  
DB: 4 Gaps: 3

US-09-719-601-5 (1-444) x US-09-227-613-35 (1-960)

```
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
Db 49 GCGCGGAGAGCGCGGCTCAGGGACCTACCGCGGCTACTTCACCTGGGAGGAGTGCC 108
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValleAspArgLysValTrpAsnLeuThr 47
Db 109 CAGCGCTCAGGCTGCGAGGCGGTGGCTAGTATCGACCGTAAGGTGTACAAATCAGC 168
QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrpAlaGlyGluAsp 67
Db 169 GAGTTCACCGCGGATCCAGGGGGTCCCGGTTCATCAGCCACTAGCGCGGCGAGAT 228
QY 66 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 229 GCCACGGATCCCTTGTGGCTCCACATCAACAAGGCGCTGTGAAGAGTATATCAAC 288
QY 86 ProLeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107
Db 289 TCTCTCCTGATGGAGAACTGTCCAGCAGCGCCAGCTTTGAGCCCAACCAAGATAAA 348
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 349 GAGCTGACAGATGAGTTCGGGAGCTGGGGCCACAGTGGAGCGGATGGGGCTCATGAG 408
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 409 GCCAACCAACGATCTCTCTGCTGACCTGTGACATCTTGTGCTGGATGTGGAGCC 468
QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 469 TGGCTCACCTTGGGTCTTTGGGAGCGCTTTTGGCCCTCTCTCTGCTGGGTGCTG 528
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
Db 529 CTCAGTGAGTTCAGGCCAGGCTGGCTGGCTGAGCATGATGATTTGGGACCTGTGGTC 588
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 589 TTCACACCTCAAGTGAAACCACTGCTATCATATTTGTGATTTGGCCACTGAAAGGG 648
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227
Db 649 GCCCGCGCAGTGTGGTGAACACATGACATCTTCAGCACCATTCGCCCACTGCTCTC 708
```

```
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 709 CGCAAGACCCAGACATCAACATG---CATCCCTCTCTTTTGGGGAAGATCCTC 765
QY 246 ProIleGluTrpGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
Db 766 TCTGTGGAGCTTGGGAAACAGAGAAATAATATATGCGGTACACCCAGCACAATAC 825
QY 266 PhePheLeuIleGlyProLeuLeuIleProMetLysPheGlnTrpGlnIleLeuMet 285
Db 826 TCTTCTTAATTTGGGCCCCCAGCCTTGTGCTCTCTACTTCCAGTGTATATTTTCTAT 885
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
Db 886 TTTGTTATCCAGCGAAAGAAAGTGGGTGGACTTTGGCTGG 924
```

## RESULT 17

US-09-439-261-5  
Sequence 5, Application US/09439261  
Patent No. 6428990  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pradiip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.P2  
CURRENT APPLICATION NUMBER: US/09/439,261  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 918  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (755)...(755)  
OTHER INFORMATION: r = g or a at position 755  
US-09-439-261-5

Alignment Scores:  
Pred. No.: 4.89e-98 Length: 918  
Score: 923.00 Matches: 167  
Percent Similarity: 74.04% Conservative: 44  
Best Local Similarity: 58.60% Mismatches: 68  
Query Match: 37.88% Indels: 6  
DB: 4 Gaps: 3

US-09-719-601-5 (1-444) x US-09-439-261-5 (1-918)

```
QY 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35
Db 7 CTTACCCCGCGTACTTTCACCTGGAGCGAGGTGGCCAGCGCTCAGGTGGAGGCGG 66
QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
Db 67 TGGCTAGTATCGACCGTAAGGTGTACAACTACATCAGCGAGTTTCACCCGCGCATCCAGG 126
QY 56 GlyGlnArgValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
Db 127 GGTCCCGGTCTATCAGCCTACCGCGGCGAGGATGCCAGGATCCCTTTGTGGCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyLeuAla 95
Db 187 CACATCAACAGGCGCTGTGTGAAGAAGTATATGAATCTCTCTCTGATTGGAGAACTGTCT 246
```

QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115  
DB 247 CCAGACACCCAGCTTGGAGCCACCAAGATTAAGAGCTACAGATGAGTTCGGGAG 306  
QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeu 135  
DB 307 CTGCGGCCACAGTGAGCGGATGGGCTCATGAAGGCCAACCATGCTCTTCTTCGTG 366  
QY 136 LeuLeuAlaHisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGly 155  
DB 367 TACCTGCTGACATCTTGTGATGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 426  
QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175  
DB 427 ACCTGCTTTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486  
QY 176 GlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHis 195  
DB 487 GGTGCTGCTGACATCTTGGGACCTTGGGACCTTGGGACCTTGGGACCTTGGGAC 546  
QY 196 LeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHis 215  
DB 547 CTGCTACATCATTTCTGATGGCCACCTGAAGGGGGCCCCCGCCAGTTGGTGAAC 606  
QY 216 ArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMet 235  
DB 607 ATGCATCTTCAGACCATGCCAGCCCACTGCTCCGCAAGAGCCAGACATCAACAT 666  
QY 236 LeuHis-----ValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLys 253  
DB 667 ---CATCCCTTCT 723  
QY 254 LeuLysTrpLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeu 273  
DB 724 AAAAAATATATGCGGTACACACACACACACATCTTCTCTCTCTCTCTCTCTCTCT 783  
QY 274 LeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrp 293  
DB 784 TTGCTGCT 843  
QY 294 ValAspLeuAlaTrp 298  
DB 844 GTGGACTTGGCTGG 858

RESULT 18  
US-09-227-613-5  
; Sequence 5, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-227-613-5

Alignment Scores:  
Pred. No.: 4, 89e-98 Length: 918  
Score: 923.00 Matches: 167  
Percent Similarity: 74.04% Conservative: 44  
Best Local Similarity: 58.60% Mismatches: 68  
Query Match: 37.86% Indels: 6  
DB: 4 Gaps: 3

US-09-719-601-5 (1-444) x US-09-227-613-5 (1-918)  
QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35  
DB 7 CCACCCCGCGCTTCTTCT 66  
QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55  
DB 67 TGGCTAGTATCAGCCGTAAGGTACACATCAGCGAGTTCACCGCGGATCCAGGG 126  
QY 56 GlyClnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75  
DB 127 GGTCTCCGGGTATCATCCACTACCGCGGCGAGGATGCCAGGATCCCTTTTGGGCTTC 186  
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95  
DB 187 CATCATCAACAGGCTTGTGAAGAGTATATGAACTCTCTCTCTCTCTCTCTCTCTCT 246  
QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115  
DB 247 CCAGACACCCAGCTTGGAGCCCAAGAAATAAAGAGCTGACATGAGTTCGGGAG 306  
QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeu 135  
DB 307 CTGCGGCCACAGTGGAGCGGATGGGCTCATGAAGCCCAACCATGCTCTTCTCTCTG 366  
QY 136 LeuLeuAlaHisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGly 155  
DB 367 TACCTGCTGACATCTTGTGCTGGATGGTGCAGCTGGCTCACCTTTTGGGCTTTGGG 426  
QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175  
DB 427 ACCTCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486  
QY 176 GlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHis 195  
DB 487 GGTCTGCTGACATGACTTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCA 546  
QY 196 LeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHis 215  
DB 547 CTGCTACATCATTTTGTGATGGCCACCTGAAGGGGGCCCCCGCCAGTTGGTGAAC 606  
QY 216 ArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMet 235  
DB 607 ATGCATCTTCAGACCATGCCAGCCCACTGCTCCGCAAGAGCCAGACATCAACAT 666  
QY 236 LeuHis-----ValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLys 253  
DB 667 ---CATCCCTTCT 723  
QY 254 LeuLysTrpLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeu 273  
DB 724 AAAAAATATATGCGGTACACACACACACATCTTCTCTCTCTCTCTCTCTCTCTCT 783  
QY 274 LeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrp 293  
DB 784 TTGCTGCT 843  
QY 294 ValAspLeuAlaTrp 298  
DB 844 GTGGACTTGGCTGG 858

RESULT 19  
US-09-389-681-425  
; Sequence 425, Application US/09389681A  
; Patent No. 6518237  
; GENERAL INFORMATION:  
; APPLICANT: Yuqui, Jiong  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND



; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C3  
; CURRENT APPLICATION NUMBER: US/09/389,681A  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-389-681-425

Alignment Scores:  
Pred. No.: 3,77e-88 Length: 446  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-389-681-425 (1-446)

QY 204 HisLeuLysGlyValAspAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
DB 2 CACTTAAGGGTGCCTCTGCCAATCTGTGGATCATCCCACTCCACACACAGCCAG 61  
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
DB 62 CCTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCAGCTGTTGTTCTGGCGAA 121  
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLys 263  
DB 122 TGGCAGCCCATCGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181  
QY 264 GluTyrPhePheLeuIleGlyProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
DB 182 GAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCATGATTTCCAGTACAGATC 241  
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303  
DB 242 ATCATGACCATGATCGTCATAGAACTGGGGAGACCTGGCGCGCTGGCGCTGAGTACTAC 301  
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323  
DB 302 ATCCGGTTCTTCATCACCTACATCCCTTTCACGACATCCCTGGAGCCCTCTTTCTCTC 361  
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
DB 362 AACCTTCATCAGTTCTCGAGAGCCACTGTTTGTGTGGTCCACAGATGAATCAGATC 421  
QY 344 ValMetGluIleAspGlnGlu 350  
DB 422 GTCATGGAGATTGACCCAGGAG 442

RESULT 20  
US-09-620-405B-425  
; Sequence 425, Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C8  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425

; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-620-405B-425

Alignment Scores:  
Pred. No.: 3,77e-88 Length: 446  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-620-405B-425 (1-446)

QY 204 HisLeuLysGlyValAspAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
DB 2 CACTTAAGGGTGCCTCTGCCAATCTGTGGATCATCCCACTCCACACACAGCCAG 61  
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
DB 62 CCTAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCAGCTGTTTCTGGCGAA 121  
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLys 263  
DB 122 TGGCAGCCCATCGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181  
QY 264 GluTyrPhePheLeuIleGlyProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
DB 182 GAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCATGATTTCCAGTACAGATC 241  
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303  
DB 242 ATCATGACCATGATCGTCATAGAACTGGGGAGACCTGGCGCGCTGGCGCTGAGTACTAC 301  
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323  
DB 302 ATCCGGTTCTTCATCACCTACATCCCTTTCACGACATCCCTGGAGCCCTCTTTCTCTC 361  
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
DB 362 AACCTTCATCAGTTCTCGAGAGCCACTGTTTGTGTGGTCCACAGATGAATCAGATC 421  
QY 344 ValMetGluIleAspGlnGlu 350  
DB 422 GTCATGGAGATTGACCCAGGAG 442

RESULT 21  
US-09-433-826B-425  
; Sequence 425, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433,826B  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-425  
Alignment Scores:  
Pred. No.: 3,77e-88 Length: 446  
Score: 834.00 Matches: 147

Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 34.21%    Indels: 0  
DB: 4    Gaps: 0

US-09-719-601-5 (1-444) x US-09-433-826B-425 (1-446)

```
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
DB 2 CACTTAAAGGGTGGCTCTGCCAACTGGTGGAAATCATGCCCACTTCAGCACCCAGCGCAAG 61
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
DB 62 CCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCAGTGTGTTCTGGGCGAA 121
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
DB 122 TGGCAGCCCATCGATGACGAGGAGAGAGAGCTGAATACCTGCCCTACATCACCAGCAC 181
QY 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
DB 182 GAATACCTTCTTCATCATCACCACCTCCCTCATCCCATGTAATTTCCAGTACCAGATC 241
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
DB 302 ATCCGGTCTTCTCATCATCACCACCTCCCTCATCCCATGTAATTTCCAGTACCAGATC 241
QY 324 AsnPheIleArgPheLeuGluSerHisTyrPheValTrpValThrGlnMetAsnHisIle 343
DB 362 AACTTCATCAGTTCCTGGAGAGCCACTGTTGTGTGGTCCACAGATGAATCACATC 421
QY 344 ValMetGluLeuAspGlnGlu 350
DB 422 GTCATGGAGATTGACCAGGAG 442
```

## RESULT 22

US-09-604-287A-425  
; Sequence 425, Application US/09604287A  
; Patent No. 6586572  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-425

Alignment Scores:  
Pred. No.: 3,77e-88    Length: 446  
Score: 834.00    Matches: 147  
Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 34.21%    Indels: 0  
DB: 4    Gaps: 0

US-09-719-601-5 (1-444) x US-09-604-287A-425 (1-446)

```
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
DB 2 CACTTAAAGGGTGGCTCTGCCAACTGGTGGAAATCATGCCCACTTCAGCACCCAGCGCAAG 61
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
DB 62 CCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCAGTGTGTTCTGGGCGAA 121
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
DB 122 TGGCAGCCCATCGATGACGAGGAGAGAGAGCTGAATACCTGCCCTACATCACCAGCAC 181
QY 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
DB 182 GAATACCTTCTTCATCATCACCACCTCCCTCATCCCATGTAATTTCCAGTACCAGATC 241
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303
DB 242 ATCATGACCATGATCTCCATAGAACTGGTGGAGCCACTGTTGTGTGGTCCACAGATGAATCACATC 421
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
DB 302 ATCCGGTCTTCTCATCATCACCACCTCCCTCATCCCATGTAATTTCCAGTACCAGATC 361
QY 324 AsnPheIleArgPheLeuGluSerHisTyrPheValTrpValThrGlnMetAsnHisIle 343
DB 362 AACTTCATCAGTTCCTGGAGAGCCACTGTTGTGTGGTCCACAGATGAATCACATC 421
QY 344 ValMetGluLeuAspGlnGlu 350
DB 422 GTCATGGAGATTGACCAGGAG 442
```

## RESULT 23

US-09-389-681-313  
; Sequence 313, Application US/09389681A  
; Patent No. 6518237  
; GENERAL INFORMATION:  
; APPLICANT: Yuqui, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C3  
; CURRENT APPLICATION NUMBER: US/09/389,681A  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-389-681-313

Alignment Scores:  
Pred. No.: 3,91e-88    Length: 456  
Score: 834.00    Matches: 147  
Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 34.21%    Indels: 0  
DB: 4    Gaps: 0

US-09-719-601-5 (1-444) x US-09-389-681-313 (1-456)

```
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
DB 3 CACTTAAAGGGTGGCTCTGCCAACTGGTGGAAATCATGCCCACTTCAGCACCCAGCGCAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
DB 63 CCTAACATCTTCCACAAGGATCCCGATGGAACATGCTGCAGTGTGTTCTGGGCGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
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Db 123 TGGGAGCCCATGAGTACGGCAGAGAGAGCTGAATATCTCCCTACATCACCAGCAC 182  
Qy 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283  
Db 183 GAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGATC 242  
Qy 284 IleMetThrMetIleValHisLysAsnTrrpValAspLeuAlaTrrpAlaValSerTyrTyr 303  
Db 243 ATCATGACCATGATGCTCCATAGAACTGGGTGGACCTGGCTGGCCGTAGCTACTAC 302  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323  
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTCTC 362  
Qy 324 AsnPheIleArgPheLeuGluSerHisTrrpPheValTrrpValThrGlnMetAsnHisIle 343  
Db 363 AACTTCATCAGTTCTCTGAGAGCCACTGGTTTGTGGTGCACACATGAATCACATC 422  
Qy 344 ValMetGluIleAspGlnGlu 350  
Db 423 GTCATGGAGATTGACCAGGAG 443

## RESULT 24

US-09-620-405B-313  
; Sequence 313, Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C8  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-620-405B-313

Alignment Scores:  
Pred. No.: 3,918-88 Length: 456  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-620-405B-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrrpAsnHisArgHisPheGlnHisAlaLys 223  
Db 3 CACTTAAAGGGTCCCTCTGCCAACTGGTGAATCATCGCCACTTCCAGCACCCGCAAG 62  
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 63 CCTAACATCTCCACAAGATCCCGATGTGAACATGCTGCACGTGTTTGTCTGGGCGAA 122  
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTrrpLeuProTyrAsnHisGlnHis 263  
Db 123 TGGCAGCCCATCGATCGGCAAGAGAGAGCTGAATATCTCCCTACATCACCAGCAC 182  
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283  
Db 183 GAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGATC 242

Qy 284 IleMetThrMetIleValHisLysAsnTrrpValAspLeuAlaTrrpAlaValSerTyrTyr 303  
Db 243 ATCATGACCATGATGCTCCATAGAACTGGGTGGACCTGGCTGGCCGTAGCTACTAC 302  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323  
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTCTC 362  
Qy 324 AsnPheIleArgPheLeuGluSerHisTrrpPheValTrrpValThrGlnMetAsnHisIle 343  
Db 363 AACTTCATCAGTTCTCTGAGAGCCACTGGTTTGTGGTGCACACATGAATCACATC 422  
Qy 344 ValMetGluIleAspGlnGlu 350  
Db 423 GTCATGGAGATTGACCAGGAG 443

## RESULT 25

US-09-339-338-313  
; Sequence 313, Application US/09339338A  
; Patent No. 6573368  
; GENERAL INFORMATION:  
; APPLICANT: Yuqiu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C2  
; CURRENT APPLICATION NUMBER: US/09/339,338A  
; CURRENT FILING DATE: 1999-06-23  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-339-338-313

Alignment Scores:  
Pred. No.: 3,918-88 Length: 456  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-339-338-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrrpAsnHisArgHisPheGlnHisAlaLys 223  
Db 3 CACTTAAAGGGTCCCTCTGCCAACTGGTGAATCATCGCCACTTCCAGCACCCGCAAG 62  
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 63 CCTAACATCTCCACAAGATCCCGATGTGAACATGCTGCACGTGTTTGTCTGGGCGAA 122  
Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLeuLysTrrpLeuProTyrAsnHisGlnHis 263  
Db 123 TGGCAGCCCATCGATCGGCAAGAGAGAGCTGAATATCTCCCTACATCACCAGCAC 182  
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283  
Db 183 GAATACTTCTTCTGATTGGGCGCGCTGCTCATCCCATGATTTCCAGTACCAGATC 242  
Qy 284 IleMetThrMetIleValHisLysAsnTrrpValAspLeuAlaTrrpAlaValSerTyrTyr 303  
Db 243 ATCATGACCATGATGCTCCATAGAACTGGGTGGACCTGGCTGGCCGTAGCTACTAC 302  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323  
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTCTACGGCATCCTGGGAGCCCTCTTTCTC 362  
Qy 324 AsnPheIleArgPheLeuGluSerHisTrrpPheValTrrpValThrGlnMetAsnHisIle 343

Db 363 AACTTCATCAGGTTCTGGAGACCACTGTTGTGTGGTGCACAGATGATCATC 422  
Qy 344 ValMetGluLeuAspGlnGlu 350  
Db 423 GTCATGGAGATTGACCAAGGAG 443  
RESULT 26  
US-09-433-826B-313  
; Sequence 313, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C4  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-313

Alignment Scores:  
Pred. No.: 3,91e-88 Length: 456  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 4 Gaps: 0  
US-09-719-601-5 (1-444) x US-09-433-826B-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
Db 3 CACTTAAAGGGTGGCTCTGCCAATCGGTGAATCATCGCCACTTCCAGCACCACGCAAG 62  
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 63 CCTAACATCTTCCACAGGATCCCGATGTGACATGTGCACGTGTTGTCTGGCGAA 122  
Qy 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263  
Db 123 TGGCAGCCCATCGAGTACGCGCAAGAAGCTGAATACCTGCCCTCAACAATCACCAGCAC 182  
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
Db 183 GAATACCTTCTTCCTGATGGGCCCGCGCTGCTATCCCATGTATTTCCAGTACCAGATC 242  
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303  
Db 243 ATCATGACCATGATCGTCCATAGAAGTGGGTGGACCTGGCGCTGGGCGCTCAGCTACTAC 302  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323  
Db 303 ATCCGGTTCCTCATCACCCTATCCCTTCTACGGCATCTCTGGAGCCCTCTTTTCTC 362  
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
Db 363 AACTTCATCAGGTTCTGGAGACCACTGGTTGTGTGGTGCACAGATGATCATC 422  
Qy 344 ValMetGluLeuAspGlnGlu 350  
Db 423 GTCATGGAGATTGACCAAGGAG 443

RESULT 27

US-09-604-287A-313  
; Sequence 313, Application US/09604287A  
; Patent No. 6586572  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C7  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-313

Alignment Scores:  
Pred. No.: 3,91e-88 Length: 456  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 4 Gaps: 0  
US-09-719-601-5 (1-444) x US-09-604-287A-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
Db 3 CACTTAAAGGGTGGCTCTGCCAATCGGTGAATCATCGCCACTTCCAGCACCACGCAAG 62  
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 63 CCTAACATCTTCCACAGGATCCCGATGTGACATGTGCACGTGTTGTCTGGCGAA 122  
Qy 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263  
Db 123 TGGCAGCCCATCGAGTACGCGCAAGAAGCTGAATACCTGCCCTCAACAATCACCAGCAC 182  
Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
Db 183 GAATACCTTCTTCCTGATGGGCCCGCGCTGCTATCCCATGTATTTCCAGTACCAGATC 242  
Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyr 303  
Db 243 ATCATGACCATGATCGTCCATAGAAGTGGGTGGACCTGGCGCTGGGCGCTCAGCTACTAC 302  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323  
Db 303 ATCCGGTTCCTCATCACCCTATCCCTTCTACGGCATCTCTGGAGCCCTCTTTTCTC 362  
Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
Db 363 AACTTCATCAGGTTCTGGAGACCACTGGTTGTGTGGTGCACAGATGATCATC 422  
Qy 344 ValMetGluLeuAspGlnGlu 350  
Db 423 GTCATGGAGATTGACCAAGGAG 443

RESULT 28  
US-09-439-261-37  
; Sequence 37, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.

```

1  APPLICANT: HUANG, YUING-SHENG
2
3  TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
4
5  FILE REFERENCE: 6295.US.P2
6
7  CURRENT APPLICATION NUMBER: US/09/439,261
8
9  PRIOR FILING DATE: 1999-11-12
10
11 CURRENT APPLICATION NUMBER: US 08/833,610
12
13 PRIOR FILING DATE: 1997-04-11
14
15 PRIOR APPLICATION NUMBER: PCT/US98/07422
16
17 PRIOR FILING DATE: 1998-04-10
18
19 PRIOR APPLICATION NUMBER: US 09/227,613
20
21 PRIOR FILING DATE: 1998-01-08
22
23 NUMBER OF SEQ ID NOS: 60
24
25 SOFTWARE: FASTSEQ for Windows Version 4.0

```

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; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-4
Alignment Scores:
Pred. No.: 2,25e-59
Score: 585.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 24.00%
Indels: 0
DB: 4
Gaps: 0

US-09-719-601-5 (1-444) x US-09-439-261-4 (1-304)
QY 151 ValPheTyrPheGlyAsnGlyTrrPheProThrLeuIleThrAlaPheValLeuAlaThr 170
Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTTACCTCATCAGCCCTTTGTCTTGTCTACC 60
QY 171 SerGlnAlaGlnAlaGlyTrrPheGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120
QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 121 CCCAAGTGGAAACACCTTTGCCAATAATTCGTCATTGGCCACCTTAAAGGGTGCCTCTGCC 180
QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 181 AACTGGTGGAAATCATGCCACTTCCAGCACCAAGCCCTAACATCTTCCACAAGGAT 240
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
Db 241 CCCGATGTGAACATGCTGCACGTGTTTCTGGCGAATGGCAGCCCATCGAGTACGGC 300
QY 251 Lys 251
Db 301 AAG 303

RESULT 32
US-09-439-261-38
; Sequence 38, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: k = g or t/u at position 5
; NAME/KEY: misc.feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: m = a or c at position 6
US-09-439-261-38
Alignment Scores:
Pred. No.: 6.79e-57
Score: 566.00
Percent Similarity: 83.33%
Best Local Similarity: 70.83%
Query Match: 23.22%
Indels: 1
DB: 4
Gaps: 0

US-09-719-601-5 (1-444) x US-09-439-261-38 (1-449)
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTAGCTCGGCTTCTCTCTACTATGCGCCACTATTGGGCTGAAAGCTTCTCTGG 68
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrrPheValThrIleMet 340
Db 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrrPheValThrIleMet 340
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Db 69 GCCTTTCTTCATA-GTCAGGTTCTGGAAAGCAACTGGTTGTGTGGGTGACACAGATG 127
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 128 AACCATATCCCATGCATGATGATCATGACCGGAACATGGACTGGTTTCCACAGCTC 187
Qy 361 ThrAlaThrCysAsnValGlnGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 188 CAGGCGACATGCAATGTCCACAAGTCTGCCATTCAATGATGCTGTTCAAGTGGACACTCAAC 247
Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisIleAla 400
Db 248 TTCAGATTGACCAATCTTTTCCACAGATGCTCCGACAAATACCAAAAGTGCT 307
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCCTGGTGCAGTCTGTGTGCCAAGCATGCGATAGAGTACCAAGTCCCAAGCCCTGCTG 367
Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db 368 TCAGCCTTGGCGACATCATCCACTCAATAAGGAGTCAAGGCGAGCTCTGGCTAGATGCC 427
Qy 441 TyrLeuHisLys 444
Db 428 TATCTTCAACAA 439

RESULT 33
US-09-227-613-37
; Sequence 37, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-37

Alignment Scores:
Pred. No.: 6,79e-57 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-227-613-37 (1-449)
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTAGTCGCTCTTCTCTCACTATGCGCACTATTGGGCGCTGAAGCTCTCTGG 68
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
Db 69 GCCTTTCTTCATA-GTCAGGTTCTGGAAAGCAACTGGTTGTGTGGGTGACACAGATG 127
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 128 AACCATATCCCATGCATGATGATCATGACCGGAACATGGACTGGTTTCCACAGCTC 187
Qy 361 ThrAlaThrCysAsnValGlnGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 188 CAGGCGACATGCAATGTCCACAAGTCTGCCATTCAATGATGCTGTTCAAGTGGACACTCAAC 247
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Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisIleAla 400
Db 248 TTCAGATTGACCAATCTTTTCCACAGATGCTCCGACAAATACCAAAAGTGCT 307
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCCTGGTGCAGTCTGTGTGCCAAGCATGCGATAGAGTACCAAGTCCCAAGCCCTGCTG 367
Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db 368 TCAGCCTTGGCGACATCATCCACTCAATAAGGAGTCAAGGCGAGCTCTGGCTAGATGCC 427
Qy 441 TyrLeuHisLys 444
Db 428 TATCTTCAACAA 439

RESULT 34
US-09-439-261-3
; Sequence 3, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-3

Alignment Scores:
Pred. No.: 1-23e-56 Length: 655
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-439-261-3 (1-655)
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 3 ACCTTCTAGTCGCTCTTCTCTCACTATGCGCACTATTGGGCGCTGAAGCTCTCTGG 62
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
Db 63 GCCTTTCTTCATA-GTCAGGTTCTGGAAAGCAACTGGTTGTGTGGGTGACACAGATG 121
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 122 AACCATATCCCATGCATGATGATCATGACCGGAACATGGACTGGTTTCCACAGCTC 181
Qy 361 ThrAlaThrCysAsnValGlnGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 182 CAGGCGACATGCAATGTCCACAAGTCTGCCATTCAATGATGCTGTTCAAGTGGACACTCAAC 241
Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisIleAla 400
Db 242 TTCAGATTGACCAATCTTTTCCACAGATGCTCCGACAAATACCAAAAGTGCT 301
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Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420  
Db 302 CCCTGCTGTCAGTCCTTGTGTGCAAGCATGGCATAGTACAGTCCAGGCCCTCTGCTG 361  
Qy 421 ArgAlaLeuLeuAspIleLeuArgSerLeuLysLysSerGlyLysLeuTyrLeuAspAla 440  
Db 362 TCAGCTTCGCCGACATCATCTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCC 421  
Qy 441 TyrLeuHisLys 444  
Db 422 TATCTTCACCAA 433  
RESULT 35  
US-09-719-601-5 (1-444) x US-09-719-601-5 (1-444)  
; Sequence 3, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 655  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; US-09-719-601-5 (1-444) x US-09-719-601-5 (1-655)

Alignment Scores:  
Pred. No.: 1,23e-56 Length: 655  
Score: 566.00 Matches: 102  
Percent Similarity: 83.33% Conservative: 18  
Best Local Similarity: 70.83% Mismatches: 24  
Query Match: 23.22% Indels: 1  
DB: 4 Gaps: 0

US-09-719-601-5 (1-444) x US-09-719-601-5 (1-655)  
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320  
Db 3 ACCTTCTACGTCGCGCTTCTTCTCCTCCTATATGTGCTATGTGGGCTGAAAGCTCTCTGG 62  
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPheValTyrValThrGlnMet 340  
Db 63 GCCTTTTCTTCATA-GTCAGGTTCTCTGAAAGCAACTGGTTGTGTGGGTGACACAGATG 121  
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeu 360  
Db 122 AACCATATTCGCATGCACATTCATGATGACCGGAACATGAGCTGGGTTCACCCAGCTC 181  
Qy 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTyrPheSerGlyHisLeuAsn 380  
Db 182 CAGGCCACATGATGTCACAGTTCCTTCATGACTGGTTCATGACACCTCAAC 241  
Qy 381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
Db 242 TTCAGATTGAGCACCATTCTTTTCCACAGATGCTGACACAAATTACCAAGTGGCT 301  
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420  
Db 302 CCCTGCTGTCAGTCCTTGTGTGCAAGCATGGCATAGTACAGTCCAGGCCCTCTGCTG 361  
Qy 421 ArgAlaLeuLeuAspIleLeuArgSerLeuLysLysSerGlyLysLeuTyrLeuAspAla 440  
Db 362 TCAGCTTCGCCGACATCATCTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCC 421

Qy 441 TyrLeuHisLys 444  
Db 422 TATCTTCACCAA 433  
RESULT 36  
US-08-834-655-1  
; Sequence 1, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUZON, DEBORAH  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,655  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RAE-VENTER, BARBARA  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CGNE.124.00US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 328-4400  
; TELEFAX: (650) 328-4477  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1617 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; US-08-834-655-1

Alignment Scores:  
Pred. No.: 1.51e-43 Length: 1617  
Score: 459.00 Matches: 118  
Percent Similarity: 43.55% Conservative: 88  
Best Local Similarity: 24.95% Mismatches: 183  
Query Match: 18.83% Indels: 84  
DB: 2 Gaps: 14  
US-09-719-601-5 (1-444) x US-08-834-655-1 (1-1617)  
Qy 17 SerValProThrPheSerTyrGluGluIle-----GlnLys 28  
Db 86 AGTGTGAGGACGCTTCTTCTGCGGCCGAGGTTTGAATGCGGAGGCTCTGAATGAGGCGAAG 145  
Qy 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThrLys 48  
Db 146 AAGGATGCGGAGCCCTCTTCTGATGATCATCGACAAAGGTTGATGTCGCGAG 205  
Qy 49 TrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAla 68  
Db 206 TTGTCCTTCATCATCCCGGTGGAAGTGTGTTCAGCAC---GTTGGCAAGGACGCGC 262  
Qy 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88



QY 49 TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAla 68  
 DB 206 TTGTCCTCCGATCATCCCGGTGGAGTGTATCTTCAGCAC--GTTGGCAAGACGGC 262  
 QY 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88  
 DB 263 ACTGAGCTTTTGACACTTTTCAACCC-----GAGGCTGCTGGAGACCTTTGCCAAC 316  
 QY 89 LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys 108  
 DB 317 TTTTACGTTGGTGATATT-----GACGAGACGACCGGATATC---AGAAATGATGAC 367  
 QY 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128  
 DB 368 TTTCGGCGGAGGTCGCGAAGCTGCTGCTGTTCCAGTCTCTGTTACTTACTTACGATTCT 427  
 QY 129 AsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrp 148  
 DB 428 TCCAGGCATATACACCTTCAAGGTCCTGTTCAACCTCTGCATCTGGGGTTTTCGACG 487  
 QY 149 PheThrValPheTyrPheGly---AsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 DB 488 GTCAATGTGCCAAGTGGGGCCAGACCTCGACCTCGCCACAGTGTCTCGGCTGGCTT 547  
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187  
 DB 548 TTGGGTCTGTTCTGGCAGCAGTGGGATGTTGGCTCAGCACTTTTTCATCACCAGTCT 607  
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 DB 608 TTCAGACCGTTCTGGGTGTATCTTTTCGGCGCTCTTTCGGAGTGTCTGCCAGGC 667  
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227  
 DB 668 TTCTCGTCCTCGTGGTGGAGGACAGCAGACACTCACCACCGCCGCCCAACGTCAC 727  
 QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247  
 DB 728 GGCAGGATCCGACATGACCCACCTCTGTTGACCTGGAGTGAG-----775  
 QY 248 GluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePhe 267  
 DB 776 -----CATCGTTGGAGATGTTCTCG 796  
 QY 268 LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMet 287  
 DB 797 GATGTCCAGATGAGGAGCTACCCGATGTGTGTCGCTTC-----ATG 841  
 QY 288 IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla 299  
 DB 842 GTCTGAACACAGCTGTTTACTTCCCATCTCTCGTTGCGCTCTCTCTCTCTGTCG 901  
 QY 300 ValSerTyrTrpIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyVala 319  
 DB 902 CTCACG---TCCATTCTTTGTGCTGCTAACCGGTGAGGCCCAAGCCCTCGGGCGG 958  
 QY 320 LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTrpPheValTrp--- 336  
 DB 959 CGTGTGCCCATCTGTTGGTGCAGCAGCTGTGCTTGGATGTCACCTGG---ACCTGGTAC 1015  
 QY 336 -----336  
 DB 1016 CTCGCCACCATGTTCTCTGTTTATCATCAAGGATCCCGTCAACATGCTGGTGTACTTTTGGTG 1075  
 QY 337 -----ValThrGlnMetAsnHisIleValMet 345  
 DB 1076 TCGAGGCGGTGTGGGAAACTTGTGTGGCGATGCTGTCTCTGCTCACCACACGATG 1135  
 QY 346 GluIle-----AspGlnGluAlaTyrArgAspTrpPheSerSerGluLeuThrAla 362  
 DB 1136 CCGTGTGATCTCGAAGGAGGAGCGGTGATATGATGTTCTTCCAGGACGATCATCAGC 1195

QY 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln 382  
 DB 1196 GGTGCGATGTCACCCGGTCTATTTCACAACTGTTTCCGGTGTGGAATGAACTATCAG 1255  
 QY 383 IleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402  
 DB 1256 ATCGACACACACTGTTCCTTCGATGCTCGCCACAACTTTTCAAGATCCAGCCTGCT 1315  
 QY 403 VallySerLeuCysAlaLysHisGlyIleGluTyrGlnGlyLysProLeuLeuArgAla 422  
 DB 1316 GTCGAGACCTGTGCAAAAAGTACATGTCGATACACACACCGGTATGATCGAGGGA 1375  
 QY 423 LeuLeuAspIleIleArgSerLeuLysLysSerGlyLys 435  
 DB 1376 ACTGCAGAGGCTTTTACCGCTCTGAACGAGGTCTCCAAG 1414  
 RESULT 38  
 US-09-363-574-1  
 ; Sequence 1, Application US/09363574  
 ; Patent No. 6136574  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KNUITZON, DEBORAH  
 ; APPLICANT: MURKERJI, PRADIP  
 ; APPLICANT: HUANG, YUNG-SHENG  
 ; APPLICANT: THURMOND, JENNIFER  
 ; APPLICANT: CHAUDHARY, SUNITA  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
 ; STREET: 2001 FERRY BUILDING  
 ; CITY: SAN FRANCISCO  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/363,574  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WARD, MICHAEL R.  
 ; REGISTRATION NUMBER: 38,651  
 ; REFERENCE/DOCKET NUMBER: CGAB-202 USA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 433-4150  
 ; TELEFAX: (415) 433-8716  
 ; TELEX: N/A  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1617 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; US-09-363-574-1  
 Alignment Scores:  
 Pred. No.: 1,518-43 Length: 1617  
 Score: 459.00 Matches: 118  
 Percent Similarity: 43.55% Conservative: 88  
 Best Local Similarity: 24.95% Mismatches: 183  
 Query Match: 18.83% Indels: 84  
 DB: 3 Gaps: 14  
 US-09-719-601-5 (1-444) x US-09-363-574-1 (1-1617)  
 QY 17 SerValProThrPheSerTrpGluGluIle-----GlnLys 28



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Query Match: 18.83% Indels: 84
DB: 4 Gaps: 14

US-09-719-601-5 (1-444) x US-09-363-526-1 (1-1617)

QY 17 SerValProThrPheSerTrpGluGluLeu-----GlnLys 28
DB 86 AGTGTGAGGACGTTTACTCGGGCGAGGTTTGAATGCGGAGGCTCTGAATGAGGCGAAG 145
QY 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTrpAsnIleThrLys 48
DB 146 AAGGATGCCGAGGACCCCTTCTTGATGATCATCGACACAAAGGTGTACGATGTCGCGGAG 205
QY 49 TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrpAlaGlyGluAspAla 68
DB 206 TTGCTCCCTGATCATCTTTCACGAC-----GAGGCTGCTTGGGAGACTCTTGCCAAAC 262
QY 69 ThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLysPro 88
DB 263 ACTGACGCTCTTGACACTTTTCAACCC-----GAGGCTGCTTGGGAGACTCTTGCCAAAC 316
QY 89 LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys 108
DB 317 TTTTACGTTGCTGATAT-----GACGAGGACGCGGATATC---AAGATGATGATAC 367
QY 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128
DB 368 TTTGCGGCGGAGGTCGCAAGCTCGGTACCTTGTCCAGTCTCTTGTGTTACTACGATTCCT 427
QY 129 AsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrp 148
DB 428 TCCAAGGCATACACGCTTCAAGGCTCTGTTCAACCTCTGCATCTGGGCTTGTGCGAG 487
QY 149 PheThrValPheTrpPheGly---AsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
DB 488 GTCATTTGCGCAAGTGGGCGACAGCTCGACCTCGCCAAAGCTGTCTCGGCTGGCTT 547
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187
DB 548 TTGGGTCTGTCTGGCAGCAGTGGGATGTTGGCTCACGACTTTTGGCATCACCAAGGTC 607
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
DB 608 TTCAGGACCGCTTCTGGGTGATCTTTTCGGCGCTTCTTGGAGGTGTCTGCCAGGCG 667
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisIleAlaLysProAsnIlePhe 227
DB 668 TTTCTCGTCTGTGTGGTGAAGGACAGACAACTCACCACCGCCGCCCCCAACGTCAC 727
QY 228 HisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIle 247
DB 728 GCGGAGATCCGACATGACCCACCTCTGTGTGACCTGGAGTGAG-----775
QY 248 GluTrpGlyLysLysLysLeuLysTrpLeuProTyrAsnHisGlnHisGluTrpPhePhe 267
DB 776 -----CATCGTGTGGAGATGTTCTCG 796
QY 268 LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTrpGlnIleMetThrMet 287
DB 797 GATGTCGCAGATGAGGAGCTGACCCGCGATGTGTGCGGCTTC-----ATG 841
QY 288 IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla 299
DB 842 GTCCTGAACAGACCTGTTTACTTCCCATTCCTCTCGTTGCGGCTCTCTCTGCTGTC 901
QY 300 ValSerTrpTrpIleArgPhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAla 319
DB 902 CTCAG---TCCATTCTTCTGTCTGCTCCCTAACGGTCAAGGTCAGGCCCAAGCCCTCGGCGCG 958
QY 320 LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTrpPheValTrp--- 336
DB 959 CGTGTGCCCATCTCGTTGGTGCAGACGCTGTGCGTTGCGATGCACTGG---ACCTGCTAC 1015

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QY 336 -----336
DB 1016 CTCGCCACCATGTTCTGTTTCATCAGGATCCCGTCAACATGCTGGTGACTTTTTGGTG 1075
QY 337 -----ValThrGlnMetAsnHisIleValMet 345
DB 1076 TCGCAGCGGTGTGCGGAAACTTTGTTGGCGATCGTGTTCGCTCAACCAACGCGTATG 1135
QY 346 GluIle-----AspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeuThrAla 362
DB 1136 CCTGTGATCTCGAAGGAGGAGGCGTGCATGATGATTTCTTCAGGACGATCATCAG 1195
QY 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln 382
DB 1196 GGTGCTGATGCCACCGGCTTATTTGCCAACTGTTGTTCCAGGTTGCGGTTGGAATATCAG 1255
QY 383 IleGluHisIleLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402
DB 1256 ATCAGACACCACTTGTTCCTTCGATGCTCGCCACCACTTTTCAMAGATCCAGCTGCT 1315
QY 403 ValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluLysProLeuLeuArgAla 422
DB 1316 GTCGAGACCTGTGCAAAAAGTACATGTCGATACCACACCGGTATGATCGAGGA 1375
QY 423 LeuLeuAspIleIleArgSerLeuLysSerGlyLys 435
DB 1376 ACTGAGAGGCTTTTACGCGTCTGACGAGGTCTCCAAAG 1414

RESULT 40
US-09-330-235-17
; Sequence 17, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:
; APPLICANT: Knutson, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO.156.00US
; CURRENT APPLICATION NUMBER: US/09/330,235
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/089,043
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; TYPE: DNA
; LENGTH: 1617
; ORGANISM: Mortierella alpina
US-09-330-235-17

Alignment Scores:
Pred. No.: 151e-43 Length: 1617
Score: 459.00 Matches: 118
Percent Similarity: 43.55% Conservative: 88
Best Local Similarity: 24.95% Mismatches: 183
Query Match: 18.83% Indels: 84
DB: 4 Gaps: 14

US-09-719-601-5 (1-444) x US-09-330-235-17 (1-1617)

```

|    |      |   |      |
|----|------|---|------|
| QY | 89   | LeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLys        | 108  |
| DB | 317  | TTTTCACGTTGGTGATATT-----GACGAGAGCGACCGCGATATC---AAGAATGATGAC        | 367  |
| QY | 109  | IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr        | 128  |
| DB | 368  | TTTTCGGCGGAGTCCGCAAGCTCGCTACCTTGTTCAGTCTCTTGGTACTACGATTCT           | 427  |
| QY | 129  | AsnHisValPhePheLeuLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrp        | 148  |
| DB | 428  | TCCAAAGCATATACGCTTCAAGAGTCTCGTTCAACCTCTGCATCTGGGGTTTGTGCGACG        | 487  |
| QY | 149  | PheThrValPheTyrPheGly---AsnGlyTyrPileProThrLeuLeuThrAlaPheVal       | 167  |
| DB | 488  | GTCAATTGTGCCAAGTGGGCGCAGACCTCGACCTCGCCACGCTGCTCTCGGTGCGCTT          | 547  |
| QY | 168  | LeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerVal        | 187  |
| DB | 548  | TTGGGTCTGTCTCGGCAGCAGTCCGATGGTGTGGCTCAGCACTTTTGTGCATCACCAAGTTC      | 607  |
| QY | 188  | TyrArgLysProLysTyrPheAsnHisLeuValHisIstysPheValIleGlyHisLeuLysGly   | 207  |
| DB | 608  | TTCCAGGACCGTTTCGGGGTGATCTTTTCGGCGCCCTTCTTGGGAGTGTCTCCAGGGC          | 667  |
| QY | 208  | AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe        | 227  |
| DB | 668  | TTCTCGTCTCCGCTGGTGGAAAGGACAGCAACAACACTCACCACGCGCGCCCAACGCTCCAC      | 727  |
| QY | 228  | HisIstysAspProAspValAsnMetLeuHisIstysValPheValLeuGlyGluTrpGlnProIle | 247  |
| DB | 728  | GGCGAGATCCCGACATTGACACCCACCCCTCTGTGTGACCTGGAGTGAG-----              | 775  |
| QY | 248  | GluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePhe        | 267  |
| DB | 776  | -----CATCGTTGGAGATGTTCTCTCG   | 796  |
| QY | 268  | LeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMet        | 287  |
| DB | 797  | GATGTCGCCAGATGAGGAGCTGACCCGCGATGTGGTCGGGTTC-----ATG                 | 841  |
| QY | 288  | IleValHisLysAsnTrp-----ValAspLeuAlaTrpAla                           | 299  |
| DB | 842  | GTCTGTAACAGACCTGGTTTACTTCCCATCTCTCGTTGCGCGTCTCTCTCGGTGC             | 901  |
| QY | 300  | ValSerTyrTyrIleArgPhePheIleThrTyrTyrIleProPheTyrGlyIleLeuGlyAla     | 319  |
| DB | 902  | CTCCAG---TCCATCTCTTTGTCTGCCCTAACGGTCAAGCCACAGCCCTCGCGCGCG           | 958  |
| QY | 320  | LeuLeuPheLeuAsnPheIleArg-----PheLeuGluSerHisTyrPheValTrp---         | 336  |
| DB | 959  | CGTGTGCCCATCTCGTTGGTCGAGCAGCTGTCTCGCTTCGATGCACCTGG---ACCTGGTAC      | 1015 |
| QY | 336  | -----   | 336  |
| DB | 1016 | CTGCCACCATGTTCTCTGTTTCATCAAGATCCCGTCAACATGCTGGTGTTACTTTTGGTG        | 1075 |
| QY | 337  | -----ValThrGlnMetAsnHisIleValMet                                    | 345  |
| DB | 1076 | TCGCAGCGGTGTGCGGAACCTGTTGGCGATCGTGTCTCTCGTCAACCAACAGCGTATG          | 1135 |
| QY | 346  | GluIle-----AspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAla            | 362  |
| DB | 1136 | CGTGTGATCTCGAAGGAGGAGCGGTGCGATATGGATTCTTTCAGAAGCAGATCATCAG          | 1195 |
| QY | 363  | ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln        | 382  |
| DB | 1196 | GGTCGTGATGCCACCCGGGTCTATTTGCCACTGTTTCAGGGTGGATTGAACATATCAG          | 1255 |
| QY | 383  | IleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu        | 402  |
| DB | 1256 | ATCGAGCACCACTTGTTCCTCTTCATGCTCGCCACCACTTTTCAAAAGATCCAGCCTGCT        | 1315 |

[illegible]

Search completed: December 10, 2003, 20:07:32  
Job time : 109 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 10:14:26 ; Search time 39 Seconds  
(without alignments)  
2937.830 Million cell updates/sec

Title: US-09-719-601-5  
Perfect score: 2438  
Sequence: 1 MGKGNQGEAGAREVSVPT.....DIIRSLKSKGKLWLDAYLHK 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID     | Description         |
|------------|--------|-------------|--------|--------|---------------------|
| 1          | 2435   | 99.5        | 444    | Q95864 | Q95864 homo sapien  |
| 2          | 2130   | 89.8        | 444    | Q92122 | Q92122 rattus norv  |
| 3          | 2189   | 89.8        | 444    | Q920R9 | Q920R9 mus musculus |
| 4          | 2111   | 86.6        | 386    | Q96H07 | Q96H07 homo sapien  |
| 5          | 2070   | 84.9        | 422    | Q9H3G3 | Q9H3G3 homo sapien  |
| 6          | 1703   | 69.9        | 311    | Q9Y3X4 | Q9Y3X4 homo sapien  |
| 7          | 1687.5 | 69.2        | 445    | Q9AY64 | Q9AY64 sparus aura  |
| 8          | 1668   | 68.4        | 454    | Q98SW7 | Q98SW7 oncorhynch   |
| 9          | 1662   | 68.2        | 452    | Q98W5  | Q98W5 oncorhynch    |
| 10         | 1653   | 67.8        | 454    | Q9QGE2 | Q9QGE2 salmo salar  |
| 11         | 1642   | 67.4        | 454    | Q90ZB8 | Q90ZB8 oncorhynch   |
| 12         | 1599   | 65.6        | 444    | Q9DEX6 | Q9DEX6 cyprinus ca  |
| 13         | 1564.5 | 64.2        | 445    | Q90ZB9 | Q90ZB9 oreochromis  |
| 14         | 1560.5 | 64.0        | 445    | Q9Y5Q0 | Q9Y5Q0 homo sapien  |
| 15         | 1551.5 | 63.6        | 449    | Q9JJE7 | Q9JJE7 mus musculus |
| 16         | 1551.5 | 63.6        | 449    | Q8C4Y5 | Q8C4Y5 mus musculus |

|    |        |      |     |    |        |                     |
|----|--------|------|-----|----|--------|---------------------|
| 17 | 1550.5 | 63.6 | 449 | 11 | Q8K1P9 | Q8K1P9 rattus norv  |
| 18 | 1545.5 | 63.4 | 449 | 11 | Q8CDZ4 | Q8CDZ4 mus musculus |
| 19 | 1516   | 62.2 | 444 | 4  | Q60427 | Q60427 homo sapien  |
| 20 | 1515   | 62.1 | 501 | 4  | Q8NG0  | Q8NG0 homo sapien   |
| 21 | 1512   | 62.0 | 444 | 4  | Q96T10 | Q96T10 homo sapien  |
| 22 | 1508   | 61.9 | 444 | 4  | Q96I39 | Q96I39 homo sapien  |
| 23 | 1508   | 61.9 | 444 | 4  | Q9NYX1 | Q9NYX1 homo sapien  |
| 24 | 1504   | 61.7 | 501 | 4  | Q8NCC7 | Q8NCC7 homo sapien  |
| 25 | 1502.5 | 61.6 | 444 | 4  | Q9NRP8 | Q9NRP8 homo sapien  |
| 26 | 1502   | 61.6 | 444 | 4  | Q96SV3 | Q96SV3 homo sapien  |
| 27 | 1473   | 60.4 | 447 | 11 | Q920R3 | Q920R3 rattus norv  |
| 28 | 1471   | 60.3 | 447 | 11 | Q920L1 | Q920L1 mus musculus |
| 29 | 1470   | 60.3 | 447 | 11 | Q8VC07 | Q8VC07 mus musculus |
| 30 | 1467   | 60.2 | 447 | 11 | Q8ROG8 | Q8ROG8 mus musculus |
| 31 | 1459   | 59.8 | 447 | 11 | Q9EPV4 | Q9EPV4 rattus norv  |
| 32 | 1090.5 | 44.7 | 287 | 11 | Q8BZX7 | Q8BZX7 mus musculus |
| 33 | 908    | 37.2 | 168 | 4  | Q96SV8 | Q96SV8 homo sapien  |
| 34 | 850.5  | 34.9 | 352 | 4  | Q60426 | Q60426 homo sapien  |
| 35 | 724    | 29.7 | 255 | 11 | Q8BV36 | Q8BV36 mus musculus |
| 36 | 651    | 26.7 | 189 | 13 | Q8AYC7 | Q8AYC7 sparus aura  |
| 37 | 531    | 21.8 | 520 | 10 | Q9LEM9 | Q9LEM9 ceratodon p  |
| 38 | 517    | 21.2 | 483 | 10 | Q9LENO | Q9LENO ceratodon p  |
| 39 | 516.5  | 21.2 | 477 | 10 | Q8RXB0 | Q8RXB0 phaeodactyl  |
| 40 | 510    | 20.9 | 525 | 10 | Q9ZRW2 | Q9ZRW2 physcomitrl  |
| 41 | 497    | 20.4 | 459 | 10 | Q944W4 | Q944W4 pythium irr  |
| 42 | 471    | 19.3 | 457 | 3  | Q9UVY3 | Q9UVY3 mortierella  |
| 43 | 470    | 19.3 | 457 | 3  | Q9HEX4 | Q9HEX4 mortierella  |
| 44 | 469    | 19.2 | 457 | 3  | Q8XI73 | Q8XI73 mortierella  |
| 45 | 467    | 19.2 | 446 | 10 | Q9ZTY9 | Q9ZTY9 ricinus com  |

ALIGNMENTS

RESULT 1

|        |   |   |              |      |         |
|--------|---|---|--------------|------|---------|
| Q95864 | ID  | Q95864                                  | PRELIMINARY; | PRT; | 444 AA. |
| AC     | Q95864;   |   |              |      |         |
| DT     | 01-MAY-1999   | (TrEMBLrel. 10, Created)                |              |      |         |
| DT     | 01-MAY-1999   | (TrEMBLrel. 10, Last sequence update)   |              |      |         |
| DT     | 01-OCT-2002   | (TrEMBLrel. 22, Last annotation update) |              |      |         |
| DE     | Delta-6 fatty acid desaturase (Fatty acid desaturase 2) (Hypothetical protein FLJ90458).  |   |              |      |         |
| GN     | FADS2.  |   |              |      |         |
| OS     | Homo sapiens (Human).   |   |              |      |         |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.   |   |              |      |         |
| OX     | NCBI_TaxID=9606;  |   |              |      |         |
| RN     | [1]   |   |              |      |         |
| RP     | SEQUENCE FROM N.A.  |   |              |      |         |
| RX     | MEDLINE=99085046; PubMed=9867867;   |   |              |      |         |
| RA     | Cho H.P., Nakamura M.T., Clarke S.D.;   |   |              |      |         |
| RT     | "Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase.";   |   |              |      |         |
| RL     | J. Biol. Chem. 274:471-477(1999).   |   |              |      |         |
| RN     | [2]   |   |              |      |         |
| RP     | SEQUENCE FROM N.A.  |   |              |      |         |
| RX     | MEDLINE=20318619; PubMed=10860662;  |   |              |      |         |
| RA     | Marquardt A., Stohr H., White K., Weber B.H.F.;   |   |              |      |         |
| RT     | "cDNA cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family.";  |   |              |      |         |
| RL     | Genomics 66:175-183(2000).  |   |              |      |         |
| RN     | [3]   |   |              |      |         |
| RP     | SEQUENCE FROM N.A.  |   |              |      |         |
| RA     | Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masubo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; |   |              |      |         |
| RT     | "NEDO human cDNA sequencing project.";  |   |              |      |         |
| RL     | Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.   |   |              |      |         |
| CC     | -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  |   |              |      |         |
| DR     | EMBL; AF126799; AAD20018.1; -.  |   |              |      |         |



DR EMBL; AF084559; AAG23121.1; --  
 DR EMBL; AX074939; BAC11305.1; --  
 DR HSP; P00171; IES1.  
 DR Genew; HGNC:3575; FADS2.  
 DR InterPro; IPR001199; Cyt\_B5.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Pfam; PF00173; heme\_1; 1.  
 DR PRINTS; PR00363; CYTOCHROMEBS.  
 DR ProDom; PD000612; Cyt\_B5; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 DR PROSITE; PS0255; CYTOCHROME\_B5\_2; 1.  
 DR Hypothetical protein; Heme.  
 KW HYPOTHETICAL PROTEIN; HEME.  
 SQ SEQUENCE 444 AA; 52259 MW; F65CE58076961A7A CRC64;

Query Match 99.5%; Score 2425; DB 4; Length 444;  
 Best Local Similarity 99.5%; Pred. No. 7.1e-209;  
 Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60  
 Db 1 MGKGNQGEAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60

QY 61 GHVAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120  
 Db 61 GHVAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120

QY 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPITLITAPVLATSOAQAGWLQH 180  
 Db 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPITLITAPVLATSOAQAGWLQH 180

QY 181 DYGLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFQHAKPNI FHKDPDVMMLHVFV 240  
 Db 181 DYGLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFQHAKPNI FHKDPDVMMLHVFV 240

QY 241 LGHQPIEYGGKKLKYLPYNHQHEYFELIGPPLIIPMYQYQIIMTMIVHKWVDLAWAV 300  
 Db 241 LGHQPIEYGGKKLKYLPYNHQHEYFELIGPPLIIPMYQYQIIMTMIVHKWVDLAWAV 300

QY 301 SYVIRFTIIPYIGILGALLFNIRFLESHWFWVTQNNHIVMEIDQAYRDFSSQL 360  
 Db 301 SYVIRFTIIPYIGILGALLFNIRFLESHWFWVTQNNHIVMEIDQAYRDFSSQL 360

QY 361 TATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLHKLAPLVKSLCAKHGIEYQEKPLL 420  
 Db 361 TATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLHKLAPLVKSLCAKHGIEYQEKPLL 420

QY 421 RALDDIIRSLKSGKWLDAYLHK 444  
 Db 421 RALDDIIRSLKSGKWLDAYLHK 444

RESULT 2  
 Q9Z122 PRELIMINARY; PRT; 444 AA.

AC Q9Z122; (Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Delta-6 fatty acid desaturase.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Sprague Dawley; TISSUE=Liver;  
 RC MEDLINE=99160394; PubMed=10049752;  
 RA Aki T., Shimada Y., Inagaki K., Higashimoto H., Kawamoto S.,  
 RA Shigeta S., Ono K., Suzuki O.;  
 RT "Molecular cloning and functional characterization of rat delta-6  
 RT fatty acid desaturase";  
 RL Biochem. Biophys. Res. Commun. 255:575-579 (1999).

CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR EMBL; AB021980; BAA75496.1; --  
 DR HSP; P00171; IES1.  
 DR InterPro; IPR001199; Cyt\_B5.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Pfam; PF00173; heme\_1; 1.  
 DR PRINTS; PR00363; CYTOCHROMEBS.  
 DR ProDom; PD000612; Cyt\_B5; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 DR PROSITE; PS0255; CYTOCHROME\_B5\_2; 1.  
 KW HYPOTHETICAL PROTEIN; HEME.  
 SQ SEQUENCE 444 AA; 52380 MW; D9AE0C7AE499A1AE CRC64;

Query Match 99.8%; Score 2190; DB 11; Length 444;  
 Best Local Similarity 87.8%; Pred. No. 8.2e-188;  
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGKGNQGEAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60  
 Db 1 MGKGNQGEAAREVSVPTFSWEEIQKNLRTDGLVIDRKVYNTKWSIQHPGQORVI 60

QY 61 GHVAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120  
 Db 61 GHVAGEDATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTA 120

QY 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPITLITAPVLATSOAQAGWLQH 180  
 Db 121 EDNMLFKTNHVFLLLAHIIALESIAWFTVFYFGNGWIPITLITAPVLATSOAQAGWLQH 180

QY 181 DYGLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFQHAKPNI FHKDPDVMMLHVFV 240  
 Db 181 DYGLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFQHAKPNI FHKDPDVMMLHVFV 240

QY 241 LGHQPIEYGGKKLKYLPYNHQHEYFELIGPPLIIPMYQYQIIMTMIVHKWVDLAWAV 300  
 Db 241 LGHQPIEYGGKKLKYLPYNHQHEYFELIGPPLIIPMYQYQIIMTMIVHKWVDLAWAV 300

QY 301 SYVIRFTIIPYIGILGALLFNIRFLESHWFWVTQNNHIVMEIDQAYRDFSSQL 360  
 Db 301 SYVIRFTIIPYIGILGALLFNIRFLESHWFWVTQNNHIVMEIDQAYRDFSSQL 360

QY 361 TATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLHKLAPLVKSLCAKHGIEYQEKPLL 420  
 Db 361 TATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLHKLAPLVKSLCAKHGIEYQEKPLL 420

QY 421 RALDDIIRSLKSGKWLDAYLHK 444  
 Db 421 RALDDIIRSLKSGKWLDAYLHK 444

RESULT 3  
 Q9ZOR9 PRELIMINARY; PRT; 444 AA.

AC Q9ZOR9; (Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Delta-6 fatty acid desaturase.  
 GN FADS2 OR FADS2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99085046; PubMed=9967867;  
 RX Cho H.P., Nakamura M.T., Clarke S.D.;  
 RA "Cloning, expression, and nutritional regulation of the mammalian  
 RT Delta-6 desaturase";  
 RL J. Biol. Chem. 274:471-477 (1999).  
 CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR EMBL; AF126798; AAD20017.1; --

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DR HSP; P00171; 115U.
DR MGD; MGI:1930079; Fads2.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 444 AA; 52387 MW; 7615D17024D3B771 CRC64;

Query Match      89.8%; Score 2189; DB 11; Length 444;
Best Local Similarity 87.2%; Pred. No. 1e-187;
Matches 387; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MGKGNQGEAGAEERVSPTFSWEIOKHNLRTDGLVIDRKVNIITKWSIQHGGQORVI 60
Db 1 MGKGNQGEAGAEERVSPTFSWEIOKHNLRTDGLVIDRKVNIITKWSIQHGGQORVI 60
Qy 61 GHYAGEDATDAFRAPHPDLFVGVKFLKPLLGELAPEPSQDHGKNSKITEDFRALKTA 120
Db 61 GHYAGEDATDAFRAPHPDLFVGVKFLKPLLGELAPEPSQDHGKNSKITEDFRALKTA 120
Qy 121 EDNLFKTNHVFLLLLAHIIALESIAWFTVYFGNGWIPITLITAFVLATSOAAGWLQH 180
Db 121 EDNLFKTNHVFLLLLAHIIALESIAWFTVYFGNGWIPITLITAFVLATSOAAGWLQH 180
Qy 181 DYGLSVYRKPKWNHVKFVIGHLKGSANWNNHRHFQHHAKPNI FHKDPDNNMLHVFV 240
Db 181 DYGLSVYRKPKWNHVKFVIGHLKGSANWNNHRHFQHHAKPNI FHKDPDNNMLHVFV 240
Qy 241 LGSEWQIEYGVKKLKYLPYNHOHEVFFLIGPLLIPMYFOYQIIMTMIVHKWVDLAWAV 300
Db 241 LGSEWQIEYGVKKLKYLPYNHOHEVFFLIGPLLIPMYFOYQIIMTMIVHKWVDLAWAV 300
Qy 301 SYIIRFFITYIPFYGILGALLFLNFIRFLESHWVWVTQNNHIVMEIDQEAIRDWFSQ 360
Db 301 SYIIRFFITYIPFYGILGALLFLNFIRFLESHWVWVTQNNHIVMEIDQEAIRDWFSQ 360
Qy 361 TATCNVEQSFNDWFSCHLNFOIEHLPTMPRHNLKIAIPLVSLCAKHGIEYQEKPLL 420
Db 361 TATCNVEQSFNDWFSCHLNFOIEHLPTMPRHNLKIAIPLVSLCAKHGIEYQEKPLL 420
Qy 421 RALLDIIRSLKSGKMLDAYLHK 444
Db 421 RALLDIIRSLKSGKMLDAYLHK 444

RESULT 4
Q96H07 PRELIMINARY; PRT; 386 AA.
ID Q96H07 AC Q96H07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fatty acid desaturase 2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC009011; AA09011.1;
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme_1; 1.

Query Match      84.9%; Score 2070; DB 4; Length 422;
Best Local Similarity 96.2%; Pred. No. 4.4e-177;
Matches 380; Conservative 0; Mismatches 5; Indels 10; Gaps 2;

Qy 53 HPGQQRVIGHYAGEDAT---DAFRAPHPDLFVGVKFLKPLLGELAPEPSQDHGKNSKI 109
Db 35 HPAS-----AGHPITGQDAPRAFPDLFVGVKFLKPLLGELAPEPSQDHGKNSKI 87

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QY 110 TEDFRALRKTAEADNMLFKTNHVFLLLAHIIAIESIAWFTVFYFGNGWIPTLITAFVLA 169
Db 88 TEDFRALRKTAEADNMLFKTNHVFLLLAHIIAIESIAWFTVFYFGNGWIPTLITAFVLA 147
QY 170 TSOAQAGWLQHDYGHLSVTRKPKNNHLVHKFVIGHLKGSANWNNHRHFQHHAKNIFHK 229
Db 148 TSOAQAGWLQHDYGHLSVTRKPKNNHLVHKFVIGHLKGSANWNNHRHFQHHAKNIFHK 207
QY 230 DPVNNMLHVFVLGEWQPIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIV 289
Db 208 DPVNNMLHVFVLGEWQPIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIV 267
QY 290 HKWVLDLAWAVSYIRFFIYIPYIGLGLALLFNIRFLESHFWFVWVQMMHIVMEIDQ 349
Db 268 HKWVLDLAWAVSYIRFFIYIPYIGLGLALLFNIRFLESHFWFVWVQMMHIVMEIDQ 327
QY 350 EAYRDMFSSQLTATCNVEQSFNDWFSGLNFOIEHLLPPTPRNHLKIAPLVKSLOAK 409
Db 328 EAYRDMFSSQLTATCNVEQSFNDWFSGLNFOIEHLLPPTPRNHLKIAPLVKSLOAK 387
QY 410 HGIEYQEKPLLRALLDIIRSLKSGKWLDAYLHK 444
Db 388 HGIEYQEKPLLRALLDIIRSLKSGKWLDAYLHK 422

RESULT 6
QY13X4 PRELIMINARY; PRT; 311 AA.
ID QY3X4 AC QY3X4
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN DXFP586C201.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050118; CAB43280.1;
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 311 AA; 37132 MW; BD9DC62CD2D7F4CD CRC64;

Query Match 69.9%; Score 1703; DB 4; Length 311;
Best Local Similarity 99.3%; Pred. No. 2.3e-144;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 AHIIALESIAWFTVFYFGNGWIPTLITAFVLATSOAQAGWLQHDYGHLSVTRKPKNNHLV 197
Db 5 AHIIALESIAWFTVFYFGNGWIPTLITAFVLATSOAQAGWLQHDYGHLSVTRKPKNNHLV 64
QY 198 HKFVIGHLKGSANWNNHRHFQHHAKNIFHKDPVNNMLHVFVLGEWQPIEYGGKKLKYLP 257
Db 65 HKFVIGHLKGSANWNNHRHFQHHAKNIFHKDPVNNMLHVFVLGEWQPIEYGGKKLKYLP 124
QY 258 PYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVLDLAWAVSYIRFFIYIPYIGIL 317
Db 125 PYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVLDLAWAVSYIRFFIYIPYIGIL 184
QY 318 GALLFLNFIREFLESHFWFVWVQMMHIVMEIDQEAYRDMFSSQLTATCNVEQSFNDWFSG 377
Db 185 GALLFLNFIREFLESHFWFVWVQMMHIVMEIDQEAYRDMFSSQLTATCNVEQSFNDWFSG 244
QY 378 HLNFOIEHLLPPTPRNHLKIAPLVKSLOAKHGIEYQEKPLLRALLDIIRSLKSGKWL 437

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Db 245 HLNFOIEHLLPPTPRNHLKIAPLVKSLOAKHGIEYQEKPLLRALLDIIRSLKSGKWL 304
QY 438 LDAYLHK 444
Db 305 LDAYLHK 311

RESULT 7
QYAY64 PRELIMINARY; PRT; 445 AA.
ID QYAY64 AC QYAY64
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative delta 6-desaturase.
GN FD6D.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OC NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Seilliez I., Panzerat S., Kaushik S., Bergot P.;
RT "Cloning, tissue distribution and nutritional regulation of a delta 6-
RT desaturase-like enzyme in gilthead seabream".
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055749; AALI7639.1;
SQ SEQUENCE 445 AA; 51920 MW; B0B98E1AF9F6C9AA CRC64;

Query Match 69.2%; Score 1687.5; DB 13; Length 445;
Best Local Similarity 65.1%; Pred. No. 9.1e-143;
Matches 291; Conservative 63; Mismatches 88; Indels 5; Gaps 2;

QY 1 MGKGG---NQEGAAAEVSVPTFSWEIQKHNLRDTSGLVIDRKVNITKWSIQHGGQ 57
Db 1 MGGGGQLTEPGEPGSRAGV--YTWEEVQSHSSRNDQWLVIDRKVNITKWKARHPGGF 58
QY 58 RVIGHYAGEDATDAFRAFPDLEFVGKFLKPLLIGELAPEEPSODHGKNGKITDDFRALR 117
Db 59 RVINHYAGEDATEAFTAFHDLKFKVQKFLKPLLIGELAAATEPSQDRKNNAAVIODFTLR 118
QY 118 KTAEDMNLFTKNHVFLLLAHIIAIESIAWFTVFYFGNGWIPTLITAFVLATSOAQAGW 177
Db 119 AOAESDGLFRAQPLFFCFLHGLHLLLEALAWLIITLWGTSGWTLTFLSIILATAQOAGW 178
QY 178 LOHDYGHLSVTRKPKNNHLVHKFVIGHLKGSANWNNHRHFQHHAKNIFHKDPVNNMLH 237
Db 179 LOHDYGHLSVTRKPKNNHLVHKFVIGHLKGSANWNNHRHFQHHAKNIFHKDPVNNMLH 238
QY 238 VFLGEMQPIEYGGKKLKYLPYNHOHEYFFLIGPPLIPMYFOYQIIMTMIVHKWVLDLA 297
Db 239 IFVLGDTQPEYGIKKIKYLPYHHQHYFLLVGPPLIPVYFHTQIIRTMTISRHDWDLA 298
QY 298 WAVSYIRFFIYIPYIGILGALLFLNFIREFLESHFWFVWVQMMHIVMEIDQEAYRDFWS 357
Db 299 WMSYLYRLCCYVPLYGLFSGVALISFVRELSHFVWVQMMHLPMDIDHEKHDLT 358
QY 358 SQTATCNVEQSFNDWFSGLNFOIEHLLPPTPRNHLKIAPLVKSLOAKHGIEYQEK 417
Db 359 MQQATCNIEKSVFNDWFSGLNFOIEHLLPPTPRNHYHLVAFLVHALCEKHGIPYQVK 418
QY 418 PLRLALLDIIRSLKSGKWLDAYLHK 444
Db 419 TWWQGIIVDIRSLKSGDLWDLAYLHK 445

RESULT 8
QY98W7 PRELIMINARY; PRT; 454 AA.
ID QY98W7 AC QY98W7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DE 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Putative delta 6-desaturase.
GN F6D6
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Sirisuv S., Yoshizaki G., Kiron V., Takeuchi T., Gen K.;
RC TISSUE=Liver;
RA Seillez I., Panserat S., Kaushik S., Bergot P.;
RT "Cloning, tissue distribution and nutritional regulation of a delta-6-
RT desaturase-like enzyme in rainbow trout.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 130:83-93(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AB074149; BAB71963.1; -.
DR HSP; P00171; IES1.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desat_fam.
DR PRINTS; PR00173; heme_1; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 454 AA; 52398 MW; 1855D811420D537 CRC64;

Query Match 68.4%; Score 1668; DB 13; Length 454;
Best Local Similarity 64.8%; Pred. No. 5.2e-141;
Matches 294; Conservative 65; Mismatches 89; Indels 10; Gaps 2;

QY 1 MGKGNQGEA--AREVSV-----TPSWEEIQKHNLRTDGLVIDRKVNITKWS 50
DB 1 MGCGGQQTESSEPVKGDGPGGRGGSAAVTWEVQKHCHRSQWLVIDREVNIQWAKR 60
QY 51 IOHPGORVIGHYAGEDATDAFRAHPDLEFVGKFLKPLLGELAPEPSODHGKNSKIT 110
DB 61 KRHPGIRVISHFAGEDATDAFVAHPDPNFVRKFLKPLLGELATTPSPDQHGKNAVIV 120
QY 111 EDPRALRTAEDMNLKFNHVPFLLLAHIIALESIAWTFVYFGNGWIPFLITAFVLAT 170
DB 121 QDFQALDRDVEREGLRLARPLFFSLYLGHILLLEALGLLWVGTSLTLLCSLMLAT 180
QY 171 SOAAGWLQHDYGHLSVVRKPKWNHLVHKFVIGHLKGASANNWNRHHPQHAKENIHKD 230
DB 181 SOSQAGWLQHDYGHLSVCKTSNNHVLHKFVIGHLKGASANNWNRHHPQHAKENVFSKD 240
QY 231 PDVNNMLHVPVLGEMOPIEYKGGKLYLPYNHGHVEFFLIGPPLIPMYFOYQIIMTVHK 290
DB 241 PDVNSLHVPVLGDKQVPEYGIKKLYMPVHHQHQYFFLIGPLVIPVFTTQIQTFWFSQ 300
QY 291 KRWDLAWAVSYIRFFITYIPFYIGLALLFLNPIRFLSHFWFVWVTQMNHIVNEIDQ 350
DB 301 RNVVDLAWAMTYLRFCCYYPFFGFGSVALISFVRFLSHFWFVWVTQMNHLPMEIDHE 360
QY 351 AYKDFSSQLTATCNVEQSFNDWFSGLNFQIEHLLPFTPRNHLKIAPLVKSCLCAKH 410
DB 361 RHQDWLTQGLSATCNIEQSTFNDWFSGLNFQIEHLLPFTPRNHLVAPLVALCEKH 420
QY 411 GIEYQKPLRLALLDIIRSLKSKGLWLDAYLHK 444
DB 421 GLPYQVKTQLQAIIDVVGSLKSGDLWLDAYLHK 454

RESULT 9
Q8UWM5 PRELIMINARY; PRT; 452 AA.
AC Q8UWM5
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative delata 6-desaturase.
OS Oncorhynchus masou (Cherry salmon) (Masu salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8020;
RN [1]
RP SEQUENCE FROM N.A.
RA Sirisuv S., Yoshizaki G., Kiron V., Takeuchi T., Gen K.;
RC "delta6-desaturase-like cDNA in masou salmon form2";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AB074149; BAB71963.1; -.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desat_fam.
DR PRINTS; PR00173; heme_1; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 452 AA; 52288 MW; 47B1857733E6CAD0 CRC64;

Query Match 68.2%; Score 1662; DB 13; Length 452;
Best Local Similarity 63.9%; Pred. No. 1.8e-140;
Matches 289; Conservative 68; Mismatches 87; Indels 8; Gaps 1;

QY 1 MGKGNQ-----GEGAAAREVSVTPFSWEEIQKHNLRTDGLVIDRKVNITKWSIQ 52
DB 1 MGCGGQQTESSEPVKGDGPGGRGGSAAVTWEVQKHCHRSQWLVIDREVNIQWAKR 60
QY 53 HPQGORVIGHYAGEDATDAFRAHPDLEFVGKFLKPLLGELAPEPSODHGKNSKIT 112
DB 61 HPQGIRVISHFAGEDATDAFVAHPDPNFVRKFLKPLLGELATTPSPDQHGKNAVIGD 120
QY 113 FRALRTAEDMNLKFNHVPFLLLAHIIALESIAWTFVYFGNGWIPFLITAFVLATSQ 172
DB 121 FOALDRDVEREGLRLARPLFFSLYLGHILLLEALGLLWVGTSLTLLCSLMLATSQ 180
QY 173 AOAGWLQHDYGHLSVVRKPKWNHLVHKFVIGHLKGASANNWNRHHPQHAKENIHKD 232
DB 181 SOAGWLQHDYGHLSVCKSGNNHKLHKFVIGHLKGASANNWNRHHPQHAKENVFSKD 240
QY 233 VNNMLHVPVLGEMOPIEYKGGKLYLPYNHGHVEFFLIGPPLIPMYFOYQIIMTVHK 292
DB 241 INSLHVPVLGDKQVPEYGIKKLYMPVHHQHQYFFLIGPLVIPVFTTQIQTFWFSQ 300
QY 293 WVDLAWAVSYIRFFITYIPFYIGLALLFLNPIRFLSHFWFVWVTQMNHIVNEIDQ 352
DB 301 WVDLAWAMTYLRFCCYYPFFGFGSVALISFVRFLSHFWFVWVTQMNHLPMEIDHERH 360
QY 353 RDNFSSQLTATCNVEQSFNDWFSGLNFQIEHLLPFTPRNHLKIAPLVKSCLCAKHGI 412
DB 361 QDWLTQGLSATCNIEQSTFNDWFSGLNFQIEHLLPFTPRNHLVAPLVALCEKHGL 420
QY 413 EYQKPLRLALLDIIRSLKSKGLWLDAYLHK 444
DB 421 PYQVKTQLQAIIDVVGSLKSGDLWLDAYLHK 452

RESULT 10
Q8QGE2 PRELIMINARY; PRT; 454 AA.
AC Q8QGE2
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative delta-6 fatty acyl desaturase.
GN FADS6.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Hastings N. Jr., Agaba M.K., Tocher D.R., Teale A.J.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
RC Freshwater Teleosts";
RC TISSUE=Liver;
RC Submitters: B. J. Agaba, M. K. Agaba, D. R. Tocher, A. J. Teale;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
RT Freshwater Teleosts";
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF478472; AAL82631.1; -.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 454 AA; 52689 MW; DAEC6D815976BDD9 CRC64;
Query Match 67.8%; Score 1653; DB 13; Length 454;
Best Local Similarity 63.4%; Pred. No. 1.2e-139;
Matches 288; Conservative 69; Mismatches 87; Indels 10; Gaps 2;
QY 1 MGKGNQGEA--AREVSVF-----TFSWEEIQKHNLRDGLVIDRKYNITKWS 50
DB 1 MGCGGQQTESSEPAKGDLFGDGGGSAVYTWEVQHSRSDQWLVIDRKYNITQWA 60
QY 51 IOHPGGORVICHVAGEDATDAFRAHPDLEFVCKFLKPLLIGELAPEEPSQDHGKNSKIT 110
DB 61 KRHPGGIRVISHFAGEDATEAFVAFHLEPNFVRKFLKPLLIGELAPTEPSQDQGNALV 120
QY 111 EDFRALKTAEDMNLFTNHFVFLLLIAHIALESIAWFTVFGNGWIPTLITAFVLAT 170
DB 121 QDFQALRDHVEREGLLARLFFSVLGHILLLEALGLLWGTWSLTLLCSLMAT 180
QY 171 SOAQAQGLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANWNNHRRHFQHHAKPNIFHKD 230
DB 181 SOAQAQGLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANWNNHRRHFQHHAKPNIFHKD 240
QY 231 PDVNLHVFVLGGEQPIEYCKKLYLPYNHQQEYFFLIGPPLLI PMYFQYQIIMTIVH 290
DB 241 PDINSLFVFLGDTQVPEYGIKKLYMPYHHQYFFLIGPPLLI VPFVFNQIIFRTMFSQ 300
QY 291 KNWVDLAWMSYIIRPITIPYFYGILGALLFNFIREFSHWFWVWTONHIVMEIDQE 350
DB 301 RDWVDLAWMSYIIRPITIPYFYGILGALLFNFIREFSHWFWVWTONHIVMEIDQE 360
QY 351 AYRDFSSQLTATCNVQSPFNDFSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKH 410
DB 361 RHQDLWLTQLSATCNIEQSTFNDFSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKH 420
QY 411 GIEYQEKPLRALDIIRSLKSKGLMDLAYLHK 444
DB 421 GVPYQVTKLOKGMTDVVRSLLKSGDLMDLAYLHK 454
RESULT 11
Q90ZE8 PRELIMINARY; PRT; 454 AA.
ID Q90ZE8
AC Q90ZE8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative delta 6-desaturase.
GN F6D6.
OS Oncorhynchus masou (Cherry salmon) (Masu salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8020;
RN [1]
RP SEQUENCE FROM N.A.
RA Hastings N., Agaba M.K., Tocher D.R., Teale A.J., Sargent J.R.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
RC Freshwater Teleosts";
RC TISSUE=Liver;
RC Submitters: B. J. Agaba, M. K. Agaba, D. R. Tocher, A. J. Teale;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
RT Freshwater Teleosts";
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AB070444; BAB63440.1; -.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 454 AA; 52480 MW; 9PAA5EB6A7A5CCF76 CRC64;
Query Match 67.4%; Score 1642; DB 13; Length 454;
Best Local Similarity 63.2%; Pred. No. 1.1e-138;
Matches 287; Conservative 70; Mismatches 87; Indels 10; Gaps 2;
QY 1 MGKGNQGEA--AREVSVF-----TFSWEEIQKHNLRDGLVIDRKYNITKWS 50
DB 1 MGCGGQQTESSEPAKGDLFGDGGGSAVYTWEVQHSRSDQWLVIDRKYNITQWA 60
QY 51 IOHPGGORVICHVAGEDATDAFRAHPDLEFVCKFLKPLLIGELAPEEPSQDHGKNSKIT 110
DB 61 KRHPGGIRVISHFAGEDATEAFVAFHLEPNFVRKFLKPLLIGELAPTEPSQDQGNALV 120
QY 111 EDFRALKTAEDMNLFTNHFVFLLLIAHIALESIAWFTVFGNGWIPTLITAFVLAT 170
DB 121 QDFQALRDHVEREGLLARLFFSVLGHILLLEALGLLWGTWSLTLLCSLMAT 180
QY 171 SOAQAQGLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANWNNHRRHFQHHAKPNIFHKD 230
DB 181 SOAQAQGLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANWNNHRRHFQHHAKPNIFHKD 240
QY 231 PDVNLHVFVLGGEQPIEYCKKLYLPYNHQQEYFFLIGPPLLI PMYFQYQIIMTIVH 290
DB 241 PDINSLFVFLGDTQVPEYGIKKLYMPYHHQYFFLIGPPLLI VPFVFNQIIFRTMFSQ 300
QY 291 KNWVDLAWMSYIIRPITIPYFYGILGALLFNFIREFSHWFWVWTONHIVMEIDQE 350
DB 301 RDWVDLAWMSYIIRPITIPYFYGILGALLFNFIREFSHWFWVWTONHIVMEIDQE 360
QY 351 AYRDFSSQLTATCNVQSPFNDFSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKH 410
DB 361 RHQDLWLTQLSATCNIEQSTFNDFSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKH 420
QY 411 GIEYQEKPLRALDIIRSLKSKGLMDLAYLHK 444
DB 421 GVPYQVTKLOKGMTDVVRSLLKSGDLMDLAYLHK 454
RESULT 12
Q9DEX6 PRELIMINARY; PRT; 444 AA.
ID Q9DEX6
AC Q9DEX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative delta-6 fatty acyl desaturase.
GN FADS6.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariphsyi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Hastings N., Agaba M.K., Tocher D.R., Teale A.J., Sargent J.R.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and

```



RT "cDNA cloning, genomic structure, and chromosomal localization of  
 RT three members of the human fatty acid desaturase family.";  
 RL Genomics 66:175-183(2000).

RP [3]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN=Muscle;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR EMBL; AF134404; AAD31282.1; -;  
 DR EMBL; AF084560; AAG23122.1; -;  
 DR EMBL; BC004901; AAH04901.1; -;  
 DR HSP; P82291; 1CXV.  
 DR InterPro; IPR001199; Cyt B5.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Pfam; PF00173; heme 1; 1.  
 DR PRINTS; PR00363; CYTOCHROMEBS.  
 DR ProDom; PD000612; Cyt B5; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 DR PROSITE; PS50255; CYTOCHROME\_B5\_2; 1.  
 KW Heme.  
 SQ SEQUENCE 445 AA; 51145 MW; 7840EFG6BE055111D CRC64;

Query Match 64.0%; Score 1560.5; DB 4; Length 445;  
 Best Local Similarity 62.3%; Pred. No. 2.2e-131;  
 Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGNQ--EGNAEREVSVPFSEIEIQHNLRTDGLVIDRKYNTKSIQHPGQR 58  
 DB 1 MGCVGPGREGPAQGPALPTFCWEQIRAHQPGDKMLVIERVYDISRMAQRHPGGR 60  
 QY 59 VIGHYAGEDATDAFAFHDPDLBFVGKFLPLIGELAPEPSQDGHKSKITEDFRALRK 118  
 DB 61 LICHGGAEDATDAFAFHQDLNFRKFLQPLIGELAPEPSQDGPLNAQLVEDFRALHQ 120  
 QY 119 TARDNMLFKTNVFFLLLAHIALESIAWFTVFVFGNGWIFTLTAFVLATSQAQWL 178  
 DB 121 AEDMKLFDASPTFFAFLLGHILAMEVLAWLIIYLLGPGWPSALAAFLAISQAQWCL 180  
 QY 179 QHDYGHLSVYRKPKMNLVHKFVIGHLKGSANWNHRRHFQHKAPNIFPKDPDYNMLHV 238  
 DB 181 QHLDLGHASIFTKSRNHNVAQR FVMGQKGFSAHWNFRHFQHKAPNIFPKDPVTAPV 240  
 QY 239 FVLGEWQPIYGGKKLKYLPYNHQBHYFFLIGPPLIPMYFOYQIMTMVHKWVDLAW 298  
 DB 241 FLLEGE--SSVEYGGKKERYLPYNQHLYFFLIGPPLILVNFVENLAYMLVCMQADLLW 299  
 QY 299 AVSYVIRFFTYIPFYGILGALLFLNFIREFLSHFWVVTOMNHVMEIDQAYRDWSS 358  
 DB 300 AASFYARFLLSYLPFYGVPGVLLFFVAVRVLSHFWVVTOMNHIPKEIGHEKRDWSS 359  
 QY 359 QLTATCNVQSFFNDWFSGLHNFQIEHLLFPMPRHNLHKIAPLVKSLCAKHGIYQKRP 418  
 DB 360 QLAATCNVPSLFTNWFSGHLNFQIEHLLFPMPRHNYRVRVAPLVKSLCAKHGLSYEVRP 419  
 QY 419 LLRALLDIIRSLKSKGLMLDAYLHK 444  
 DB 420 FLTALVDIVSLKSKGDIWLDAYLHQ 445

RESULT 15

Q9JUE7 PRELIMINARY; PRT; 449 AA.  
 ID Q9JUE7  
 AC Q9JUE7  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Brain cDNA, clone MNCB-0629, similar to Homo sapiens delta-6 fatty  
 DE acid desaturase (CYB5RP) mRNA.  
 GN FADS3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL;  
 RA Osada N.; Kusuda J.; Tanuma R.; Ito A.; Hirata M.; Sugano S.;  
 RA Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library  
 RT made by oligo-capping method.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR EMBL; AB041560; BAA95044.1; -;  
 DR HSP; P04166; IAMP.  
 DR MCD; MGI:1928740; Fada3.  
 DR InterPro; IPR001199; Cyt B5.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Pfam; PF00173; heme 1; 1.  
 DR PRINTS; PR00363; CYTOCHROMEBS.  
 DR ProDom; PD000612; Cyt B5; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 DR PROSITE; PS50255; CYTOCHROME\_B5\_2; 1.  
 KW Heme.  
 SQ SEQUENCE 449 AA; 51497 MW; 6FDB74EC8C07750B CRC64;

Query Match 63.6%; Score 1551.5; DB 11; Length 449;  
 Best Local Similarity 61.6%; Pred. No. 1.4e-130;  
 Matches 277; Conservative 61; Mismatches 105; Indels 7; Gaps 2;

QY 1 MGKGNQGEAAARE-----VSPFSEIEIQHNLRTDGLVIDRKYNTKSIQHP 54  
 DB 1 MGCVGPGREGPAQGPALPTFCWEQIRAHQPGDKMLVIERVYDISRMAQRHP 60  
 QY 55 GGORVIGHYAGEDATDAFAFHDPDLBFVGKFLPLIGELAPEPSQDGHKSKITEDFR 114  
 DB 61 GGSLLIGHGGAEDATDAFAFHQDLNFRKFLQPLIGELAPEPSQDGAQNAQLIEDFR 120  
 QY 115 ALKRTADNMLFKTNVFFLLLAHIALESIAWFTVFVFGNGWIFTLTAFVLATSQAQ 174  
 DB 121 ALRQAEDMKLFDADTFFALLGHILAMELAWLIIYLLGPGWSSIIAAILAISQAQ 180  
 QY 175 AGWLQHDYGHLSVYRKPKMNLVHKFVIGHLKGSANWNHRRHFQHKAPNIFPKDPDYN 234  
 DB 181 CWCLQHDLGHASIFTKSRNHNVAQR FVMGQKGFSAHWNFRHFQHKAPNIFPKDPVT 240  
 QY 235 MLHVFLVGEWQPIYGGKKLKYLPYNHQBHYFFLIGPPLIPMYFOYQIMTMVHKWV 294  
 DB 241 VAPVFLLEGE--SSVEYGGKKERYLPYNQHLYFFLIGPPLILVNFVENLAYMLVCMQMT 299  
 QY 295 DLAWAVSYVIRFFTYIPFYGILGALLFLNFIREFLSHFWVVTOMNHVMEIDQAYRD 354  
 DB 300 DLLWAASFYARFLLSYLPFYGVPGVLLFFVAVRVLSHFWVVTOMNHIPKEIGHEKRD 359  
 QY 355 WFSQLTATCNVQSFFNDWFSGLHNFQIEHLLFPMPRHNLHKIAPLVKSLCAKHGIY 414  
 DB 360 WASSQLAATCNVPSLFTNWFSGHLNFQIEHLLFPMPRHNYRVRVAPLVKAFCAKGLHY 419  
 QY 415 QEKPLLRALLDIIRSLKSKGLMLDAYLHK 444  
 DB 420 EVKFFLTALVDIVSLKSKGDIWLDAYLHQ 449

RESULT 16

Q8C4Y5 PRELIMINARY; PRT; 449 AA.  
 ID Q8C4Y5  
 AC Q8C4Y5  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Fatty acid desaturase 3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Cerebellum;
EX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK080414; BAC37908.1; -- OCC365378D479989 CRC64;
SQ SEQUENCE 449 AA; 51455 MW; 0CC365378D479989 CRC64;

Query Match 63.6%; Score 1551.5; DB 11; Length 449;
Best Local Similarity 61.6%; Pred. No. 1.4e-130;
Matches 277; Conservative 61; Mismatches 105; Indels 7; Gaps 2;

QY 1 MGKGNQGEAAARE-----VSVPTFSWBIQKHLRTDGLVIDKVNITKWSIQHP 54
DB 1 MGVGEPGGPGREGAPLCPAPLIFRWQIRQHDLPQDKWLVIERRVDIRWAQRHP 60
QY 55 GQORVGHYAGEDATDAFRPHDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFR 114
DB 61 GGSRLIGHGAEADATDAFHAFQDLHFVRKFLKPLLIGELAPEEPSQDGAQNAQIEDFR 120
QY 115 ALRKAEDMNLKTNHVFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAQ 174
DB 121 ALRQAEDMKLFEADSTFFALLGHILAMELLAWLIIYLLGPGWVSSILAALILASOAQ 180
QY 175 AGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGSANWNHRRHFOHAKPNIHKPDVYN 234
DB 181 CWCLQHDLGHASIFTKSRWNHVAQFVNGQLKGFSAHWNFRHFOHAKPNIHKPDVDT 240
QY 235 MLHFVFLGEMQPIEVGKKLKYLPYNHCHVEFFLIGPLIPMYFOYQIIMTVHKWV 294
DB 241 VAPVFLIGE--SSVEGKKRRYLPYNHCHLFFLIGPLIPMLVNFVENLAYMLVCMQWT 299
QY 295 DLAWAVSYIRFFIYIPFYGILGALLFNIRFLESHWFVVTQMNHIVMEIDQAYRD 354
DB 300 DLLWAASYSRFFLSYSPFYGATGTLIIFFAVRVLESWFVVTQMNHVPKEIGEKHRD 359
QY 355 WFSQLTATCNVEQSFNDWFSGLNFQIEHLFTMPRHNLHKLAPLVKSLCAKHGIEY 414
DB 360 WASSQLAATCNVEPSLFDWFSGLNFQIEHLFTMPRHNRVAVPLVAFKACGHLY 419
QY 415 QEKPLLRALLDIIRSLKSGKWLDAYLHK 444
DB 420 EVKPFALTALVDIIGSLKSGDIWLDAYLHQ 449

RESULT 17
Q8KIP9 PRELIMINARY; PRT; 449 AA.
AC Q8KIP9;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-WAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative fatty acid desaturase.
GN FADS3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley; Tissue=Liver;
RA D'Andrea S., Guillou H., Jan S., Daval S., Rioux V., Legrand P.;
RT "Characterization of a novel putative fatty acid desaturase from
RT rat.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ494720; CAD38527.1; --
DR InterPro; IPR001199; Cyt_B5.

DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000812; Cyt_B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
KW Heme.
KW PROSITE; PS0255; CYTOCHROME_BS_2; 1.
SQ SEQUENCE 449 AA; 51467 MW; E2E33662095855AB CRC64;

Query Match 63.6%; Score 1550.5; DB 11; Length 449;
Best Local Similarity 61.8%; Pred. No. 1.8e-130;
Matches 278; Conservative 61; Mismatches 104; Indels 7; Gaps 2;

QY 1 MGKGNQGEAAARE-----VSVPTFSWBIQKHLRTDGLVIDKVNITKWSIQHP 54
DB 1 MGVGEPGGPGREGAPLCPAPLIFRWQIRQHDLPQDKWLVIERRVDIRWAQRHP 60
QY 55 GQORVGHYAGEDATDAFRPHDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFR 114
DB 61 GGSRLIGHGAEADATDAFHAFQDLHFVRKFLKPLLIGELAPEEPSQDGAQNAQIEDFR 120
QY 115 ALRKAEDMNLKTNHVFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAQ 174
DB 121 ALRQAEDMKLFEADSTFFALLGHILAMELLAWLIIYLLGPGWVSSILAALILASOAQ 180
QY 175 AGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGSANWNHRRHFOHAKPNIHKPDVYN 234
DB 181 CWCLQHDLGHASIFTKSRWNHVAQFVNGQLKGFSAHWNFRHFOHAKPNIHKPDVDT 240
QY 235 MLHFVFLGEMQPIEVGKKLKYLPYNHCHVEFFLIGPLIPMYFOYQIIMTVHKWV 294
DB 241 VAPVFLIGE--SSVEGKKRRYLPYNHCHLFFLIGPLIPMLVNFVENLAYMLVCMQWT 299
QY 295 DLAWAVSYIRFFIYIPFYGILGALLFNIRFLESHWFVVTQMNHIVMEIDQAYRD 354
DB 300 DLLWAASYSRFFLSYSPFYGATGTLIIFFAVRVLESWFVVTQMNHVPKEIGEKHRD 359
QY 355 WFSQLTATCNVEQSFNDWFSGLNFQIEHLFTMPRHNLHKLAPLVKSLCAKHGIEY 414
DB 360 WASSQLAATCNVEPSLFDWFSGLNFQIEHLFTMPRHNRVAVPLVAFKACGHLY 419
QY 415 QEKPLLRALLDIIRSLKSGKWLDAYLHK 444
DB 420 EVKPFALTALVDIIGSLKSGDIWLDAYLHQ 449

RESULT 18
Q8CDZ4 PRELIMINARY; PRT; 449 AA.
AC Q8CDZ4;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Fatty acid desaturase 3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK029318; BAC26393.1; --
SQ SEQUENCE 449 AA; 51495 MW; 4F0B689C90F22185 CRC64;

Query Match 63.4%; Score 1545.5; DB 11; Length 449;
Best Local Similarity 61.3%; Pred. No. 4.9e-130;
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DR PRINTS: PR00363; CYTOCHROMEBS.
DR ProDom: PD000612; Cyt B5; 1.
DR ProDom: PD001081; FA_desat_fam; 2.
DR ProSITE; PS00255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 444 AA; 51954 MW; B288BA9346A8A8A CRC64;

Query Match 61.9%; Score 1508; DB 4; Length 444;
Best Local Similarity 61.7%; Pred. No. 1.1e-126;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKNLRTDSGLVIDRKYNIITKWSIOHPGQGVIGHYAGED 67
DB 7 AAEATAAGPTPRYFTDWEVAQRSGCEERWLVIDRKYNISEFTRRHPPGSGRVISHYAGQD 66
QY 68 ATDAFAFAPDLFEVGFVKPLKPLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLFK 127
DB 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSFPTKNEKLTDFEFLRATVERMGLMK 126
QY 128 TNHVFLLLAHIALESIAFTVYFGNGWPTLTITAPVLATSOAQAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHLLDGAALTLWVFGTSFPLLCVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHLVHKFVIGHLKASANNWNRHFFQHHAKPNIFHKDPDYNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLHFFVIGHLKGPASWNNHWFQHHAKPNCFRKDPDINN-HPFFPALGKIL 245
QY 246 PIEYGGKKLYLPYNHQBHYFFLIGPPLIPYFQYQIIMTVIHKWVVDLAWAVSYIR 305
DB 246 SVELGQKKKYPYNNHQBHYFFLIGPPLIPYFQYQIIMTVIHKWVVDLAWAVSYIR 305
QY 306 FFITYPFYIGLALLFLNFIRESHFVFWVQNNHIVNEIDQEAAYRDFSSQLTATCN 365
DB 306 FFITYPVLGLKAFGLGFFIVFLESNFWVQNNHIVNEIDQEAAYRDFSSQLTATCN 365
QY 366 VEGSFNDWFSGLNFQIEHLLFPTPRNLHKLAPLVKSLCAKHGIEYQERPLRLALLD 425
DB 366 VHKSAFNDWFSGLNFQIEHLLFPTPRNLHKLAPLVKSLCAKHGIEYQERPLRLALLD 425
QY 426 IIRSLKSGKWLDAYLHK 444
DB 426 IIRSLKSGKWLDAYLHQ 444

RESULT 24
Q8NCC7 PRELIMINARY; PRT; 501 AA.
AC Q8NCC7, 2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90338.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NDO human cDNA sequencing project";
RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AK074819; BAC11229.1;
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.

Q9NYX1 PRELIMINARY; PRT; 444 AA.
AC Q9NYX1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Delta-5 fatty acid desaturase.
GN FADS5
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Leonard A.E., Kelder B., Bobik E.G., Chuang L.-T., Parker-Barnes J.M.,
RA Thurmond J.W., Kroeger P.E., Kopchick J.J., Huang Y.-S., Mukerji P.;
RT "cDNA cloning and characterization of human delta-5 desaturase
RT involved in the biosynthesis of arachidonic acid.";
RL Biochem. J. 347:719-724(2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF226273; AA70457.1;
DR HSP; P04166; IBSM.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA_desat_fam.
DR PRINTS; PR00363; CYTOCHROMEBS.

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DR PROSITE, PSS0255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
SQ SEQUENCE 501 AA; 57827 NW; C729B0DA3C54053C CRC64;

Query Match
Best Local Similarity 61.7%; Score 1504; DB 4; Length 501;
Matches 270; Conservative 63; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAESEVSVPT---FSWEEIQKHLRTDGLVIDRKYNTKWSIQHPGGQORVIGHYAGED 67
DQ 64 AAEAAQGGTPRYFTWDEVAQSGCEERLWIDRKYNTSEPTREHFGSGSRVISHYAGD 123
QY 68 ATDAFRAHPDLEFVGKFLKPLIGELAPEBSQDHGKNSKITEDFRALRKTAEADNMLFK 127
DQ 124 ATDPFVAHINKGLVKYKYNLSLIGELPEQSPFETKNEKLTDFRELRATVERMGLMK 183
QY 128 TNHVFLLLAHIIALESIAWTFVFGNGWIPITLITAFVLATSOAQAGWLQHDYGHLSV 187
DQ 184 ANHVFLLYLLHLLDGAWLTLWFGTSFLPFLLCVLLSAVQAQAGWLQHDYGHLSV 243
QY 188 YRKPKNHLVHKFVGHILKASANNWNRHFOHAKPNIFHKDPVNMJH--VFVLGEWQ 245
DQ 244 FTSKWNHLHFFVGHILKASANNWNRHFOHAKPNIFHKDPVNMJH--VFVLGEWQ 302
QY 246 PIEYGGKKLYLPYNHGEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIR 305
DQ 303 SVELGQKKKYNPNHGEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIR 362
QY 306 PFTIIPFVIGLALFNFRFLSHWFWVVTQNNHIVMEIDQAYRDWFSSQLTATCN 365
DQ 363 FLLTVPLGLKAFGLFVFRFLSHWFWVVTQNNHIVMEIDQAYRDWFSSQLTATCN 422
QY 366 VEQSFNDFWFSHNLFOIEHLFPMPRNHLKIAPLVKSACAKHGLEVOEKPLLRALLD 425
DQ 423 VKKSAFNDWFSHNLFOIEHLFPMPRNHLKIAPLVKSACAKHGLEVOEKPLLRALLD 482
QY 426 IIRSKGSKGLWLDAYLHK 444
DQ 483 IIRSKGSKGLWLDAYLHQ 501

RESULT 25
Q9NRP8 PRELIMINARY; PRT; 444 AA.
AC Q9NRP8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Delta-5 desaturase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20069725; PubMed=10601301;
RA Cho H.P., Nakamura M., Clarke S.D.;
RT "Cloning, expression, and fatty acid regulation of the human delta-5
RT desaturase.";
RL J. Biol. Chem. 274:37335-37339(1999).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF199596; AAF29378.1; -.
DR HSP; P04166; 1BSM.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 444 AA; 51980 NW; 78D476EB107891B2 CRC64;

Query Match
Best Local Similarity 62.4%; Score 1502.5; DB 4; Length 444;
Matches 266; Conservative 62; Mismatches 95; Indels 3; Gaps 2;

QY 21 FSWEEIQKHLRTDGLVIDRKYNTKWSIQHPGGQORVIGHYAGEDATDAFRAHPDLE 80
DQ 20 FTWDEVAQSGCEERLWIDRKYNTSEPTREHFGSGSRVISHYAGDATDPFVAHINKG 79
QY 81 FVCKFLKPLIGELAPEBSQDHGKNSKITEDFRALRKTAEADNMLFKTNHVFLLLAHI 140
DQ 80 LVKKYKYNLSLIGELPEQSPFETKNEKLTDFRELRATVERMGLMKANHVFLLYLLHI 139
QY 141 IALESIAWTFVFGNGWIPITLITAFVLATSOAQAGWLQHDYGHLSVYRKPKNHLVHKF 200
DQ 140 LLDGAAWLTLWFGTSFLPFLLCVLLSAVQAQAGWLQHDYGHLSVYRKPKNHLVHKF 199
QY 201 VIGHLKGASANNWNRHFOHAKPNIFHKDPVNMJH--VFVLGEWQPIEYGGKKLYLP 258
DQ 200 VIGHLKGASANNWNRHFOHAKPNIFHKDPVNMJH--VFVLGEWQPIEYGGKKLYLP 258
QY 259 YNHQHEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIRFITYIPFYGILG 318
DQ 259 YNHQHEYFPLIGPPLIPMYFOYQIIMTMIHKNWVDLAWAVSYVIRFITYIPFYGILG 318
QY 319 ALLFNLFRFLSHWFWVVTQNNHIVMEIDQAYRDWFSSQLTATCNVQSFNDFWFSGH 378
DQ 319 FLGLFTFVFRFLSHWFWVVTQNNHIVMEIDQAYRDWFSSQLTATCNVQSFNDFWFSGH 378
QY 379 LNFQIEHLFPMPRNHLKIAPLVKSACAKHGLEVOEKPLLRALLDIRSKGSKGLW 438
DQ 379 LNFQIEHLFPMPRNHLKIAPLVKSACAKHGLEVOEKPLLRALLDIRSKGSKGLW 438
QY 439 DAYLHK 444
DQ 439 DAYLHQ 444

RESULT 26
Q96SV3 PRELIMINARY; PRT; 444 AA.
AC Q96SV3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ14616.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayaishi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Watanabe M., Hosoi R. T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Nanamiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AK027522; BAB55173.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
SQ SEQUENCE 444 AA; 51934 NW; 4B7046AE343058B CRC64;
```

Query Match 61.6%; Score 1502; DB 4; Length 444;  
 Best Local Similarity 61.7%; Pred. No. 3.9e-126;  
 Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKHLRTDGLVIDRKYVNIWKSIQHPGQORVIGHYAGED 67  
 DB 7 AETAAGGTPPYFTWDEVAQSGCEERWLVIDRKYVNISEFTRRHPGGSRVISHYAGD 66

QY 68 ATDAFAFADLEFVCKFLKPLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFK 127  
 DB 67 ATDFPFAFINKLVKYNLSLIGELSPESQSFSEFTKNELTDBFRELRATVERMGLMK 126

QY 128 THNVFLLLAHIALESIAFWTFVFGNGWPTLITAFVLATSAQAQWLOHGYCHLSV 187  
 DB 127 ANHVFFLLVLLHLLDGAWLTLWVGTSFLPFLLCVLLSAVQAQWLOHDFGLSV 186

QY 188 YRPKPNHLVHKVIGHLKGASANNVHHRFHQHAKEPNIFHKDPDNNMLH--VFVLGHWQ 245  
 DB 187 FSTSKVNLHLHFEVIGHLKGASANNVHHRFHQHAKEPNIFHKDPDNNMLH--HPFFFGALGKIL 245

QY 246 PIEYGGKKLYLPYNHGHYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIR 305  
 DB 246 SVELGQKKKYPYNHGHYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIR 305

QY 306 FFIYIPFYGILGALLFLNFIRESHFWVWVTQNNHIVMEIDQEAIRDWFSQLTATCN 365  
 DB 306 FELTYVPLGLKAFGLFTVRESNFWVWVTQNNHIVMEIDQEAIRDWFSQLTATCN 365

QY 366 VEGSFNDPFGHLNFIRESHFWVWVTQNNHIVMEIDQEAIRDWFSQLTATCN 425  
 DB 366 VHSASFNDPFGHLNFIRESHFWVWVTQNNHIVMEIDQEAIRDWFSQLTATCN 425

QY 426 IIRSLKSGKMLDAYLHK 444  
 DB 426 IIRSLKSGKMLDAYLHK 444

RESULT 27  
 Q920R3 PRELIMINARY; PRT; 447 AA.

AC Q920R3 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Delta-5 fatty acid desaturase.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC TISSUE=Liver;  
 RA Ingaki K., Aki T., Shimada Y., Kawamoto S., Shigeta S., Ono K.,  
 RA Suzuki O.;  
 RA "Cloning and expression of rat liver delta-5 fatty acid desaturase";  
 RC Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RL -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR EMBL; AB052085; Cyt B5.  
 DR InterPro; IPR001199; Cyt B5.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Pfam; PF00173; heme\_1; 1.  
 DR PRINTS; PR00363; CYTOCHROME B5.  
 DR ProDom; PD000612; Cyt B5; 1.  
 DR ProDom; PD01081; FA\_desat\_fam; 2.  
 DR PROSITE; PS02055; CYTOCHROME\_B5\_2; 1.  
 KW Heme  
 SQ SEQUENCE 447 AA; 52482 MW; 764D7D7C9AA3F7BE CRC64;

Query Match 60.4%; Score 1473; DB 11; Length 447;  
 Best Local Similarity 61.8%; Pred. No. 1.5e-123;

Matches 264; Conservative 59; Mismatches 100; Indels 4; Gaps 3;

QY 21 PSNEEI-QKHLRTDGLVIDRKYVNIWKSIQHPGQORVIGHYAGEDATDAFRAHPDL 79  
 DB 22 FTWEEVAQSGRGRKWLVIDRKYVNIWFSRRHPGGSRVISHYAGQDAIDFVAFHINK 81

QY 80 EFYVKELKPLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFKTNHVFLLLAH 139  
 DB 82 GLVRKYNLSLIGELAPEEPSPEPTKNELTDBFRELRATVERMGLMKANHLFFFLYLLH 141

QY 140 IIALESIAFWTFVFGNGWPTLITAFVLATSAQAQWLOHGYCHLSVYRKPKNHLVHK 199  
 DB 142 ILLDVAAWTLWVGTSFLPFLLCVLLSAVQAQWLOHDFGLSVFSTWTNHLVHH 201

QY 200 FVIGHLKGASANNVHHRFHQHAKEPNIFHKDPDNNMLH--VFVLGHWQPIEYGGKKLYL 257  
 DB 202 FVIGHLKGASANNVHHRFHQHAKEPNIFHKDPDNNMLH--HPLFFALGKVLSELGKEKKCHM 260

QY 258 PYNHGHYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIRFIPTIYFVIGIL 317  
 DB 261 PYNHGHYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIRFIPTIYFVIGIL 320

QY 318 GALLFLNFIRESHFWVWVTQNNHIVMEIDQEAIRDWFSQLTATCNVEQSFNDWFSG 377  
 DB 321 GLCLCFIVRESNFWVWVTQNNHIVMEIDQEAIRDWFSQLTATCNVEQSFNDWFSG 380

QY 378 HLNFQIEHHLFPTPRNHLKIAPLVKSACAKGIEYQEKPLLRALLDIIRSLKSGKML 437  
 DB 381 HLNFQIEHHLFPTPRNHLKIAPLVKSACAKGIEYQEKPLLRALLDIIRSLKSGKML 440

QY 438 LDAYLHK 444  
 DB 441 LDAYLHQ 447

RESULT 28  
 Q920L1 PRELIMINARY; PRT; 447 AA.

AC Q920L1 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Delta-5 desaturase.  
 GN 0710001003RIK OR D5D.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6; TISSUE=Liver;  
 RA Matsuzaka T., Shimano H.;  
 RT "Dual gene regulation of mouse delta-5 and -6 desaturases by SREBP-1  
 and PPAR alpha";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR EMBL; AB072976; BAC69894.1; -.  
 DR EMBL; AK083959; BAC39079.1; -.  
 DR MGD; MGI:1923517; 0710001003RIK.  
 DR InterPro; IPR001199; Cyt B5.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Pfam; PF00173; heme\_1; 1.  
 DR PRINTS; PR00363; CYTOCHROME B5.

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DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 447 AA; 52333 MW; 1C69B61DF919A009 CRC64;

Query Match 60.3%; Score 1471; DB 11; Length 447;
Best Local Similarity 61.6%; Pred. No. 2.3e-123;
Matches 263; Conservative 62; Mismatches 98; Indels 4; Gaps 3;

QY 21 FSWEBI-QKHNLRITDGLVIDRKVNITKWSIQHPGQGVICHYAGEDATDAFRAHPDL 79
DB 22 FTWEEVAQSGREKRWLVDRKVNISDFSRHPGGSRVISHYAGQDATDFVAFHINK 81
QY 80 EYVGLKPLLLIGELAPESPDSODHGKNSKITEDFRALRKTAEADMLFKTNHVFLLLLAH 139
DB 82 GLVRKYMSLLIGELAPESPDPKTKALTDRELRATVERMGLMKNHLLFVYLLH 141
QY 140 IIALESIAWTFVYFGNGWIPITLITAFVLATSAQAGWLQHDYGHLSVYRKPNHVLHK 199
DB 142 ILLDVAWLTLWIFGTSVLPFCALLSTVQAQAGWLQHDYGHLSVYRKPNHVLHK 201
QY 200 FVIGHLKASANNWNRHFRHAKENI PHKDPDVMNLH--VFVLGEWQPIEYGGKKLYL 257
DB 202 FVIGHLKAPASANNWNRHFRHAKENI PHKDPDVMNLH--HPLFFALGKVLPELGRKKCHM 260
QY 258 PYNHOHEVFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITYIPFYGIL 317
DB 261 PYNHQKVFLLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITYIPFYGIL 320
QY 318 GALLFLNFRFLESWFVWVTQNMHIVMEIDQEAAYRDWFSQATATCNVEQSFENDWFSG 377
DB 321 GFLGFFIVRFLESWFVWVTQNMHIVMEIDQEAAYRDWFSQATATCNVEQSFENDWFSG 380
QY 378 HLNFOIEHLPTMPRHNLKIAPLVKSICAKHGYEOEKPLLRALLDITIRSLKSKGLW 437
DB 381 HLNFOIEHLPTMPRHNLKIAPLVKSICAKHGYEOEKPLLRALLDITIRSLKSKGLW 440
QY 438 LDAYLHK 444
DB 441 LDAYLHQ 447

RESULT 29
Q8VC07 PRELIMINARY; PRT; 447 AA.
AC Q8VC07;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 23, Last annotation update)
DE Hypothetical 52.3 kDa protein.
GN 0710001003RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC Tissue=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC022139; AAH26831.1;
DR EMBL; BC026831; AAH26831.1;
DR MGD; MGI:1923517; 0710001003RIK.
DR InterPro; IPR001199; Cyt B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat_fam.
DR Pfam; PF00487; FA desaturase; 1.

DR ProDom; PD00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
SQ SEQUENCE 447 AA; 52337 MW; FOAFCCAL2919B8B2 CRC64;

Query Match 60.3%; Score 1470; DB 11; Length 447;
Best Local Similarity 61.4%; Pred. No. 2.9e-123;
Matches 262; Conservative 63; Mismatches 98; Indels 4; Gaps 3;

QY 21 FSWEBI-QKHNLRITDGLVIDRKVNITKWSIQHPGQGVICHYAGEDATDAFRAHPDL 79
DB 22 FTWEEVAQSGREKRWLVDRKVNISDFSRHPGGSRVISHYAGQDATDFVAFHINK 81
QY 80 EYVGLKPLLLIGELAPESPDSODHGKNSKITEDFRALRKTAEADMLFKTNHVFLLLLAH 139
DB 82 GLVRKYMSLLIGELAPESPDPKTKALTDRELRATVERMGLMKNHLLFVYLLH 141
QY 140 IIALESIAWTFVYFGNGWIPITLITAFVLATSAQAGWLQHDYGHLSVYRKPNHVLHK 199
DB 142 ILLDVAWLTLWIFGTSVLPFCALLSTVQAQAGWLQHDYGHLSVYRKPNHVLHK 201
QY 200 FVIGHLKASANNWNRHFRHAKENI PHKDPDVMNLH--VFVLGEWQPIEYGGKKLYL 257
DB 202 FVIGHLKAPASANNWNRHFRHAKENI PHKDPDVMNLH--HPLFFALGKVLPELGRKKCHM 260
QY 258 PYNHOHEVFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITYIPFYGIL 317
DB 261 PYNHQKVFLLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITYIPFYGIL 320
QY 318 GALLFLNFRFLESWFVWVTQNMHIVMEIDQEAAYRDWFSQATATCNVEQSFENDWFSG 377
DB 321 GFLGFFIVRFLESWFVWVTQNMHIVMEIDQEAAYRDWFSQATATCNVEQSFENDWFSG 380
QY 378 HLNFOIEHLPTMPRHNLKIAPLVKSICAKHGYEOEKPLLRALLDITIRSLKSKGLW 437
DB 381 HLNFOIEHLPTMPRHNLKIAPLVKSICAKHGYEOEKPLLRALLDITIRSLKSKGLW 440
QY 438 LDAYLHK 444
DB 441 LDAYLHQ 447

RESULT 30
Q8ROG8 PRELIMINARY; PRT; 447 AA.
AC Q8ROG8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical 52.4 kDa protein.
GN 0710001003RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; BC026848; AAH26848.1;
DR MGD; MGI:1923517; 0710001003RIK.
DR InterPro; IPR001199; Cyt B5.
DR ProDom; PD000612; Cyt B5.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA desat_fam; 2.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
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KW Hypothetical protein; Heme.
SQ SEQUENCE 447 AA; 52351 MW; 4AE76A132B809C9 CRC64;

Query Match      60.2%; Score 1467; DB 11; Length 447;
Best Local Similarity 61.1%; Pred. No. 5.3e-123;
Matches 261; Conservative 64; Mismatches 98; Indels 4; Gaps 3;

QY 21 FSWEEI-QKHNLRDGLVIDRKVNITKWSIOHFGGQVIGHYAGEDATDAFAPHDL 79
DB 22 FTWEEVAQRSGREKERLWVIDRKVNISDFSRHFGGSRVISHYAGODATDPFVAFHINK 81
QY 80 EFGVKELKPLLIGELAPEESQDHGKNSKITDPRALRKTAEEDMNLKTNHVFLLLLAH 139
DB 82 GLVEKYNLSLIGELAPEQSFEPTKNKALTDEFRELATVERMGLMKANHLFFLYLLH 141
QY 140 IIALESIANFTVPYFGNGWPTLITAFVLATSOAQAGWLQHDYGHLSVYRKPKNHLVHK 199
DB 142 ILLLDVAAMLTLWFTGSLVPFTLCVLLSTVQAQAGWLQHDYGHLSVSTSTWNLVHH 201
QY 200 FVIGHLKGASANNWNRHFOHAKPNI FHKDPDNNMLH--VFVLGEWQPIEYKKKLYL 257
DB 202 FVIGHLKGAPASANNWNRHFOHAKPNCFRKDPDNNM-HPLFFALGKVLPLVELGREKKHM 260
QY 258 PYNHQEYFFELIGPPLLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFIYIFYGIL 317
DB 261 PYNHQHYFFELIGPPLLIPYFQWYIFVYVQKWKWDLAWMLSFYRVFFTYMPLLLGLK 320
QY 318 GALLFNLFIRFLESHFWVWVTQNNHIVMEIDQAYRDWFSOLTATCNVEQSFENDWFSG 377
DB 321 GFLGLFFVFRFLESNFWVWVTQNNHIVMEIDHNRNVDWSTQLQATCNHQSAFNWFSG 380
QY 378 HLNFOIEHLFPMPRHNHKLAPLVKSLCAKHIGIEYQEKPLLRALLDIIIRSLKSGKLM 437
DB 381 HLNFOIEHLFPMPRHNHKLAPLVQSLCAKIGIKYESKPLLTAFADIVYSLKESGQLW 440
QY 438 LDAYLHK 444
DB 441 LDAYLHQ 447

RESULT 31
Q9EPV4 PRELIMINARY; PRT; 447 AA.
AC Q9EPV4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Delta-5 desaturase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis; TISSUE=Liver;
RX MEDLINE=21308414; PubMed=1414679;
RA Zolfighari R., Cifelli C.J., Banta M.D., Ross A.C.;
RT "Fatty acid delta(5)-desaturase mRNA is regulated by dietary vitamin A
RT and exogenous retinoic acid in liver of adult rats.";
RL Arch. Biochem. Biophys. 391:8-15(2001).
CL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF320509; AAC35068.1; -.
DR HSSP; P04166; IBSM.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROMES.
DR ProDom; PD000612; Cyt_B5_1.
DR ProDom; PD001081; FA_desat_fam; 2; 1.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 447 AA; 52470 MW; 4232F0ABFD55CD94 CRC64;
```

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Query Match      59.8%; Score 1459; DB 11; Length 447;
Best Local Similarity 61.4%; Pred. No. 2.8e-122;
Matches 262; Conservative 59; Mismatches 102; Indels 4; Gaps 3;

QY 21 FSWEEI-QKHNLRDGLVIDRKVNITKWSIOHFGGQVIGHYAGEDATDAFAPHDL 79
DB 22 FTWEEVAQRSGREKERLWVIDRKVNISDFSRHFGGSRVISHYAGODATDRFVAFHINK 81
QY 80 EFGVKELKPLLIGELAPEESQDHGKNSKITDPRALRKTAEEDMNLKTNHVFLLLLAH 139
DB 82 GLVEKYNLSLIGELAPEQSFEPTKNKALTDEFRELATVERMGLMKANHLFFLYLLH 141
QY 140 IIALESIANFTVPYFGNGWPTLITAFVLATSOAQAGWLQHDYGHLSVYRKPKNHLVHK 199
DB 142 ILLLDVAAMLTLWFTGSLVPFTLCVLLSTVQAQAGWLQHDYGHLSVSTSTWNLVHH 201
QY 200 FVIGHLKGASANNWNRHFOHAKPNI FHKDPDNNMLH--VFVLGEWQPIEYKKKLYL 257
DB 202 FVIGHLKGAPASANNWNRHFOHAKPNCFRKDPDNNM-HPLFFALGKVLPLVELGREKKHM 260
QY 258 PYNHQEYFFELIGPPLLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFIYIFYGIL 317
DB 261 PYNHQHYFFELIGPPLLIPYFQWYIFVYVQKWKWDLAWMLSFYRVFFTYMPLLLGLK 320
QY 318 GALLFNLFIRFLESHFWVWVTQNNHIVMEIDQAYRDWFSOLTATCNVEQSFENDWFSG 377
DB 321 GLGLFFVFRFLESNFWVWVTQNNHIVMEIDHNRNVDWSTQLQATCNHQSAFNWFSG 380
QY 378 HLNFOIEHLFPMPRHNHKLAPLVKSLCAKHIGIEYQEKPLLRALLDIIIRSLKSGKLM 437
DB 381 HLNFOIEHLFPMPRHNHKLAPLVQSLCAKIGIKYESKPLLTAFADIVYSLKESGQLW 440
QY 438 LDAYLHK 444
DB 441 LDAYLHQ 447

RESULT 32
Q8BZX7 PRELIMINARY; PRT; 287 AA.
AC Q8BZX7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Delta-5 desaturase (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK033308; BAC28228.1; -.
FT NON TER
SQ SEQUENCE 287 AA; 33955 MW; 9CE3575BD7BE2577 CRC64;

Query Match      44.7%; Score 1090.5; DB 11; Length 287;
Best Local Similarity 65.6%; Pred. No. 1.7e-89;
Matches 189; Conservative 40; Mismatches 56; Indels 3; Gaps 2;

QY 159 IPTLITAFVLATSOAQAGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFF 218
DB 1 VPFILCAVLLSTVQAQAGWLQHDYGHLSVFGTSTWNLHHLHFFVIGHLKGAPASANNWNRHF 60
QY 219 QHAKPNI FHKDPDNNMLH--VFVLGEWQPIEYKKKLYLKYLPNNHOFYFLGPPLIP 276
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DB 61 CHHAKPNCRKDPDINM-HPLFFALGKVLPELGREKKKHPYNHQHKYFFELGIPGALLP 119
QY 277 MYFQIIMTMVHNKNDLAWAVSYIRFFITVIPPYIGLALLFLNFIREFLESHFWV 336
DB 120 LYFQWYIFVQKKNVDLAWLSFYARIFFTNPLGLGKGFGLFFVREFLESHFWV 179
QY 337 VTQNMHIWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 396
DB 180 VTQNMHIWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 239
QY 397 HKIAPLVKSLCAKHGIEQEPFLRALLDIIRSLKSKGLWLDAYLHK 444
DB 240 HKVAPLVKSLCAKHGIEQEPFLRALLDIIRSLKSKGLWLDAYLHQ 287

RESULT 33
Q96SV8 PRELIMINARY; PRT; 168 AA.
AC Q96SV8
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ14607.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.
RT "NEBO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027513; BAB55167.1; -.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR Hypothetical protein.
KW SEQUENCE 168 AA; 20218 MW; 4EE3991624210E12 CRC64;

Query Match 37.2%; Score 908; DB 4; Length 168;
Best Local Similarity 98.8%; Pred. No. 1.9e-73;
Matches 166; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 277 MYFQIIMTMVHNKNDLAWAVSYIRFFITVIPPYIGLALLFLNFIREFLESHFWV 336
DB 1 MYFQIIMTMVHNKNDLAWAVSYIRFFITVIPPYIGLALLFLNFIREFLESHFWV 60
QY 337 VTQNMHIWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 396
DB 61 VTQNMHIWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 120
QY 397 HKIAPLVKSLCAKHGIEQEPFLRALLDIIRSLKSKGLWLDAYLHK 444
DB 121 HKIAPLVKSLCAKHGIEQEPFLRALLDIIRSLKSKGLWLDAYLHK 168

RESULT 34
OS0426 PRELIMINARY; PRT; 352 AA.
AC O60426
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE BC269730.1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

DB 61 CHHAKPNCRKDPDINM-HPLFFALGKVLPELGREKKKHPYNHQHKYFFELGIPGALLP 119
QY 277 MYFQIIMTMVHNKNDLAWAVSYIRFFITVIPPYIGLALLFLNFIREFLESHFWV 336
DB 120 LYFQWYIFVQKKNVDLAWLSFYARIFFTNPLGLGKGFGLFFVREFLESHFWV 179
QY 337 VTQNMHIWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 396
DB 180 VTQNMHIWEIDQAYRWFSQLTATCNVQSFNDWFSQHLNFIQIEHLLFPTMPRHNL 239
QY 397 HKIAPLVKSLCAKHGIEQEPFLRALLDIIRSLKSKGLWLDAYLHK 444
DB 240 HKVAPLVKSLCAKHGIEQEPFLRALLDIIRSLKSKGLWLDAYLHQ 287

RESULT 35
Q8BV36 PRELIMINARY; PRT; 255 AA.
AC Q8BV36
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Delta-5 desaturase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080706; BAC37985.1; -.
SQ SEQUENCE 255 AA; 29221 MW; 345E537DC5AF741B CRC64;
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OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Coleman M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomey M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a human BAC containing the FEN1 DNA repair
RT gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004770; AAC23396.1; -.
DR Genew; HGNC:3576; PADS3.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
FT NON TER 1
SQ SEQUENCE 352 AA; 39851 MW; 488341D5A1672399 CRC64;

Query Match 34.9%; Score 850.5; DB 4; Length 352;
Best Local Similarity 61.4%; Pred. No. 7.1e-68;
Matches 151; Conservative 35; Mismatches 59; Indels 1; Gaps 1;

QY 70 DAFRAPHDLFEVKGKFLKLLIGELAPEPSQDHGKNSKITEDFRALRKTAEDMNLFTKN 129
DB 1 DAFRAPHDLNFKVRFKFLQPLLIGELAPEPSQDGLNAGLVEDFRALHQAEDMKLFDS 60
QY 130 HVFFLLLLAHITALESIATFTVYFGNGWIPFLITAFVLATSOAQAGWLOHGYHLSVTR 189
DB 61 PTFPFFLLGHILAMEVLAWLLIYLLPGWVPSALAAFTILASQAQSWCLQDLGHASIFK 120
QY 190 KPKWNHLVKFVIGHLKGSANWNHRRHPQHAKNIPHKDPVNMHLHVFLGEGQPIEY 249
DB 121 KSWNHVAQKFMVQGLKGSANWNHRRHPQHAKNIPHKDPVNTVAPVFLIGE-SSVEY 179
QY 250 GKKKLYLPYNHGHYFFLIGPPLIPYFYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 309
DB 180 GKKKRYLPYNQOHLFFLIGPPLTLVNFVEVENLAYMLVCMQWADLLWAASFYARFFLS 239
QY 310 YLPFYG 315
DB 240 YLPFYG 245

RESULT 35
Q8BV36 PRELIMINARY; PRT; 255 AA.
AC Q8BV36
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Delta-5 desaturase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080706; BAC37985.1; -.
SQ SEQUENCE 255 AA; 29221 MW; 345E537DC5AF741B CRC64;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=wt3; TISSUE=Protonemata;
RX  MEDLINE=20307617; PubMed=10848999;
RA  Sperling P., Lee M., Girke K., Zaehring U., Stymne S., Heinz E.;
RT  "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
RT  moss Ceratodon purpureus. A new member of the cytochrome b5
RT  superfamily.";
RL  Eur. J. Biochem. 267:3801-3811(2000).
CC  -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR  EMBL: AJ250734; CAB94992.1; -.
DR  HSSP: P04166; 1BSM.
DR  InterPro: IPR001199; Cyt_B5.
DR  InterPro: IPR005804; FA_desat_fam.
DR  Pfam: PF00487; FA_desaturase; 1.
DR  Pfam: PF00173; heme_1; 1.
DR  ProDom: PD000612; Cyt_B5; 1.
DR  ProDom: PD001081; FA_desat_fam; 2.
DR  PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW  Heme.
SQ  SEQUENCE 483 AA; 54857 MW; C451D042169AB1C2 CRC64;

Query Match      21.2%; Score 517; DB 10; Length 483;
Best Local Similarity 30.5%; Pred. No. 8.4e-38;
Matches 140; Conservative 85; Mismatches 176; Indels 58; Gaps 18;

Qy  3 KGGNOGGAAREV---SVPTFSWEEIOKHLRTDGLVIDRKVYNITKMSIQHPGQRV 59
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  42 QGKTAGQTLRQSRVQDKKPGTYSADVASHDRPGDCWNVKVKYDISRFADDPFGG-TV 100
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  60 IGHVAGEDATDAFRAHFDLDFVGFKFLPLIGELAPEEPSQDHGKSKITEDPRALRKT 119
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  101 ISTYGRGTDFATFHPPAAW--KQNDYVIGDLAREEPLDE-----LLKYRDMRAE 152
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  120 AEDMNLFTNNHVFLLLAHIALESIAWTFVFGNGWIPTLTAFVLATSOQAQWLQ 179
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  153 FVREGLFKSSKAWFLLQTLNAALFAASIAICYDKSYW-AIVLSASIMGLFVQCCWLA 211
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  180 HDYGHLSVYRKPKNHLVHKVIGHL-----KGASANNWNRHFFQHAKNIFHK----- 229
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  212 HDFLHQVFE---NRTANSP-FGLFCNVLGVSWMRTKNIHTAPNECDEQVTP 266
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  230 DPDVNMHVFVLGEWQ-----PIEYKKKLYLPYNHQHEYFFLIGPPLIPMY----- 278
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  267 DEDIDTLPPIA---WSKEILATVE-SKRLRVLOVQH-----YMLPLLFMARYSWTFGS 317
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  279 ----FOYQIIMTM-IVHKWVDLAWVSYIYRFTITYPFYIGLALLFLNFIREFLESHW 333
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  318 LLFTFNPOLSTKGLIEKGTVAFYAWFSWAAPHI--LP--GVAKPLAWVATLVAGLL 373
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  334 FVWVTQNMHIVMEIDQEAIRDWFSQTLATCNVQSPFNDFWFSGLHNFQIEHHLFPTMPR 393
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  374 LGFVFTLSHGKGVNES-KDFVRAQVITRTKRGWENDFNFTGGLDTQIEHHLFPTMPR 432
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  394 HNLKXIAFLVSLCKKHGIEQKPELLRALLDIIRSLKK 432
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  433 HNPXIAFQVEALCKKHGLEVDNVSVGASVAVVVKALKE 471
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 39
Q8RXB0 PRELIMINARY; PRT; 477 AA.
ID Q8RXB0
AC Q8RXB0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Delta 6 fatty acid desaturase D6.
GN D6
OS Phaeodactylum tricornutum.
OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
OC Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
OX NCBI_TaxID=2850;
RN [1]

```

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RP  SEQUENCE FROM N.A.
RC  STRAIN=UTEX 646;
RA  Donergue F., Lerchl J., Zaehring U., Heinz E.;
RT  "Cloning and functional characterization of Phaeodactylum tricornutum
RT  front-end desaturases involved in eicosapentaenoic acid
RT  biosynthesis.";
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC  -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR  EMBL: AY082393; AAL92563.1; -.
DR  InterPro: IPR001199; Cyt_B5.
DR  InterPro: IPR005804; FA_desat_fam.
DR  Pfam: PF00487; FA_desaturase; 1.
DR  Pfam: PF00173; heme_1; 1.
DR  ProDom: PD000612; Cyt_B5; 1.
DR  ProDom: PD001081; FA_desat_fam; 1.
DR  PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW  Heme.
SQ  SEQUENCE 477 AA; 53452 MW; 2A4B8E30F8BDF99F CRC64;

Query Match      21.2%; Score 516.5; DB 10; Length 477;
Best Local Similarity 29.3%; Pred. No. 9.2e-38;
Matches 146; Conservative 75; Mismatches 170; Indels 107; Gaps 20;

Qy  1 MKGGG---NQEGGAAREVSVPTFSWEEIOKHLRTDGLVIDRKVYNITKMSIQHPGQ 56
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  57 QRVIGHAGEDATDAFRAHFDLDFVGFKFLPLIGELAPE-----EPSQDHGKSKITE 111
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  54 AVIFTH-AGDDMTDIFAAHAPGSG---SLMKFYIGELLPETTGKEPQ-----IAPEK 104
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  112 DPALEKTAEDMNLFTNNHVFLLLAHIALESIAWTFVFGNGWIPTLTAFVLATSL 171
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  105 GYRDLRSKLIMGMFKSKNKFYVYKLSNMALWAAACALVFYSDRFVW-HLASAVMLGTF 163
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  172 QQAQGLWLDYGHLSVYRKPKNHLVHKVIGHLKGASANNWNRHFFQHAKNIF----- 227
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  164 FQSGSLAHDFLHHQVFTKRKHGDLGLFWGNLMQGVSYQWKNKHGHHAVPNLHCSA 223
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  228 ---HKDPVNMHVFVLGEWQPIEY-----OKKK--LKLYPNHQHEYFFLIGPPLIP 276
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  224 VAQDGDPTDITPLLAWSQQASYRELQADGKDSGLVKFMIRNQSIFYF-----PILLA 279
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  277 MY-----FOYQII--MTMIVHKWVDLAWVSYIYR 306
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  280 RLSWLNESFKAFGLGAASENNAELKAGLOYPLEKAGILLHYAW--MLTVSGFGF 337
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  307 FITYIPFY-----GILGALLFLNFIREFLESHWVWVWVQNMHIV-EIDQEAIRDWFS 357
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  338 SFAYTAFYELTATASCGFLLAIVF-----GLGHNGMATYNADARPDEWK 381
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  358 SOLTATCNVE-----QSPFNDFWFSGLHNFQIEHHLFPTMPRNLKXIAFLVSLCKKHG 412
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  382 LQVTTTRNTGTHGHPQAFVDFWFCGGLQYQVDHLLFPSPRNLAKTHALVESPFCKEWG 441
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  413 EYQEKPLRALLDIIRSL 430
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  442 QYHEADLVGDTMVLHLL 459
Db  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 40
Q9ZNNW2 PRELIMINARY; PRT; 525 AA.
ID Q9ZNNW2
AC Q9ZNNW2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DELTA6-acyl-lipid desaturase.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
OC Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;

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Search completed: December 9, 2003, 10:19:01  
Job time : 42 secs



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FT CDS 180..1514
FT /*tag= a
FT /product= "HOP-5"
XX
PN W020000622-A2.
XX
XX 06-JAN-2000.
XX
XX 29-JUN-1999; 99NO-US14711.
XX
XX 30-JUN-1998; 98US-0091177.
XX 16-JUL-1998; 98US-0155241.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandnan O, Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ;
XX PI Gorgone GA, Baughn MR;
XX
XX WPI; 2000-117171/10.
XX P-PSDB; AAY59182.
XX
XX New polypeptide, its antagonist useful for treatment and prevention of
XX neurological, inflammatory, reproductive, endocrine, cell proliferative
XX and smooth muscle disorders
XX
XX Claim 7; Page 85; 88pp; English.
XX
XX The invention provides human oxidoreductase proteins (HOP)
XX (AAY59178-183) and nucleic acid sequences (AAZ48243-248) encoding HOP-1
XX to HOP-6. The HOP proteins can be expressed by standard recombinant
XX technology. Pharmaceutical compositions comprising the HOP proteins are
XX useful for preventing or treating disorders associated with decreased
XX expression or activity of HOP while HOP antagonists are useful for
XX preventing or treating disorders associated with increased expression of
XX HOP. Such disorders include neurological, autoimmune, reproductive,
XX cell proliferative, vesicle trafficking, endocrine disorders and cancer
XX in mammal, especially in humans. HOP is useful for producing antibodies
XX and for drug screening using libraries of compounds. HOP polynucleotides
XX and their antibodies are useful for diagnosis of disorders associated
XX with HOP expression. The present sequence represents a cDNA encoding
XX the HOP-5 protein.
XX
XX Sequence 3184 BP; 648 A; 956 C; 929 G; 651 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3e-258 Length: 3184
Score: 2438.00 Matches: 444
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-719-601-5 (1-444) x AAZ48247 (1-3184)
Qy 1 MetGlyLysGlyLysAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
Db 180 ATGGGGAAGGAGGAGGACCAAGGGCGAGGGGGCGCGGAGGAGGTGTCGGTGGCCACC 239
Qy 21 PheSerTrpGluGluGlnGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
Db 240 TTACGCTGGAGGAGATTTCAGAGCATTAACCTCGCACCGACAGTGGGTGTCATTGAC 299
Qy 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 300 CGCAAGGTTTACACATCACAAATGTCATCCAGCACCCCGGGGGCCAGCGGGTTCATC 359
Qy 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 360 GGGGACATACGCTGGAGGAATGCAACGGATGCTTCGGGCCCTTCCACCTGACCTGGAA 419
Qy 81 PheValGlyLysPheLeuLysProLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 420 TTCGTGGGCAAGTCTTGAACCCCTGCTGATTGGTGAACCTGGGAGGCTGTGGCTGGACGCC 479

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Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 480 CAGGACCACGGCAAGAACTCAAGATCACTAGAGACTTCGGGCCCTCGAGAAAGCGGCT 539
Qy 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db 540 GAGGACATGAACCTGTTCAAGACCAACACCGTGTCTTCCTCCTCCTCGGCCCAATC 599
Qy 141 IleAlaLeuGluSerIleAlaTTPheThrValPheTyrPheGlyAsnGlyTTPilePro 160
Db 600 ATCCCTCGGAGAGCATGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 659
Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
Db 660 ACCCTCATCAGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT 719
Qy 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200
Db 720 GATTATGGCCACCTGTCTGTCTACAGAAACCAACCAAGTGAACCACTTGTCCAAATTC 779
Qy 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db 780 GTCATGGCCACCTTAAAGGGTGTCTGTCCCACTGTGTGAATCATCGCCACTTCCAGCAC 839
Qy 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 840 CACGCCAAGGCTTAAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCAGTGTGTGT 899
Qy 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
Db 900 CTGGCGCAATGGCAGCCATCGAGTAGCGCAAGAGAGCTGAATACCTGCTGCCACAT 959
Qy 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
Db 960 CACCAGCAGCAATACTTCTTCTGATTGGCGCGCTGCTCATCCCATGTTATTTCCAG 1019
Qy 281 TyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTTPalaVal 300
Db 1020 TACCAGATCATGACCATGATGCTCCATAGACTGGGTGGACCTGGCTGGCGCTC 1079
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 1080 AGCTACTATACATCCGTTCTTTCATCACCTATACCTTCTTACGGCATCTCTGGAGGCCCTC 1139
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340
Db 1140 CTTTCTCTCACTTCAATCAGTTTCTCGAGAGCCACTGGTTTGTGGGTACACAGATG 1199
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 1200 AATCACATCGTATGGAGATTGACCAAGAGGCTTACCGTACTGTGTTCAGTAGCAGCTG 1259
Qy 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 1260 ACAGCCACCTGCAACGTGGAGCAGTCTCTTCAACACACTGGTTTCTAGTGACACCTTAAC 1319
Qy 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db 1320 TTCCAGATTGAGCACCACTCTTCCCAACCATGTCGCCCGGCACAACTTACACAGATCGCC 1379
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluLysProLeuLeu 420
Db 1380 CCGTGTGTGAGTCTCTATGTGCCAGCATGGCATTTGAAATACCAGGAGAGCGGCTACTG 1439
Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db 1440 AGGCGCTGTGTGACATCATCAGTCTCTTGAAGAGTCTGGGAGGCTGTGGCTGGACGCC 1499
Qy 441 TyrLeuHisLys 444
Db 1500 TACCTTCACAAA 1511

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DB: 22 Gaps: 0  
US-09-719-601-5 (1-444) x AAD19403 (1-1335)

QY 1 MetGlyValGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
Db 1 ATGGGAAGAGCGGAAACAGGCGAGGGGGCGCGAGCGGAGGTGTGGTGCCACC 60  
QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
Db 61 TTCAGCTGGGAGGAGATTTCAGAGCATTAACCTCGCCACCGACAGGTGGCTGTCATTGAC 120  
QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlnArgValIle 60  
Db 121 CGCAAGGTTTACAAACATACCAAATCGTCCATCCAGCACCCGGGGGGCCAGCGGTCATC 180  
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
Db 181 GGSCACTACGCTGGAGAGATGCAACGGATGCTTCGGGCGCTTCCACCTGACTGGAA 240  
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100  
Db 241 TTCGTGGGCAAGTTCCTTGAACCCCTCGCTGATTGGTGAATGGCCCGCGAGGAGCCAGC 300  
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
Db 301 CAGACACCGCGAAGAACTCAAGATCACTGAGGACTTCCGGGCCCTTGAGGAAGCGCT 360  
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
Db 361 GAGGACATGAACCTGTTCAAGACCAACACGCTGTTCTTCCTCTCTCTGGGCCACATC 420  
QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
Db 421 ATCGCCCTGAGAGCATGTGATGGTTCACGTCTTTTACTTTGGCAATGCTGGATTCCT 480  
QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
Db 481 ACCCTCATCAGCGCTTTGTCTTGCTACTCTCAGGCCCAACGTGGATGGCTGCAACAT 540  
QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisIleValHisLysPhe 200  
Db 541 GATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGGAAACACCATGTGCCCAAAATC 600  
QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpAsnHisArgHisPheGlnHis 220  
Db 601 GTCAITGGCCACTTAAAGGTGCCTCTGCCAACTGGTGGATCATGCCACTTCCAGCAC 660  
QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
Db 661 CAGGCCAAGCCTAACATCTTCCACAGGATCCCGATGTGAACATGTGTGACCGTGTGTGTT 720  
QY 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysTyrLeuProTyrAsn 260  
Db 721 CTGGCGAATGGCAGCCCATCGAATGCGCAAGCAAGAACTGAATACCTTGCCTCCATCAAT 780  
QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280  
Db 781 CACCAGCAGCAATACTTCTTCCTGATTGGGCGCGCTGCTCATCCCATGTATTTCAG 840  
QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
Db 841 TACCAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACTGCGCCTGGGCGCTC 900  
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320  
Db 901 AGCTACTACATCGGTTCCTTCATCACCTACATCCCTTTCTACGGCATCTCTGGGAGCCCTC 960  
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340  
Db 961 CTTTTCCTCAACTTCATCAGGTTCTGTGAGAGCCACTGTGTTGTGTGGGTGCACACAGATG 1020  
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360

DB 1021 AATCATCGTCATGGAGATTGACAGAGAGCCCTACCGTGACTGGTTTCAGTAGCCAGCTG 1080  
 QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380  
 DB 1081 ACAGCCACCTGCAACGTCAGAGCAGTCCCTTCTTCAACGACTGGTTTCAGTAGCCAGCTTAAC 1140  
 QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
 DB 1141 TTCAGATGAGCACCACCTCTTCCCAACCATGCCCGGCGCAACTTACCAAGATCGCC 1200  
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420  
 DB 1201 CGCTGGTGAAGTCTCTAATGTCGAAGCATGCGATTGAATACAGGAGAGCCGCTACTG 1260  
 QY 421 ArgAlaLeuLeuAspIleAlaArgSerLeuLysLysSerGlyLysLeuTyrLeuAspAla 440  
 DB 1261 AGGGCCCTGCTGGACATCATCAGGTCCCTGGAAGTCTGGGAAGCTGTGGCTGGACGCC 1320  
 QY 441 TyrLeuHisLys 444  
 DB 1321 TACCTTCACAA 1332

RESULT 3  
 AAK94346  
 ID AAK94346 standard; cDNA; 3083 BP.

AC AAK94346;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 3049.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-0114089.

XX 08-JUL-1999; 99JP-0194486.

XX 11-JAN-2000; 2000JP-0118774.

XX 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX P-PSDB; AAK93425.

XX 830 Primers useful for synthesizing full length cDNA clones and their

XX use in genetic manipulation -

XX Claim 8; SEQ ID NO 3049; 1380pp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5' and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a full length  
 CC human cDNA of the invention.

XX Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.

SQ Sequence 3083 BP; 615 A; 937 C; 884 G; 647 T; 0 other;

Alignment Scores:  
 Pred. No.: 7,78e-257 Length: 3083  
 Score: 2425.00 Matches: 442  
 Percent Similarity: 99.55% Conservative: 0  
 Best Local Similarity: 99.55% Mismatches: 2  
 Query Match: 99.47% Indels: 0  
 DB: 22 Gaps: 0

US-09-719-601-5 (1-444) x AAK94346 (1-3083)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
 DB 91 ATGGGGAAGGAGGAAACCCAGGGCGAGGGGGCGCGAGCGAGGTGTGCGTGGCCACC 150  
 QY 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
 DB 151 TTCAGCTGGGAGAGATTCCGAAGCATACCTGCCACCGACAGGTGGTGGTCAATTGAC 210  
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
 DB 211 CGCAAGGTTTACAACATCACCAATGGTCCATCCAGCACCCCGGGGGCGCGAGGTGCATC 270  
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
 DB 271 GGGCACTACGCTGGAGAGATGCAACGGATGCTTCCGGCGCTTCCACCTGACTGGAA 330  
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100  
 DB 331 TTCGTGGCAAGTTCCTTGAACCCCTGCTGATTGGTAACCTGGCCCGGAGAGCCACATC 390  
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
 DB 391 CAGGACCCAGGCAAGAACTCAAGATCACTAGGACTTCCGGGCGCTTGGAGAGACGGCT 450  
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
 DB 451 GAGGACATGAACCTGTTCAAGCAACCAACCGTGTCTCTCTCTCTCTCTCTCTCTCTCT 510  
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
 DB 511 ATCGCCCTGGAGAGCATTCATGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570  
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
 DB 571 ACCCTCATCAAGCCCTTGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 630  
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
 DB 631 GATTATGGCCACCTGTGTCTACAGAAACCCCAAGTGAACCCACCTTGTCCACAAATTC 690  
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
 DB 691 GTCAATGGCCACTTAAGGGTGTCTGTCCAACTGTGTGGATCATCGCCATTCAGCAC 750  
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
 DB 751 CAGCCCAAGCCTAACATCTTCCCAAGGATCCCGATGTCGAACATGTCGACGTGTGTGT 810  
 QY 241 LeuGlyLutTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLys 260  
 DB 811 CTGGCGGAATGGGAGCCCATCGAGTACGGCAGAGAGAGCTGAATACCTGCCCTACAT 870  
 QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280  
 DB 871 CACCAGCAGCAATATCTTCTTCTGATTGGGCGCGCTGCTCATCCCATGTATTTCCAG 930  
 QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
 DB 931 TACCAGATCATCATGACATGATGCTCCATGAAGACTGGGTGGACCTGGCTGGCGGCTC 990  
 QY 301 SerTyrTrpIleArgPhePheIleThrTyrIleProPheTyrGlyLysLeuGlyAlaLeu 320





101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
Db  
321 CAGGACCCAGCGAAGAACTCAGAGATCAGTGGAGCTTCGGGCGCTTCAGGAGACCGCT 380  
Qy  
121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
Db  
381 GAGGACATGAACCTGTTCAAGACCAACACAGCTGTTCTTCCTCTCTCTGGGCCACATC 440  
Qy  
141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
Db  
441 ATCGCCCTGAGAGCATGTCATGGTTCATCTTTTACCTTTGGCAATGGCTGGATTCCT 500  
Qy  
161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
Db  
501 ACCCTCATCAGCGCTTGTCTTGTCTGTCTCAGGCCCAAGCTGGATGGCTGCAACAT 560  
Qy  
181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
Db  
561 GATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGGAACCACTTGTCCAAATTC 620  
Qy  
201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
Db  
621 GTCATGGCCACTTAAAGGGTGCCTCTGCCAATCTGGTGGAAATCATGCCACTTCCAGCAC 680  
Qy  
221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
Db  
681 CACGCCAAGCCTAATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTTTGTGT 740  
Qy  
241 LeuGlyGluTrpGlnProIleGlyLysLysLysLysLysLysLysLysLysLysLys 260  
Db  
741 CTGGGCGATGGCAGCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTACAT 800  
Qy  
261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280  
Db  
801 CACGAGCAGCAATATCTTCTCTGATTGGCGCGCTGCTCATCCCATGTATTTCCAG 860  
Qy  
281 TyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
Db  
861 TACGAGATCATGACCATCATGATCTCTCATAGACTGGTGGACCTGGCTGGCGCTC 920  
Qy  
301 SerTyrTyrIleArgPheIleThrTyrIleProPheTyrGlyLysLeuGlyAlaLeu 320  
Db  
921 AGCTACTACATCCGGTCTTCTCATCCTCATCCTTCTACGGCATCCCTGGAGCCCTC 980  
Qy  
321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValTrpGlnMet 340  
Db  
981 CTTTCTCTCAACTTCATCAGTTCCTGGAGAGCCACTGGTTGTGGTGGTGCACACAGATG 1040  
Qy  
341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360  
Db  
1041 AATCAGATCGTTCATGGAGATTGACAGAGGCCCTACCGTACCTGTTTCACTAGCCAGCTG 1100  
Qy  
361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380  
Db  
1101 ACAGCCACCTGCAACGCGGAGCAGTCTCTTCAACGACTGGTTCAGTGGACACCTTAAC 1160  
Qy  
381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
Db  
1161 TTCCAGATTGAGCACCCTCTTCCACCACCATGCCCGGCACCACTTACACAGATCGCC 1220  
Qy  
401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420  
Db  
1221 CCGTGTGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACAGGAGAGCGGCTACTG 1280  
Qy  
421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440  
Db  
1281 AGGGCCCTGCTGGACATCATCAGTCTCTGAGAGTCTGGGAAGTCTGGCTGGAGGCC 1340  
Qy  
441 TyrLeuHisLys 444  
Db  
1341 TACCTTCACAAA 1352

## RESULT 6

AAI66599  
ID AAI66599 standard; DNA; 1335 BP.  
XX  
AC AAI66599;  
XX  
DT 29-JAN-2002 (first entry)  
XX  
DE Rat fatty acid desaturase gene.  
XX  
KW Rat; fatty acid desaturase; unsaturated long-chain fatty acid production; fermentation; ds.  
XX  
OS Rattus norvegicus.  
XX  
FH Key Location/Qualifiers  
FT 1..1335  
FT /\*tag= a  
FT /product= "fatty acid desaturase"  
XX  
PN WO200175069-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 31-MAR-2000; 2000WO-JP02129.  
XX  
PR 31-MAR-2000; 2000WO-JP02129.  
XX  
PA (IDEM ) IDEMITSU PETROCHEM CO LTD.  
XX  
PI Suzuki O, Ono K, Aki T, Shimauchi T, Nakajima T, Kondo A;  
XX  
DR WPI: 2001-648552/74.  
DR P-PSDB; AAM51801.  
XX  
PT New microorganism for the efficient expression of long-chain unsaturated fatty acids into the medium, comprises Saccharomyces transformed by a fatty acid desaturase gene -  
XX  
PS Disclosure; Page 22-25; 29pp; Japanese.  
XX  
CC The present invention relates to a microorganism transformed by a gene encoding a fatty acid desaturase and having the ability to secrete lipids into the medium. This can be used for the efficient production of unsaturated long-chain fatty acids by fermentation. The present sequence is the fatty acid desaturase gene from Rattus norvegicus.  
XX  
SQ Sequence 1335 BP; 311 A; 395 C; 326 G; 303 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1,928-231 Length: 1335  
Score: 2190.00 Matches: 390  
Percent Similarity: 93.6% Conservative: 26  
Best Local Similarity: 87.8% Mismatches: 28  
Query Match: 89.8% Indels: 0  
DB: Gaps: 0  
  
US-09-719-601-5 (1-444) x AAI66599 (1-1335)  
Qy 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
Db 1 ATGGGAGAGGAGGAGTAAACAGGAGAGGGAGGACCGAGCTCCAGGCTCCGATGCCAC 60  
Qy 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
Db 61 TTCGCTGGAGAGATTCAGAGCAACCTGGCCAGCCGCTGGCTGCTCATCGAC 120  
Qy 41 ArgLysValTyrAsnIleThrIleTrpSerIleGlnHisProGlyGlyGluArgValIle 60  
Db 121 CGCAAGGCTCACAGCTTACCAATGGTCCAGCGGACCCAGGGGGGACCGGTGTATC 180  
Qy 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80

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Db 181 GGACACTATTCCGGAGAGAGTCTACCGATGCCTTCCTCGCTCCACCTGGACCTGGAT 240
Qy 81 PheValGlyysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 241 TTCGTGGGCAAGTCTTTGAAGCCCTCTGCTATTGCTGAGCTGGCCCGAGAGAGCCGAGC 300
Qy 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 301 CTGGACCGGGCAAAAGCTCTCATCATCAGAGACTTCAGGGCCCTGAAGAGAGACTGCT 360
Qy 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuLeuAlaHisIle 140
Db 361 GAGGACATGAACCTTTCAAACCAACCAACCTGTTCTTTCTTCCTCTGTCGCCAATC 420
Qy 141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTyrIlePro 160
Db 421 ATCGTCAATGGAAGATCGCTGGTTTCATCTCTGCTATTCGGCAATGGCTGATTCCTC 480
Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHis 180
Db 481 ACCGTCAATCAGGCTGTTGCTCTGCTACCTCCAGGCCCCAAGCTGGATGGCTACAACAT 540
Qy 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPhe 200
Db 541 GATTATGCCCACTTTCTGTCTAAGAAATCCATATGGAACCAATTTGTCACCAAGTTT 600
Qy 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHis 220
Db 601 GTCATGGCCACTTAAGGGTGGCTCCGCCCACTGGTGAACCATCGACATTTCCAGCAC 660
Qy 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 661 CATGCGAAGCCCAACATCTTCACCAAGGACCCCGACATAAAGAGCCCTGCACGTGTTGTC 720
Qy 241 LeuGlyGluTyrGluProIleGlyTyrGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
Db 721 CTTGAGAGAGTGGCACCCCTCGAGTATGGCAGAGAGAGCTGAATATCTGCCCTCAAC 780
Qy 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
Db 781 CACCAGCATGAATACTTCTTCGTATCGGACCCGACCCGCTGCTCATCCCTATGATCTCCAG 840
Qy 281 TyrGlnIleMetThrMetIleValHisLysAsnTyrValAspLeuAlaTyrAlaVal 300
Db 841 TACCAGATCATATGACCATGATGATGACGACGAGACTGGTGGACTTGGCTTGGCCATC 900
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeu 320
Db 901 AGCTACTATGCAGTTTCTTACACCTATATCCCTTCTATGGCATCTTGGAGCCCTG 960
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPheValTyrValThrGlnMet 340
Db 961 GTTTTCTCACTTATATCAGTTCTCGAGGCCACTGTTTGTGTGGTTCACAGATG 1020
Qy 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTyrPheSerSerGlnLeu 360
Db 1021 AACCAATTTGTCAGAGATTGATCTGTATCACTACCGGAGCTGGTTCAGACAGCCAGCTG 1080
Qy 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTyrPheSerGlyHisLeuAsn 380
Db 1081 GCAGCCACCTGCAATGTGAGCAGTCTTCTTCAATGACTGTTTGTGGGGGACCTCAAT 1140
Qy 381 PheGlnIleGluHisIleLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db 1141 TTCACATTTGAGCACCACTCTCCCACTATGCGAAGACACAACTTGCACAAAGATTGCC 1200
Qy 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 1201 CCACCTGGTGAAGTCTCTCTGCGCAAGCATGTCATTTGAATACCAAGAGAGCCGCTGCTG 1260
Qy 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTyrPheLeuAspAla 440
Db 1261 AGGGCCCTGCTGACATTTGAGATTCTACTGAAGAGTCTGGGAGGCTGTGGTGGATGCC 1320
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Qy 441 TyrLeuHisLys 444
Db 1321 TACCTCCACAA 1332
RESULT 7
ID AAD19402
ID AAD19402 standard, DNA; 1335 BP.
XX AAD19402;
AC AAD19402;
XX 18-DEC-2001 (first entry)
DE Rat delta-6-desaturase (rD6D-1) coding region.
XX Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
XX mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
XX gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
XX endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
XX cardiovascular disease; Crohn's disease; congenital liver disease;
XX schizophrenia; diabetic neuropathy; nephropathy; cancer;
XX arterial hypertension; atherosclerosis; chronic inflammatory disorder;
XX autoimmune disorder; hypercholesterolaemia; atopic disorder; rD6D-1;
XX gene therapy; rat; ds.
OS Rattus sp.
XX Key
XX 1..1335 Location/Qualifiers
XX CDS
XX /*tag= a "Rat D6D-1 protein"
XX /product= (pos:718..720, aa:Val)
XX /transl_except= (pos:718..720, aa:Val)
XX W0200170993-A2.
XX 27-SEP-2001.
XX 26-MAR-2001; 2001WO-CA00398.
XX 24-MAR-2000; 2000CA-2301158.
XX (SCOT-) SCOTIA HOLDINGS PLC.
XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
XX WPI; 2001-611507/70.
XX P-PSDB; AAEL1081.
XX Nucleic acid encoding delta-6-desaturase gene useful for treating
XX atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
XX gastrointestinal disorders, viral infections and post viral fatigue -
XX Example 3; Fig 3; 164pp; English.
XX The invention relates to polynucleotides that control delta-6
XX desaturase genes (D6D) and methods useful for identifying compounds
XX which inhibit or promote the activity of mammalian D6D. Compounds
XX which modulate D6D gene segments are useful for treating lipid
XX metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
XX arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
XX infections and post viral fatigue, pre-menstrual syndrome,
XX endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
XX cardiovascular disease, Crohn's disease, cancer, congenital liver
XX disease, schizophrenia, diabetes and diabetic complications including
XX diabetic neuropathy, nephropathy and retinopathy. Compounds of the
XX invention are also useful for inhibiting progressive and acute
XX disorders such as arterial hypertension, atherosclerosis, chronic
XX inflammatory and autoimmune disorders, hypercholesterolaemia and
XX other atopic disorders. D6D genes are useful in gene therapy. The
XX present sequence is rat delta-6-desaturase (rD6D-1) coding region.
XX Sequence 1335 BP; 311 A; 396 C; 326 G; 302 T; 0 other;
```





CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a full length  
 CC human cDNA of the invention. The present sequence is a full length  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.

XX  
 SQ Sequence 2825 BP; 562 A; 868 C; 778 G; 617 T; 0 other;

## Alignment Scores:

Pred. No.: 1,538-217 Length: 2825  
 Score: 2068.50 Matches: 378  
 Percent Similarity: 99.44% Conservatives: 0  
 Best Local Similarity: 99.44% Mismatches: 3  
 Query Match: 84.84% Indels: 3  
 DB: 22 Gaps: 1

US-09-719-601-5 (1-444) x AAK94377 (1-2825)

QY 64 AlaGlyGluAspAlaThr-----AspAlaPheArgAlaPheHisProAspLeuGlu 80  
 DB 7 GCAGGACACCCCAATCACCGGGCAACAGGATGCTTCCGCGCTTCCACCTGACCTGGAA 66  
 QY 81 PheValGlyLysPheLeuLysProLeuLeuGlyGluLeuAlaProGluGluProSer 100  
 DB 67 TTCGTGGGCAAGTTCTTGAAACCTCTGCTGATTGTGTAAGTGGCCCGGAGAGCCGAGC 126  
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
 DB 127 CAGGACACCGGCAAGAACTCAAGATCACTGAGGACTTCCGCGCTTCCGAGGAGAGCGCT 186  
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
 DB 187 GAGGACATGAACCTGTTCAAGACCAACACAGTGTTCTTCTCTCTCTCTCTCTCTCTCTCT 246  
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheThrGlyAsnGlyTrpIlePro 160  
 DB 247 ATCGCCCTGGAGAGCATTCATGTTCTACTGTCTTTTACTTGGCAATGGCTGGATTCCT 306  
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
 DB 307 ACCCTCATCAGCGCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366  
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
 DB 367 GATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGAACCACTTGTCCACAAATTC 426  
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
 DB 427 GTCAATTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGAATCATCGCCACTTCCAGCAC 486  
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
 DB 487 CACGCCAACCTTAACATCTTCCAAAGATCCCGATGTGAACATCTGCACGTGTTCCTT 546  
 QY 241 LeuGlyGluTrpGlnProIleGluTrpGlyLysLysLysLysLysLysLysLysLysLys 260  
 DB 547 CTGGGCGAATGGCAGCCCATCATGAGTACGGCAAGAAAGCTGAAATACCTGCGCTTACAA 606  
 QY 261 HisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280  
 DB 607 CACCAGACAGATATCTTCTCTGATTGGCGCGCTGCTGCTCATCTCCCATGATTTTCAG 666  
 QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
 DB 667 TACCAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726  
 QY 301 SerTyrTyrIleArgPheIleThrTrpIleProPheThrGlyIleLeuGlyAlaLeu 320  
 DB 727 AGCTACTACATCCGGTCTTCTACATCACTACATCCCTTCTACGCAATCTCGGAGCCCTC 786  
 QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340  
 DB 787 CTTTCTCTCACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTCAACAGATG 846

QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeu 360  
 DB 847 AATCATCATGTCATGAGATTGACCCAGGAGGCTTACCGTACTGTTTCAGTAGCCAGCTG 906  
 QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380  
 DB 907 ACAGCCACCTCAACGTGGAGCAGTCCTTCTTCAACGACTGGTTCAGTGGACACCTTAAC 966  
 QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
 DB 967 TTCCAGATTGAGCACCACCTTTCCTCCACCATGCCCGGCACAACTTACACAAATCGCC 1026  
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420  
 DB 1027 CCGCTGTTGAAGTCTCTATGTGCCAAGCATGTCATGAATACCCAGGAGAGCGCTACTG 1086  
 QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440  
 DB 1087 AGGCGCTCTCTGGACATCATCAGTCCCTGAAGAGTCTGGGAAGCTGTGGCTGGACGCC 1146  
 QY 441 TyrLeuHisLys 444  
 DB 1147 TACCTTCACAAA 1158  
 RESULT 9  
 AAV63643  
 ID AAV63643 standard; cDNA; 2257 BP.  
 XX  
 AC AAV63643;  
 XX  
 XX 15-FEB-1999 (first entry)  
 DT  
 XX  
 DE Contig 253538a encoding a human desaturase enzyme.  
 KW Fatty acid; desaturase; polyunsaturated fatty acid;  
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome; human;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
 XX  
 OS Homo sapiens.  
 FN WC9846763-A1.  
 XX  
 XX 22-OCT-1998.  
 PD  
 XX 10-APR-1998; 98WO-US07126.  
 PF  
 XX 11-APR-1997; 97US-0834655.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX  
 XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 DR WPI; 1998-594582/50.  
 XX P-PSDB; AAW84156.  
 PT New isolated fatty acid desaturase enzymes - used for the production  
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
 XX compositions, nutritional compositions, cosmetics or animal feed  
 PS Example 12; Pages 117-118; 165pp; English.  
 CC The present sequence encodes a human desaturase enzyme. The sequence was  
 CC identified based on homology between human cDNA sequences and Mortierella  
 CC alpina desaturase gene sequences. The specification describes methods for  
 CC desaturating a fatty acid and for producing a desaturated fatty acid by  
 CC expressing increased levels of a desaturase. The enzyme can be used for  
 CC desaturating fatty acids. The enzyme can be used to produce

CC polyunsaturated fatty acids, which can be used for treating malnutrition,  
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The  
 CC polyunsaturated fatty acids can be used for treating e.g. stenosis  
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma, They  
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They  
 CC can also be used to inhibit platelet aggregation, cause vasodilation,  
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth  
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding  
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,  
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic  
 CC encephalomyelitis and chronic fatigue after viral infections, treat  
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and  
 CC inflammatory skin disorders.

XX .  
 SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

# Alignment Scores:

Pred. No.: 5,92e-203 Length: 2257  
 Score: 1935.00 Matches: 352  
 Percent Similarity: 88.84% Conservative: 30  
 Best Local Similarity: 81.86% Mismatches: 44  
 Query Match: 79.37% Indels: 4  
 DB: 19 Gaps: 2

US-09-719-601-5 (1-444) x AAV63643 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluGluGlnHisAsnLeuArgThrAspSer 35  
 DB 7 CCTACCCCGCGCTACTTTCATCTGGGAGAGTGGCCAGCGCTCAGGGTGGAGGCGG 66  
 QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55  
 DB 67 TGGCTAGTATCGACCGTAAAGTGTACACATCAGGAGTTCACCCCGCGATCCAGGG 126  
 QY 56 GlyGlnArgValIleGlyHisTyAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75  
 DB 127 GGCCTCCCGGTCATCAGCAGCTACGCGGCGGAGGATGCCAGGATCCCTTTGTGGCCTTC 186  
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95  
 DB 187 CATATCAACAGGCGCTTGTGAAGATATATGAACTCTCTCCCTGATGGAGAACTGCT 246  
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115  
 DB 247 CCAGAGCAGCCAGCTTGTAGCCACCAAGATTAAGAGCTGACAGATGATGATTCGCGGAG 306  
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135  
 DB 307 CTGCGGCGCACAGTGGAGCGGATGGGCTCATGAAGGCCAACCATGTCTTCTTCCTGCTG 366  
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGly 155  
 DB 367 TACCTGTGTGCACATCTTGTCTGCTGATGGTGTGACGCTGGCTCACCTTTGGTCTTTGGG 426  
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174  
 DB 427 ACGTCTCTTTTGGCCTCTCTCTCTGTGCGGTGCTGCTCAGTGCAGTTCAGCGAGGCCAA 486  
 QY 175 AlaGlyTrpLeuGlnHisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsn 194  
 DB 487 GCTGGATGGCTGCACATGATTATGGCCACCTGTCTCTACAGAAACCCAGTGGAAAC 546  
 QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214  
 DB 547 CACCTTGTCCACAAATTCGTCAATGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAAT 606  
 QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234  
 DB 607 CATGCCACTTCCAGCACCAGCCAGCCTTAACATCTTCCACAGAGATCCCGATGTGAAC 666  
 QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGlyLysLysLysLeu 254  
 DB 667 ATGCTGCACGTGTTGTTCTCGGGGAATGGCAGGCCCATCGAGTACGCGCAAGAGAGCTG 726

QY 255 LysTyrLeuProTyAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274  
 DB 727 AAATACCTGCTCCCTCAATACACGACGCAAACTTCTTCTGATGGGCGCGCTGCTC 786  
 QY 275 IleProMetTyPheGlnTyGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294  
 DB 787 ATCCCATGATTTCCAGTACCATGATCATGACCATGATCGTCCATTAAGAACTGGGTG 846  
 QY 295 AspLeuAlaTrpAlaValSerTyTrpIleArgPheIleThrTyIleProPheTy 314  
 DB 847 GACCTGGCGCTGGCGCTGAGCTACATCCGGTTCCTTCATCACCTATATCCCTTTCAC 906  
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334  
 DB 907 GGCATCTCTGGGAGCCCTCTTTCCTCAACTTCATGAGTTCCTGGAGAGCCACTGTTT 966  
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyTrpAsp 354  
 DB 967 GTGTGGGTGCACACATGATCATGCTCATGAGATTGACAGGAGGCGCTACCGTGCAC 1026  
 QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374  
 DB 1027 TGGTTTCAGTAGCCAGCTGCAGCAGCCACTTCAAGCTGGAGCAGTCTCTTTCACGACTGG 1086  
 QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394  
 DB 1087 TTCAGTGGACACCTTAACTTCCAGATTGAGCACCACCTCTTCCACCACCATGCCCGGAC 1146  
 QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTy 414  
 DB 1147 AACTTACACAGATCGCCCGCTGTGTGAAGTCTATGTGCAAGCATGGCATTAATAC 1206  
 QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434  
 DB 1207 CAGGAGAAAGCCCTACTCAGGCGCCCTGTGGACATCATCAGTCCCTCGAAGAGTCTGGG 1266  
 QY 435 LysLeuTrpLeuAspAlaTyIleHisLys 444  
 DB 1267 AAGCTGTGGTGGAGCGCTACCTTTCACAA 1296  
 RESULT 10  
 AAX00910  
 ID AAX00910 standard; DNA; 2257 BP.  
 XX  
 AC AAX00910;  
 XX  
 DT 26-MAR-1999 (first entry)  
 XX  
 DE Human desaturase gene contig 253538a.  
 XX  
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUPA; oil;  
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;  
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;  
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;  
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;  
 KW diabetes; cosmetic; animal feed; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2256  
 FT /tag= a  
 FT /note= "contains internal stop codons"  
 XX  
 PN WO9846764-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 10-APR-1998; 98WO-US07421.  
 XX  
 PR 24-OCT-1997; 97US-0956985.  
 PR 11-APR-1997; 97US-0833610.

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11-APR-1997; 97US-0834033.
11-APR-1997; 97US-0834655.
(ABBO ) ABBOTT LAB.
(CALJ ) CALGENE LLC.
Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
Thurmond J;
WPI; 1999-080739/07.
P-PSDB; AAW95514.
Nucleic acid construct able to express fatty acid desaturase in
plants - useful in human or animal nutrition, as cosmetics and
therapeutically, e.g. for restenosis, cancer and diabetes
Claim 48; Page 161-162; 210pp; English.
The invention relates to a nucleic acid construct that contains at least
one of the nucleotide sequences (AAX00889 to AAX00891) encoding
Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to
AAW95506) respectively, coupled to an expression control sequence
functional in plants. Recombinant plant cells containing at least one DNA
encoding a M. alpina fatty acid desaturase (FAD), can be used for the
production of polyunsaturated fatty acid (PUFA). These recombinant cells
or plants containing them are used to produce oils such as linoleic
acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic
acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils
are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
dietary supplements or substitutes, for use in humans or animals; (iii)
for treating disorders associated with inadequate consumption or
production of PUFA for their metabolites such as prostaglandins), e.g.
restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,
and (v) as animal feeds. Fragments of the DNA are used as probes to
isolate related coding sequences. Recombinant plants can produce high
yields of PUFA, since new pathways can be created and unwanted ones
suppressed. Plants can be engineered to express oils of particular PUFA
composition, e.g. one similar to that in human milk, and product recovery
is simpler than with e.g. fish. Sequences AAX00904-910 represent DNA
sequences of various contigs of human desaturase genes which are similar
to the M. alpina desaturase sequences.
XX
SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;
Alignment Scores:
Pred. No.: 5,92e-203 Length: 2257
Score: 1935.00 Matches: 352
Percent Similarity: 88.84% Conservative: 30
Best Local Similarity: 81.86% Mismatches: 44
Query Match: 79.37% Indels: 4
DB: 20 Gaps: 2
US-09-719-601-5 (1-444) x AAX00910 (1-2257)
QY 19 ProThr-----PhSerTrpClnuIleGlnLysHisAsnLeuArgThrAspSer 35
Db 7 CTAACCCCGCGTACTTCACCTGGACAGGTGCCAGCGCTCAGGTCGCGAGGAGCGG 66
QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
Db 67 TGGCTAGTGTATCGACCGTAAGGTGTACACATCAGCGAGTTCACCCCGCGCATCCAGG 126
QY 56 GlyGlnArgValIleGlyHisTyTrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
Db 127 GGTCTCCGGGTTCATCAGGCACCTACGCCCGGCGAGGTGCCAGGATCCCTTTTGGGCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
Db 187 CACATCACACAGGCCCTTGTGAAGACGATATATGAACTCTCTCTCATTTGGAGACTGTCT 246
QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115

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QY 395 AnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleLeuTyr 414  
 DB 1147 AACTTACACAAATCGCCCGTGTGAAGTCTCTATGTGCCAAGCATGGCATTAATAC 1206  
 QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleLeuArgSerLeuLysSerGly 434  
 DB 1207 CAGGAGACCCGCTACTAGGCGCCCTGTGGACATCATCAGTCCCTGAAGAAGTCTGGG 1266  
 QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 DB 1267 AAGCTGTGGTGGAGCCCTACCTTACAAA 1296

RESULT 12

ID AAA49939 standard; cDNA; 2257 BP.

XX AAA49939;

DT 10-OCT-2000 (first entry)

XX Human delta-5-desaturase-related contig 253538A.

DE Delta-5-desaturase; human; polyunsaturated fatty acid;  
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;  
 KW docosahexaenoic acid; nutrition; feedstuff; ss.  
 OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..1299

FT /\*tag= a

XX WO200040705-A2.

XX 13-JUL-2000.

XX 29-DEC-1999; 99WO-US311163.

XX 08-JAN-1999; 99US-0227613.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JW;

XX WPI; 2000-465975/40.

XX P-PSDB; AA195446.

PT New polypeptide useful for preparation of nutritional supplements based  
 PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids  
 PT at carbon 5 -

XX Example 1; Fig 8; 127pp; English.

XX The present sequence is that of contig 253538A, a contig produced  
 CC from overlapping contigs 2535 (see AAA49939) and 384933 (see  
 CC AAA49936), which were isolated from the Incyte Lifeseq database on  
 CC the basis of homology to Mortierella alpina delta-5-desaturase and  
 CC delta-6-desaturase cDNA sequences. The contig includes a partial  
 CC open reading frame that aligns with M. alpina delta-5- and  
 CC delta-6-desaturase sequences. The contig was utilised in the  
 CC isolation of cDNA (see AAA49932) encoding human delta-5-desaturase  
 CC (see AA195445). Delta-5-desaturase catalyzes the conversion of  
 CC dihomogamma-linolenic acid to arachidonic acid and of 20:4n-3 to  
 CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic  
 CC or eukaryotic hosts using the isolated human delta-5-desaturase  
 CC cDNA, can be used in the production of polyunsaturated fatty acids  
 CC that may be added to nutritional, veterinary and pharmaceutical  
 CC compositions.

XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

SQ Alignment Scores:

Pred. No.: 5.92e-203 Length: 2257

Score: 1935.00 Matches: 352  
 Percent Similarity: 88.84% Conservative: 30  
 Best Local Similarity: 81.86% Mismatches: 44  
 Query Match: 79.37% Indels: 4  
 DB: 21 Gaps: 2

US-09-719-601-5 (1-444) x AAA49939 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35  
 DB 7 CCTACCCCGCGCTACTTCCCTGGACGAGGTGCCCGCCAGCGTCCAGGTGGCAGAGCGG 66  
 QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55  
 DB 67 TGGCTAGTGTATGACCGTAACTAGGTGTACACATCAGCGAGTTACCCCGCGCATCCAGGG 126  
 QY 56 GlyGluArgValIleGlyHisTyrAlaGlyLysAlaThrAspAlaPheArgAlaPhe 75  
 DB 127 GGTCCCGGTTCATCAGCCACTACGCGGCGGACGATGCCAGCATCCCTTTGTGGCTTC 186  
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95  
 DB 187 CACATCAACAAGGCGCTTGTGAAGAAGTATATGAATCTCTCTCTGATTGGAGAACTGTCT 246  
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115  
 DB 247 CCAGAGCAGCCGCTTTGAGCCCAACCAAGAGCTGACAGATGATTCGCGGAG 306  
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135  
 DB 307 CTGCGGCGCACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCCTTCCTCGCTG 366  
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155  
 DB 367 TACCTGTGTGCATCTTGTCTGTGGATGGTGCAGCGCTGGCTACCCCTTTGGCTTTGGG 426  
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174  
 DB 427 ACCTCTTTTGGCCCTTCTCTCTGTGCGGTGTGTCTAGTCAGTCAGTCAGCGGCCAA 486  
 QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194  
 DB 487 GCTGGATGGCTGCAACATGATTATGGCCACTGTCTCTACAGAAACCCCAAGTGGAAC 546  
 QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214  
 DB 547 CACCTTGTCCACAAATTCGTTCATTGGCCACTTAAAGGGTGCCTCTGCAATCGTGGTGAAT 606  
 QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234  
 DB 607 CATGCCCACTTCCAGCACCGCCCAAGCCTAACATCTTCCCAAGGATCCCGATGTGAAC 666  
 QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254  
 DB 667 ATGTGTCAGGTGTGTGTCTGGCGAATGGCAGCCCATCGAGTACGGCAAGAAAGCTG 726  
 QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274  
 DB 727 AAATACCTGGCCCTCAATCACAGCAGCAATCTTCTTCGATTTGGCCCGCCCTGCTC 786  
 QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294  
 DB 787 ATCCCATGTATTTCAGTACCAGATCATCATGACCATGATCGTCCATAGAACTGGTG 846  
 QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314  
 DB 847 GACCTGGCCCTGGCGCGTACACTACATCCGGTTCCTTCATCAGTACATCCCTTTCTAC 906  
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334  
 DB 907 GGCATCTCTGGGAGCCCTCTTCTCACTTCATCAGGTTCTCTGGAGAGCCACTGGTTT 966  
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354

Db 967 GTGTGGGTCACACAGATCAATCACATCGTCATGAGATTGACGAGGCGCTACCGTGAC 1026

Qy 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374

Db 1027 TGGTTTCATGACGCTGACGACCACTGCAACGTGGAGCAGTCTCTTTCACAGACTGG 1086

Qy 375 PheSerGlyHisLeuAsnPhelGlnHisHisLeuPheProThrMetProArgHis 394

Db 1087 TTCAGTGACACCTTAATTCAGATTGAGCACCACCTCTTCCCAACCATGCCCGGCAC 1146

Qy 395 AsnLeuHisValIleAlaProLeuValIleValSerLeuValLeuHisGlyIleGluTyr 414

Db 1147 AACCTTACACAGATCGCCCGCTGTGTGAGTCTCTATGTGCCAGCATGGCAATTGAATAC 1206

Qy 415 GlnGluYsProLeuLeuArgAlaLeuLeuAspIleLeuArgSerLeuLeuYsSerGly 434

Db 1207 CAGGAGAGCGCTACTAGGCGCCCTGCTGCACATCATCAGTCCCTGAGAGTCTGGG 1266

Qy 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444

Db 1267 AGCTGTGGTGGACGCTACCTTACAAA 1296

RESULT 13

AAA09453

ID AAA09453 standard; DNA; 2257 BP.

XX AC AAA09453;

XX DT 10-AUG-2000 (first entry)

XX DE Human contig 2535 DNA encoding desaturase homologue.

XX KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;

XX KW transgenic insect cell; polyunsaturated long chain fatty acid;

XX KW antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;

XX KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;

XX KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;

XX KW antiaggregant; vasotropic; ss.

XX OS Homo sapiens.

XX FH Key

FT mat\_peptide

FT 1..2256

FT \*tag= a

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FT /transl\_except= (pos:1375..1377, aa:Xaa)

FT /transl\_except= (pos:1785..1788, aa:Xaa)

FT /transl\_except= (pos:1885..1887, aa:Xaa)

FT /transl\_except= (pos:1963..1965, aa:Xaa)

FT /transl\_except= (pos:2017..2019, aa:Xaa)

FT /transl\_except= (pos:2062..2064, aa:Xaa)

FT /note= "Xaa not defined"

XX WO200020602-A2.

XX PN 13-APR-2000.

XX PD 29-SEP-1999; 99WO-US22686.

XX PF 05-OCT-1998; 98US-0103110.

XX PR (ABBO ) ABBOTT LAB.

XX PA Mukerji P, Huang Y, Parker-barnes JM, Das T;

XX PI WPI; 2000-328935/28.

XX DR P-PSDB; AA92618.

XX PT Novel transgenic insect cells comprising a nucleotide sequences which

XX PT encode delta-6-desaturase or delta-12- desaturase, useful for producing

XX PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid

PS Example 13; Page 161-162; 170pp; English.

XX AAA09447-52 are human DNA sequences identified based on homology to

CC Mortierella alpina delta-5 and delta-6 desaturase genes. The human

CC DNA's were aligned based on areas of homology to form a contig.

CC Consensus sequences were assembled. A contig, 2511785 overlaps with

CC contig 3506132, and this new contig was called 2535 (AAA09453).

CC The fatty acid desaturases are able to catalyse the conversion of oleic

CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of

CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells

CC comprising a nucleotide sequence which encodes a polypeptide comprising

CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6

CC desaturase (AA92599), or comprising delta-12 desaturase (AA92600) are

CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated

CC from the recombinant insect cells are also claimed. Production of

CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many

CC advantages, as insect cells have greatly simplified lipid compositions,

CC are not subject to external variable fluctuations, and can easily be

CC maintained and manipulated. The oils are used in pharmaceutical

CC compositions, infant formulas, dietary supplements or substitutes, and

CC cosmetics (all claimed). The PUFA supplements have antiinflammatory,

CC antirheumatic, antiasthmatic, antipsoriatic, osteopathic, cytostatic,

CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,

CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic

CC activity.

XX SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Alignment Scores:

Pred. No.: 5.92e-203 Length: 2257

Score: 1935.00 Matches: 352

Percent Similarity: 88.84% Conservative: 30

Best Local Similarity: 81.86% Mismatches: 44

Query Match: 79.37% Indels: 4

DB: 21 Gaps: 2

US-09-719-601-5 (1-444) x AAA09453 (1-2257)

Qy 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35

Db 7 CTTACCCCGCGCTACTTTCCTGGGACGAGTGGCCCGCTCAGGGGCGGAGGCGG 66

Qy 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55

Db 67 TGGCTAGTATCGACCGTAAAGTGTCAACATCAGCGAGTTCACCCCGCGGATCCAGG 126

Qy 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75

Db 127 GGCTCCGGGTATATGACCATCTACCGCGGCGAGGATGCCACGGATCCCTTTGTGGCTTC 186

Qy 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95

Db 187 CACATCAACAAGGGCGCTTGTGAAGAGTATATGAACCTCTCTCTGATTGGAGACTGTCT 246

Qy 96 ProGluLupProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115

Db 247 CCAGAGCAGCCCGCTTTGAGCCCAAGATAAAGACTGACAGATGATGTTCCGGAG 306

Qy 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135

Db 307 CTGGGGCCACAGCTGGAGCGGATGGGGCTCATGAGGCCAACCATGTCTTCTCTGCTG 366

Qy 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGly 155

Db 367 TACCTGCTGCACATCTTGTGCTGGATGGTGCAGCTGCTCACCCTTTGGGTCTTTGGG 426

Qy 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174

Db 427 ACCTCTTTTGGCT 486

Qy 175 AlaglyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194

Db 487 GCTGGATGGCTGCAACATGATTATGCCACCTGTCTGTCTACAGAAAACCCCAAGTGAAC 546

```
QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214
Db 547 CACCTGTGTCACAAATTCGTATTGGCCACATTAAGGGTGCCTTCGCAACTGTGTGAAT 606
QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
Db 607 CATGCCCACTCCAGCACCGCCAGAGCTTAACATCTTCCCAAGGATCCCGATGTGAAC 666
QY 235 MetLeuHisValPheValLeuGlyLysTrpGlnProlIleGlyLysLysLysLeu 254
Db 667 ATGCTGCACGTGTTGTTCTGGGCGAATGGCAGCCATCGAGTACGGCAAGAAAGAGCTG 726
QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274
Db 727 AATACCTGCGCTACAAATCACAGACAGATACATCTTCTGATTTGGCGCCGCTGCTC 786
QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
Db 787 ATCCCGCATGATTTCAGTACCAGATCATCATGACCATGCTGCTCAATGAAGAACTGGTG 846
QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
Db 847 GACCTGGCCCTGGCGGTGAGTACTACATCCGTTCTTCATCACCTACATCCCTTTCTAC 906
QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPhelIleArgPheLeuGluSerHisTrpPhe 334
Db 907 GGCATCCTGGAGCCCTCTTTCCTCAACTTCATCAGGTTCTCTGGAGAGCACTGGTGT 966
QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354
Db 967 GTGTGGGTACACAGATGAATCACATCGTCAATGGAGATTGACAGAGGCTACCGTGAC 1026
QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
Db 1027 TGTTTCAGTAGGAGCTGACAGCCACTGCAACGTTGGAGCACTCTTCTTCAACGACTGG 1086
QY 375 PheSerGlyHisLeuAsnPhelGlnIleGluHisLysLeuPheProThrMetProArgHis 394
Db 1087 TTCAGTGGACACTTAACCTTCAGATTGAGCACCTCTTCCCAACATGCCCCGGCAC 1146
QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
Db 1147 AACTTACACAGATCCCGCGCTGGTGAAGTCTCTATGTCACAGCATGCGCATTAATAC 1206
QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434
Db 1207 CAGGAGAAGCGGTACTGAGGGCCCTGCTGGACATCATCAGGTCCCTGGAAGAGTCTGG 1266
QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1267 AAGCTGTGGTGGACGCTACCTTTCACAA 1296
RESULT 14
AAAI4594
ID AAI4594 standard; DNA; 2257 BP.
XX
AC AAI4594;
XX
DT 08-AUG-2000 (first entry)
XX
DE Nucleotide sequence of a contig of a human desaturase enzyme.
XX
KW Deltas-desaturase; poly-unsaturated long chain fatty acid; PUFA;
KW arachidonic acid; infant formula; dietary supplement; dietary substitute;
KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;
KW malabsorption; resenosis; angioplasty; inflammation; kidney stone;
KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;
KW cancer; cachexia; diabetes; cachexia; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder;
KW blood score; platelet aggregation; vasodilatation;
KW gastro-intestinal bleeding; ss.
```

```
XX Homo sapiens.
OS WO200020603-A1.
XX
PD 13-APR-2000.
XX
PF 29-SEP-1999; 99WO-US22692.
XX
PR 05-OCT-1998; 98US-0103109.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Mukerji P, Huang Y, Parker-Barnes JH, Das T;
XX WPI; 2000-364599/31.
XX DR P-PSDB; AAY84703.
XX
PT Novel transgenic insect cell with modified delta-5-desaturase
XX production, useful for altering fatty acid biosynthesis -
XX
XX Example 9; Page 148-149; 161pp; English.
XX
XX AAA14588-94 represent contigs of a human desaturase. The specification
XX describes a Mortierella alpina deltas-desaturase. The protein is
XX involved in the biosynthesis of poly-unsaturated long chain fatty
XX acids (PUFAs). The polynucleotide is to produce PUFAs, especially
XX arachidonic acid. The oils produced by the invention are used in
XX pharmaceutical compositions, infant formulas, dietary supplements,
XX used to treat normal individuals temporality exposed to stress, or
XX individuals having specialized needs due to chronic or acute diseases
XX (e.g. metabolic disorders such as gastrointestinal difficulties and/or
XX malabsorption, and other disorders such as restenosis after angioplasty,
XX symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,
XX osteoporosis, kidney stones, tract stones, cancer, cachexia associated
XX with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,
XX myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,
XX acute respiratory syndrome, hypertension, inflammatory skin disorders,
XX as well as reduce blood score, inhibit platelet aggregation, cause
XX vasodilatation, inhibit proliferation of vessel wall smooth muscle and
XX fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for
XX geriatric treatments).
XX
XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;
XX
Alignment Scores: 5.92e-203 Length: 2257
Pred. NO.: 1935.00 Matches: 352
Score: 1935.00 Conservative: 30
Percent Similarity: 88.84% Mismatches: 44
Best Local Similarity: 81.86% Indels: 4
Query Match: 79.37% Gaps: 2
Dbs: 21
US-09-719-601-5 (1-444) X ABAI4594 (1-2257)
QY 19 ProThr-----PheSerTrpGluGluIleGlnLysHisLeuArgThrAspSer 35
Db 7 CCTACCCCGCGCTACTTCACTGGAGCGGTGCCCGACGCGTCCAGGGTCCGAGGACGG 66
QY 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
Db 67 TGGTAGTGTATCGACCGTACAGGTGTATACATCAGCGAGTTCACCGCGCATCCAGGG 126
QY 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
Db 127 GGCTCCCGGGTCAATCAGCCACTAGCGCGGCGAGGATCCCGGATCCCTTTGTGGCCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
Db 187 CACATCAACAAGGGCGCTTGTGAAGATATATGACTCTCTCTGATGGAGAACTGTCT 246
QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
```



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Db 247 CCAGAGCAGCCAGCTTTGAGCCCAAGAGCTACAGATGAGTTCGGGAG 306
Qy 116 LeuArgLysThrAlaGluAspValLeuPheLysThrAsnHisValPheLeuLeu 135
Db 307 CTGCGGGCCACAGTGGAGCGGATGGGCTCATGAAGGCCAACCATGCTCTTCTGCTG 366
Qy 136 LeuLeuAlaHisIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
Db 367 TACCTGTGTCACATCTTGCTGTGATGGTGGAGCTGGCTCACCTTTGGTCTTTGGG 426
Qy 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGluAlaGln 174
Db 427 AGCTCTCTTTTGGCCCTTCTCTGTGTGGGTGCTCAGTGCAGTTCAGCAGGCCCAA 486
Qy 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194
Db 487 GTGTGATGGCTGCACATGATTATGGCCACCTGTCTCTACAGAAACCCCAAGTGGAC 546
Qy 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpAsn 214
Db 547 CACCTTGTCCACAAATTCGTATTGGCCACTTAAAGGTGCTCTGCAACTGGTGAAT 606
Qy 215 HisArgHisPheGlnHisIleAlaLysProAsnIlePheHisLysAspProAspValAsn 234
Db 607 CATCGCCACTTCCAGCACCCAGCCCTAACATCTTCCACAGGATCCCGATGTGAAC 666
Qy 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254
Db 667 ATGCTGCAGCTGTTGTTCTGGGCAATGGCAGCCCATCGAGTACGGCAAGAGCTG 726
Qy 255 LysTyrLeuProTyrAsnHisGlnHisIleGluTyrPhePheLeuIleGlyProProLeuLeu 274
Db 727 AAATACCTGCGCTACAAATCACAGCAGCAATACATCTTCTGATGGGCCCGCTGCTC 786
Qy 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
Db 787 ATCCCCATGATTTCAGTACAGATCATCATGACCATGATCGTCCATAAGATGGGTG 846
Qy 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
Db 847 GACCTGGCTGGCGCGTCACTACTACATCCGGTTCCTCATCAGTACATCCCTTTCTAC 906
Qy 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
Db 907 GGCATCTGGAGGCCCTCTTTCTCACTCATCAGTTCTCGAGAGCCACTGGTTT 966
Qy 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354
Db 967 GTGTGGGTACACAGATGAATCACATCGTCATGGAGATTGACAGGAGGCCCTACCGTGAC 1026
Qy 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPheAsnAspTrp 374
Db 1027 TGGTTTCAGTAGCAGCTGACAGCCACCTGCAACGTGGAGCAGTCTCTTCAACGATCGG 1086
Qy 375 PheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHis 394
Db 1087 TTCAGTGAGCACCTTAATTCAGATTGAGCACCACTCTTCCCAACATGCCCGGCAC 1146
Qy 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
Db 1147 AACTTACAAAGATGCCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCATTAATAC 1206
Qy 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysGly 434
Db 1207 CAGGAGAGCCGCTACTGAGGCCCTGCTGGACATCATCAGTCTCTTGAAGATCTGGG 1266
Qy 435 LysLeuTrpLeuAspAlaTyrIleuHisLys 444
Db 1267 AAGCTGTGGCTGGAGCCCTACCTTCCACAA 1296
```

RESULT 15  
ABS71826

```
ID ABS71826 standard; DNA; 2257 BP.
XX ABS71826;
AC
XX
XX 02-DEC-2002 (first entry)
DT
XX
XX Human deltas-desaturase gene #8.
DE
XX
XX Human; deltas-desaturase; polyunsaturated fatty acid; DGLA;
KW dihomo-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;
KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;
KW gene; ds.
XX
XX Homo sapiens.
OS
XX
XX US6432684-B1.
PN
XX
XX 13-AUG-2002.
PD
XX
XX 08-JAN-1999; 99US-0227613.
PF
XX
XX 11-APR-1997; 97US-0833610.
PR
XX
XX 10-APR-1998; 98WO-US07422.
XX
XX (ABBO ) ABBOTT LAB.
PA
XX
XX Mukerji P, Leonard AB, Huang Y, Das T;
PI WPI; 2002-689761/74.
XX
XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing
PT the conversion of dihomo-gamma-linolenic acid to arachidonic acid and
PT in the conversion of 20:4n-3 to eicosapentaenoic acid -
XX
XX Example 1; Figure 8; 88pp; English.
XX
XX The invention relates to an isolated human deltas-desaturase nucleotide
CC sequence (I) which desaturates polyunsaturated fatty acids at
CC carbon 5. The nucleotide sequence (I) may be used in the recombinant
CC production of vectors and host cells for the production of deltas-
CC desaturase. Deltas-desaturase may be utilised in the conversion of
CC dihomo-gamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the
CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or
CC polyunsaturated fatty acids produced from it may be added to
CC pharmaceutical compositions, nutritional compositions, animal feeds, as
CC well as other products such as cosmetics. ABS71819-ABS71854
CC represent human deltas-desaturase coding sequences and PCR primers of
CC the invention.
XX
XX SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;
```

Alignment Scores:

| Pred. No.:             | 5,92e-203 | Length:       | 2257 |
|------------------------|-----------|---------------|------|
| Score:                 | 1935.00   | Matches:      | 352  |
| Percent Similarity:    | 88.84%    | Conservative: | 30   |
| Best Local Similarity: | 81.86%    | Mismatches:   | 44   |
| Query Match:           | 79.37%    | Indels:       | 4    |
| DB:                    | 24        | Gaps:         | 2    |

US-09-719-601-5 (1-444) x ABS71826 (1-2257)

```
Qy 19 ProThr-----PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSer 35
Db 7 CCTACCCCGCGCTACTTCACTGGGACGAGGTGGCCAGCGCTCAGGTGGCAGGCGG 66
Qy 36 GlyLeuValIleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGly 55
Db 67 TGCTAGTATCAGCGGTAAAGGTGTACACATCAGCGAGTTCCACCGCGCGCATCCAGG 126
Qy 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
Db 127 GGCTCCCGGGTTCATCAGCCACTACCGCGGACAGATGCCACGATCCCTTTGTGGCTTC 186
```



CC topical ointments. The PUFAs produced by this method are useful in  
 CC producing pharmaceutical compositions for treating rough or aging skin,  
 CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
 CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,  
 CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
 CC platelet aggregation, inducing vasodilation, reducing cholesterol  
 CC levels, inhibiting proliferation of fibrous tissue, treating  
 CC endometriosis, and myalgic cephalomyelitis. The gene for delta5  
 CC desaturase is located on chromosome 11q12. The present sequence  
 CC is a partial cDNA for a human delta5 desaturase.

XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

## Alignment Scores:

Pred. No.: 5.92e-203 Length: 2257  
 Score: 1935.00 Matches: 352  
 Percent Similarity: 88.84% Conservative: 30  
 Best Local Similarity: 81.86% Mismatches: 44  
 Query Match: 79.37% Indels: 4  
 DB: 24 Gaps: 2

US-09-719-601-5 (1-444) x ABS76713 (1-2257)

QY 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35  
 DB 7 CCTACCCCGCGCTACTTCCCTGGGACGAGTGGCCCGCGCTCAGGGTCCGAGGACGG 66  
 QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55  
 DB 67 TGGCTAGTAGTCGACCGCTAAGGTGTACAAATCAGGAGTTCACCCGCGCATCCAGGG 126  
 QY 56 GlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75  
 DB 127 GGCTCCCGGGTCATCAGCCATCAGCCGGGAGAGTCCAGGATCCCTTTGTGGCCTTC 186  
 QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95  
 DB 187 CACATCAACAGGGCGCTTGTGAAGAGTATATGAATCTCTCTCTGATTTGGAGACTGTCT 246  
 QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115  
 DB 247 CCAGAGCAGCCCGCTTTGGCCCAACCAAGAAATGAAGAGCTGACAGATGATTCGCGGAG 306  
 QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135  
 DB 307 CTGCGGGCCACAGTCGAGCGGATGGGCTCATGAAGCCCAACCATGCTCTTCTCTGCTG 366  
 QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155  
 DB 367 TACTGTCTGCACATCTTGTCTGTGATGGTGCAGCTGGCTCACCCCTTTGGTCTTTGGG 426  
 QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174  
 DB 427 ACGTCTTTTGGCCCTTCTCTCTGTCGGTGTCTGCTCAGTCAGTTCAGAGGCCCA 486  
 QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194  
 DB 487 GCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAAACCCAACTGGAAC 546  
 QY 195 HisLeuValHisLysPheValIleGlyHisIleLysGlyAlaSerAlaAsnTrpTrpAsn 214  
 DB 547 CACCTTGTCACAAATTCGTATTGGCCACCTTAAGGGTGGCTCTGCCAACTGGTGGAA 606  
 QY 215 HisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234  
 DB 607 CATGCCACTTCCAGCACACCGCCAGCGCTAACATCTTCCACAGGATCCCGATGTGAAC 666  
 QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254  
 DB 667 ATGCTGCACGTGTTGTTGCTGGCGCAATGGGACCCCATCGAGTACGGCAAGAGAGCTG 726  
 QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeu 274

DB 727 AAATACCTGGCCCTCAATCAATCACCAGCAGCAATACTTCTTCTGATGGCGCGCTGCTC 786  
 QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisAsnTrpVal 294  
 DB 787 ATCCCATGATATTTCCAGTACCAGATCATCATGACCATGATCGTCCATTAAGAACTGGGTG 846  
 QY 295 AspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314  
 DB 847 GACCTGGCTGGCGCTCAGCTACTACATCCGGTTCTTTCATCACCTACATCCCTTCTAC 906  
 QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334  
 DB 907 GGCATCCTGGAGCCCTCTTCTTCTCAACTTCATCAGGTTCTCTGGAGAGCCACTGGTTT 966  
 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354  
 DB 967 GTGTGGGTACACATGATGATCATCGTCTATGGAGATTGACAGAGGCTTACCGTGAC 1026  
 QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374  
 DB 1027 TGGTTTCAGTAGCCAGCTGACAGCCACCTGCAACGTCGAGCACTCTCTTCTCAACACTGG 1086  
 QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394  
 DB 1087 TTCAGTGGACACTTAACTTCCAGATTGAGCAACCACTTCTTCCCACCATGCGCCGGCAC 1146  
 QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414  
 DB 1147 AACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTCGAATAC 1206  
 QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGly 434  
 DB 1207 CAGGAGAACCCCTACTGAGGGCCCTGCTGGACATCATCAGTCTCCCTGAAGAAGTCTGG 1266  
 QY 435 LysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 DB 1267 AAGCTGTGCTGGACGCTTACCTTACAAA 1296

RESULT 17  
 ABT10758  
 ID ABT10758 standard; cDNA; 2621 BP.  
 XX  
 AC ABT10758;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human breast cancer associated coding sequence SEQ ID NO: 892.  
 XX  
 KW Human; breast specific gene; breast cancer; differential expression;  
 KW cytostatic; gene therapy; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200259271-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 25-JAN-2002; 2002WO-US02176.  
 XX  
 PR 25-JAN-2001; 2001US-263757P.  
 PR 25-APR-2001; 2001US-286090P.  
 PR 23-MAY-2001; 2001US-292517P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Orr MS, Nation M, Diggins JC, Zeng W;  
 XX  
 DR MPI; 2002-674803/72.  
 XX  
 PT Diagnosing breast cancer in a patient comprises detecting the level of  
 PT gene expression in cell or tissue samples, where a differential gene  
 PT expression is indicative of breast cancer -

|    |     |   |     |
|----|-----|---|-----|
| Db | 614 | ACACAGATGAATCACATCGTTCATGGAGATTGACACGAGGCCCTACCGTGACCTGGTTTCAGT | 677 |
| Qy | 358 | SerGlnLeuThrAlaThrCysAsnValcIuGlnSerPhePheAsnAspTrpPheSerGly    | 377 |
| Db | 674 | ASCCAGCTGACAGCCACCTCGCAACGTCGAGCAGTCTCTTCTTCAACGACTGGTTCAGTGGA  | 733 |
| Qy | 378 | HisLeuAsnPheGlnIleGluHisIleuPheProThrMetProArgHisAsnLeuHis      | 397 |
| Db | 734 | CACCTTTACTTCCAGATTGACACACCACTCTTCCCCACCATGCCCGGCACCACTTACAC     | 793 |
| Qy | 398 | LysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluLys    | 417 |
| Db | 794 | AGATCGCCCGCTGGTGAATCTTATGTGCCAAGCATGGCATGAATACCAAGGAAG          | 853 |
| Qy | 418 | ProLeuLeuArgAlaLeuLeuAspIleAlaArgSerLeuLysLysSerGlyLysLeuTrp    | 437 |
| Db | 854 | CGCTACTGAGGGCCCTCTCGACATCATCAGGACCCTGATGAAGTCTGGGAAGCTGTGG      | 913 |
| Qy | 438 | LeuAspAlaTyrLeuHisLys   | 444 |
| Db | 914 | CTGGACGCCTACCTTCAAAA  | 934 |

RESULT 18  
 ABL90108  
 ID ABL90108 standard; CDNA; 1575 BP.  
 XX  
 AC ABL90108;  
 XX  
 DT 24-MAY-2002 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 670.  
 DE

|    |   |
|----|---|
| XX | Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;     |
| KW | antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;    |
| KW | vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;        |
| KW | cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; |
| KW | neurological disease; infection; human; secreted protein; gene; ss.       |
| XX |   |
| OS | Homo sapiens.   |
| XX |   |
| XX | WO200190304-A2.   |
| XX |   |
| PD | 29-NOV-2001.  |
| XX |   |
| XX | 18-MAY-2001; 2001WO-US16450.  |
| PF |   |
| XX | 19-MAY-2000; 2000US-205515P.  |
| XX |   |
| PA | (HUMA-) HUMAN GENOME SCI INC.   |
| XX |   |
| PI | Birse CE, Rosen CA;   |
| XX |   |
| XX | WPI; 2002-122018/16.  |
| DR | P-PSDB; ABB93699.   |
| XX |   |
| XX | Novel 1405 isolated polypeptides, useful for diagnosis, treatment and     |
| PT | prevention of neural, immune system, muscular, reproductive,              |
| PT | gastrointestinal, pulmonary, cardiovascular, renal and proliferative      |
| PT | disorders -   |
| XX |   |
| XX | Claim 4; SEQ ID NO 670; 2081pp + Sequence Listing; English.               |
| PS |   |
| XX |   |
| XX | The invention relates to novel genes (ABL89449-ABJ90853) and proteins     |
| CC | (ABB89040-ABB90444) useful for preventing, treating or ameliorating       |
| CC | medical conditions e.g. by protein or gene therapy. The genes are         |
| CC | isolated from a range of human tissues disclosed in the specification.    |
| CC | The nucleic acids, proteins, antibodies and (ant)agonists are useful      |
| CC | in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast    |
| CC | and ovarian cancer and other cancers of the adrenal gland, bone, bone     |
| CC | marrow, breast, gastrointestinal tract, liver, lung, or urogenital;       |
| CC | (b) immune disorders e.g. Addison's disease, allergies, autoimmune;       |
| CC | haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's    |
| CC | disease, multiple sclerosis, rheumatoid arthritis and ulcerative          |

CC colitis; (c) cardiovascular disorders such as myocardial ischemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

SQ Sequence 1575 BP; 313 A; 500 C; 386 G; 368 T; 8 other;

## Alignment Scores:

Pred. No.: 7,918-174 Length: 1575  
 Score: 1669.00 Matches: 298  
 Percent Similarity: 99.67% Conservative: 0  
 Best Local Similarity: 99.67% Mismatches: 1  
 Query Match: 68.46% Indels: 0  
 DB: 24 Gaps: 0

US-09-719-601-5 (1-444) x ABL90108 (1-1575)

QY 146 IleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAla 165  
 Db 3 ATTGCATGGTTCACTGCTTTTACTTTGGCAATGGCTGATTCCTACCCICATCAGGCC 62  
 QY 166 PheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeu 185  
 Db 63 TTTGTCTGTGTACCTCTCAGGCCCAAGCTGKATGGCTGCAACATGATTATGGCCACCTG 122  
 QY 186 SerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeu 205  
 Db 123 TCTGTCTACAGAAACCCCAAGTGGACCACTTGTCCACAAATTCGTCATTTGGCCACTTA 182  
 QY 206 LysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsn 225  
 Db 183 AAGGGTGCCTCTGCCAACTGGTGGGAATCATCGCCACTTCCAGCACCAAGCCCAAGCTAAC 242  
 QY 226 IlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlyTrpGln 245  
 Db 243 AICTTCCACAGAGATCCCGATGTGAACATGCTGCACGTTGTTGTTCTGGGCGAATGGCAG 302  
 QY 246 ProfileGlyTyrGlyLysLysLysLysLysTyrLeuProTyrAsnHisGlnHisGlyTyr 265  
 Db 303 CCCATCGAGTACGGCAAGAAGCTGAATACCTGCCCTACAATCACCAGCAGCAAGATAC 362  
 QY 266 PhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285  
 Db 363 TTCTTCCATGATGGCGCGCTGCTCATCCCATGTTATTTCCAGTACAGATCATCATG 422  
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305  
 Db 423 ACCATGATGCTCCATAAGAAGCTGGTGGACCTGGCGCTGGCGCTCAGCTACTACATCGG 482  
 QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325  
 Db 483 TTCTTCATCACTATACCTCTTCACGGCATCTCGGAGGCCCTCTTTTCTCAACTTC 542  
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345  
 Db 543 ATCAGGTTCCTGGAGGCCACTGTTGTTGGTGCACACAGATGAATCATCATGTCATG 602  
 QY 346 GluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365  
 Db 603 GAGATTGACAGAGGCGCTTACCGTACCTGTTTCACTAGCCAGCTCAGACCCACCTGCAAC 662  
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385  
 Db 663 GTGGAGCAGTCTCTTTCACCAAGCTGTTTCAGTGGACACCTTAATTCAGATTGAGCAG 722  
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405  
 Db 723 CACCTTCTCCCAACCATGCCCCGGCACAACTTACAAAGATGCCCGCTGTGTGAAGTCT 782  
 QY 406 LeuCysAlaLysHisGlyIleGlyTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425

Db 783 CTATGTGCCAAGCATGGCATTCGAATCACCAGGAGAGCGCTACTGAGGGCCCTGCTGGAC 842  
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 Db 843 ATCATCAGTCCCTGGAAGTCTGGGAAGTCTGGTGGACGCTTACCTTACCAA 899  
 RESULT 19  
 AAK94786  
 ID AAK94786 standard; cDNA; 2558 BP.  
 XX  
 AC AAK94786;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DT Human full-length cDNA, SEQ ID NO: 3894.  
 XX  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114089.  
 XX  
 PR 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 WIPI: 2001-524255/58.  
 P-PSDB; AAM93830.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 3894; 1380pp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesising the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a full length  
 CC human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX  
 SQ Sequence 2558 BP; 502 A; 777 C; 710 G; 569 T; 0 other;

Alignment Scores:  
 Pred. No.: 2,12e-173 Length: 2558  
 Score: 1668.00 Matches: 297  
 Percent Similarity: 99.67% Conservative: 1  
 Best Local Similarity: 99.33% Mismatches: 1  
 Query Match: 68.42% Indels: 0  
 DB: 22 Gaps: 0

US-09-719-601-5 (1-444) x AAK94786 (1-2558)

QY 146 IleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAla 165  
 Db 1 ATTGCATGGTTCACTGCTTTTACTTTGGCAATGGCTGATTCCTACCCICATCAGGCC 60

QY 166 PheValLeuAlaThrSerGlnhlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeu 185  
 DB 61 TTTGTCCTTGTACCTCTCAGCCCAAGCTGGATGGCTGCAACATGATTAAGCCACCTG 120  
 QY 186 SerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeu 205  
 DB 121 TCTGTCTACAGAAACCCCAAGTGAACACCTTGTCCACAAATTCATCATTTGGCCACTTA 180  
 QY 206 LysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsn 225  
 DB 181 AAGGGTGCCTCTGCCAACTGGTGAATCATGCCACTTCCACACCCAGCCCAAGCCTAAC 240  
 QY 226 IlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyLutPgin 245  
 DB 241 ATCTTCCACAGGATCCCATGTGAACATGCTGCACGTGTGTCTGGGGGAATGGCAG 300  
 QY 246 ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265  
 DB 301 CCCATCGAGTACGGCAAGGAAGCTGAAATACCTGCCCTACCAATCACACGACCAAGATAC 360  
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMet 285  
 DB 361 TTCTTCTGATGGGGCGCGCTGCTCATCCCATGTATTTCCAGTACCATCATCATG 420  
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrileArg 305  
 DB 421 ACCATGATGTCATTAAGAACTGGGTGGACCTGGCTGGCGCTCAGCTACTACATCCGG 480  
 QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325  
 DB 481 TTCTTCTCATCCTTACATCCCTTTCTACGGCATCCCTGGGAGCCCTCTTTCTCTCACTTC 540  
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345  
 DB 541 ATCAGGTTCCTGGAGAGCCACTGTTTGTGGTCCACACAGATGAATCACATGCTCATG 600  
 QY 346 GluIleAspGlnCluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365  
 DB 601 GAGATTGACAGAGAGCCCTACCGTGTCTGTTGAGTGGAGTGGAGTGGAGTGGAGTGGAG 660  
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385  
 DB 661 GTGGAGCAGTCTCTTCAAGACTGTTTCAGTGGACACCTTAACCTCCAGATTGAGCAC 720  
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405  
 DB 721 CACCTCTTCCCAACCATGCCCGGCACTTACACAGATCGCCCGCTGTGTGAAGTCT 780  
 QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425  
 DB 781 CTATGTGCCAAGCATGGCATTGATACCGGGGAGAGCCGCTACTGAGGCGCCTGTGGAC 840  
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 DB 841 ATCATCAGTCTCCTGAAGAGTCTGGGAGCTGTGGAGCTGTGGAGCTGTGGAGCTGTGGAG 897  
 RESULT 20  
 AAV63642  
 ID AAV63642 standard; cDNA; 1843 BP.  
 XX  
 AC AAV63642;  
 XX  
 DT 15-FEB-1999 (first entry)  
 XX  
 DE Contig 2535 encoding a human desaturase enzyme.  
 XX  
 KW Fatty acid; desaturase; polyunsaturated fatty acid;  
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome; human;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

OS Homo sapiens.  
 XX  
 PN W09846763-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 10-APR-1998; 98WO-US07126.  
 XX  
 PR 11-APR-1997; 97US-0834655.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX  
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 XX  
 DR WPI: 1998-594582/50.  
 DR P-PSDB; AAW841155.  
 XX  
 PT New isolated fatty acid desaturase enzymes - used for the production  
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
 PT compositions, nutritional compositions, cosmetics or animal feed  
 XX  
 PS Example 12; Pages 116-117; 165pp; English.  
 XX  
 CC The present sequence encodes a human desaturase enzyme. The sequence was  
 CC identified based on homology between human cDNA sequences and Mortierella  
 CC alpina desaturase gene sequences. The specification describes methods for  
 CC desaturating a fatty acid and for producing a desaturated fatty acid by  
 CC expressing increased levels of a desaturase. The enzyme can be used for  
 CC desaturating fatty acids. The enzyme can be used to produce  
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,  
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The  
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis  
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma,  
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They  
 CC can also be used to inhibit platelet aggregation, cause vasodilation,  
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth  
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding  
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,  
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic  
 CC encephalomyelitis and chronic fatigue after viral infections, treat  
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and  
 CC inflammatory skin disorders.  
 XX  
 SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,46e-171 Length: 1843  
 Score: 1646.00 Matches: 294  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 67.51% Indels: 0  
 DB: 19 Gaps: 0  
 US-09-719-601-5 (1-444) x AAV63642 (1-1843)  
 QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170  
 DB 1 GTCCTTTTACITTTGGCAATGGCTGGATTCCTACCTCATCGGCTTTGTCTGTCTACC 60  
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTTATGGCCACTGTCTGTCTCAGAAA 120  
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210  
 DB 121 CCCAAGTGGAAACCACTTGTCCCAAAATTCGTCTATGGCCACTTAAGGGTGGCTCTGCC 180  
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230  
 DB 191 AACTGGTGGATCATCGCACTTCCAGCACCCAGCCCAAGCTTAACATCTTCCCAAGGAT 240

QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250  
 Db 241 CCCGATGTGACATCTGACATGTTGTTTCTGGCGAATGGCAGCCATCGATACGGC 300  
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270  
 Db 301 AAGAAAGAGCTGAATACCTGCGCTACCAATCACCAGCAGCAATATCTTCTCTGATTGGG 360  
 QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290  
 Db 361 CGCGCGCTGCTCATCCCATGATTTCCAGTACCAAGATCATCATGACCATCATCGTCCAT 420  
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleAArgPhePheIleThrTyr 310  
 Db 421 AAGAACTGGGTGACCTGGCTGGCGCTGAGTACTACTACATCGGTTCTTCATCACCTAC 480  
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuPheLeuPheLeuAsnPheIleAArgPheIleGlu 330  
 Db 481 ATCCCTTTCTACGGCATCTGGAGCCCTCTTTCTCAACTTCATCAGGTTCTCTGGAG 540  
 QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350  
 Db 541 AGCCACTGGTTGTGGGTACACAGATGAATCATCGTCATGGAGATTGACCGAG 600  
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370  
 Db 601 GCTACCGTGTGCTGTTGAGTACGAGCTGACAGCCCTGCAACGCTGGAGCAGTCTCTTC 660  
 QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390  
 Db 661 TTCACGACTGTTGAGTGACACCTTAATTCAGATTGAGCACCCTCTTCCACC 720  
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCGCGCACAACTTACACAGATGCGCCGCTGGTGAATCTCTATGTGCCAAGCAT 780  
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleAArgSerIleu 430  
 Db 781 GGCATTGAATACAGAGAGAGCGCTACTAGGCGCCCTGCTGGACATCATCAGGTCCCTG 840  
 QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 Db 841 AAGAAAGCTGTGGAAGCTGTGGTGGAGCGCTACCTACCTTCAAAA 882

RESULT 21  
 AAX00909 standard; DNA; 1843 BP.  
 XX AC AAX00909;  
 XX DT 26-MAR-1999 (first entry)  
 XX DE Human desaturase gene contig 2535.  
 XX KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;  
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;  
 KW stearidonic acid; eicosapentaenoic acid; main nutrition; feeding formula;  
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;  
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;  
 KW diabetes; cosmetic; animal feed; human; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT 1.1842  
 XX CDS /tag= a  
 XX FT /note= "contains internal stop codons"  
 XX FN W09846764-A1.  
 XX PD 22-OCT-1998.  
 XX XX 10-APR-1998; 98WO-US07421.

XX 24-OCT-1997; 97US-0958985.  
 PR 11-APR-1997; 97US-0833610.  
 PR 11-APR-1997; 97US-0834033.  
 PR 11-APR-1997; 97US-0834655.  
 XX (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX Chaudhary S, Huang Y, Knutzon D, Leonard AS, Mukerji P;  
 PI Thurmond J;  
 XX WPI; 1999-080739/07.  
 DR P-PSDB; AAW95513.  
 XX Nucleic acid construct able to express fatty acid desaturase in  
 PT plants - useful in human or animal nutrition, as cosmetics and  
 FT therapeutically, e.g. for restenosis, cancer and diabetes  
 XX Claim 48; Page 160-161; 210pp; English.  
 XX The invention relates to a nucleic acid construct that contains at least  
 CC one of the nucleotide sequences (AAX00889 to AAX00891) encoding  
 CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to  
 CC AAW95506) respectively, coupled to an expression control sequence  
 CC functional in plants. Recombinant plant cells containing at least one DNA  
 CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the  
 CC production of polyunsaturated fatty acid (PUFA). These recombinant cells  
 CC or plants containing them are used to produce oils such as linoleic  
 CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic  
 CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils  
 CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or  
 CC dietary supplements or substitutes, for use in humans or animals; (iii)  
 CC for treating disorders associated with inadequate consumption or  
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.  
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,  
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,  
 CC and (v) as animal feeds. Fragments of the DNA are used as probes to  
 CC isolate related coding sequences. Recombinant plants can produce high  
 CC yields of PUFA, since new pathways can be created and unwanted ones  
 CC suppressed. Plants can be engineered to express oils of particular PUFA  
 CC composition, e.g. one similar to that in human milk, and product recovery  
 CC is simpler than with e.g. fish. Sequences AAX00904-910 represent DNA  
 CC sequences of various contigs of human desaturase genes which are similar  
 CC to the M. alpina desaturase sequences.  
 XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,46e-171 Length: 1843  
 Score: 1646.00 Matches: 294  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 67.51% Indels: 0  
 DB: 20 Gaps: 0  
 US-09-719-601-5 (1-444) x AAX00909 (1-1843)  
 QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170  
 Db 1 GTCTTTACTTTGGCAATGGCTGGATTCTTACCTCATCAGGCTTTGCTTGTGTAC 60  
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 Db 61 TCTCAGGCCCAAGCTGGATGGCTGCACCATGATTATGGCCACCTGCTGTCTACAGAAA 120  
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210  
 Db 121 CCCAAGTGAACCACTTGTCCCAATTCGTATTGGCCACTTAAGGTGCTCTGCC 180  
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230  
 Db 181 AACTGGTGAATCATCGCCACTTCCAGCACCACCGCCCAAGCTTAACATCTTCCACAGGAT 240







QY 371 PheAsnAspTTPPhSeGlyHisLeuAsnPhenGlnIleGluHisLeuPheProThr 390  
 Db 661 TTCAACGACTGGTTCAGTGGACACCTTAACTTCCAGATTGAGCACCACTCTTCCCCACC 720  
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCGGCACACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780  
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerIleu 430  
 Db 781 GGCATTGAATACAGGAGAACCGCTACTAGGCGCCCTGCTGGACATCATCAGGTCCCTG 840  
 QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 Db 841 AAGAAGCTGGGAAGCTGTGGTGGACGCTACCTTCAAAA 882

RESULT 24  
 AAA09452  
 ID AAA09452 standard; DNA; 1843 BP.  
 AC AAA09452;  
 XX 10-AUG-2000 (first entry)  
 DT  
 XX Human contig DNA encoding desaturase homologue.  
 DE  
 XX  
 KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;  
 KW transgenic insect cell; polyunsaturated long chain fatty acid;  
 KW antiinflammatory; antirheumatic; antisthmatic; antipsoriatic;  
 KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;  
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;  
 KW antiaggregant; vasotropic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT mat\_peptide 1..1842  
 FT /\*tag= a  
 FT /transl\_except= (pos:883..885, aa:Xaa)  
 FT /transl\_except= (pos:961..963, aa:Xaa)  
 FT /transl\_except= (pos:1371..1374, aa:Xaa)  
 FT /transl\_except= (pos:1471..1473, aa:Xaa)  
 FT /transl\_except= (pos:1549..1551, aa:Xaa)  
 FT /transl\_except= (pos:1648..1650, aa:Xaa)  
 FT /note= "Xaa not defined"  
 XX  
 XX W0200020602-A2.  
 XX  
 XX 13-APR-2000.  
 XX  
 XX 29-SEP-1999; 99WO-US22686.  
 XX  
 XX 05-OCT-1998; 98US-01031110.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Mukerji P, Huang Y, Parker-barnes JM, Das T;  
 XX  
 XX WPI; 2000-328935/28.  
 XX P-PSDB; AAY92617.  
 XX  
 XX Novel transgenic insect cells comprising a nucleotide sequences which  
 XX encode delta-6-desaturase or delta-12- desaturase, useful for producing  
 XX poly-unsaturated long chain fatty acids, e.g. arachidonic acid  
 XX  
 XX Example 13; Page 160-161; 170pp; English.  
 XX  
 XX AAA09447-52 are human DNA sequences identified based on homology to  
 XX Mortierella alpina delta-5 and delta-6 desaturase genes. The human  
 XX DNA's were aligned based on areas of homology to form a contig.  
 XX Consensus sequences were assembled. A contig, 2511785 overlaps with  
 XX contig 3506132, and this new contig was called 2535 (AAA09453).

CC The fatty acid desaturases are able to catalyse the conversion of oleic  
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of  
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells  
 CC comprising a nucleotide sequence which encodes a polypeptide comprising  
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6  
 CC desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are  
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated  
 CC from the recombinant insect cells are also claimed. Production of  
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many  
 CC advantages, as insect cells have greatly simplified lipid compositions,  
 CC are not subject to external variable fluctuations, and can easily be  
 CC maintained and manipulated. The oils are used in pharmaceutical  
 CC compositions, infant formulae, dietary supplements or substitutes, and  
 CC cosmetics (all claimed). The PUFA supplements have antiinflammatory,  
 CC antirheumatic, antisthmatic, antipsoriatic, osteopathic, cytostatic,  
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,  
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic  
 CC activity.  
 XX  
 SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;  
 Alignment Scores:  
 Pred No.: 3,46e-171 Length: 1843  
 Score: 1646.00 Matches: 294  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 67.51% Indels: 0  
 DB: 21 Gaps: 0  
 US-09-719-601-5 (1-444) x AAA09452 (1-1843)  
 QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170  
 Db 1 GTCTTTTACTTGGCAATGGCTGGATTCCTACCTCATACAGCCCTTGTCTTGTTACC 60  
 QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 Db 61 TCTCAGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 120  
 QY 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyValAspAla 210  
 Db 121 CCCAAGTGGACCACTTGTGCCAAATTCGTATTGGCCACCTTAAAGGGTGGCTCTGCC 180  
 QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230  
 Db 191 AACTGGTGGATCATCGCCACTTCCAGCACCCAGCCCAAGCCTTAACATCTTCCACAGGAT 240  
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250  
 Db 241 CCGCATGTGAACATGCTGCACGTGTTTGTCTGGCGGAATGGCAGCCCATCGAGTACGGC 300  
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270  
 Db 301 AAGAAGAGCTGAAATACCTGCCCTACATACCCAGCACGAATACTTCTTCTGATTGGG 360  
 QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290  
 Db 361 CCGCGCTGCTCATCCCATGATTTTCCAGTACCAGATCATCATGACCATGATCGTCCAT 420  
 QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
 Db 421 AAGAACTGGGTGGACCTGGCTGGCGCTGAGCTACTACATCCCGTTCCTCATCACCTAC 480  
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330  
 Db 481 ATCCCTTTTCTACGGCATCCTGGAGCCCTCCCTTTTCTCACTTCACTCAGGTCTCTGGAG 540  
 QY 331 SerHisTrpPheValTrpValThrClnMetAsnHisIleValMetGluIleAspGlnGlu 350  
 Db 541 AGCCACTGGTGTGTGGGTGCACAGATGAATCATCATCTGTCATGGAGATTGACACGAG 600  
 QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370

Db 601 GCCTACCGTGACTGTTTCAGTAGCCAGCTGACAGCCACTGCAACGCTGGAGCGTCTTC 660  
 Qy 371 PheAsnAspTrpPheSerGlyHisLeuAsnPhenIleGluHisHisLeuPheProThr 390  
 Db 661 TTCAACGAGCTGTTTCAGTGAGCACCTTAACTTCCAGATTGAGCACCACTTCTCCACC 720  
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCGGCGACAACTTACACAGATGCGCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780  
 Qy 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleAlaArgSerLeu 430  
 Db 781 GCATGTGAATACAGAGAGCGCTACTAGAGGCGCTGCTGACATCATCAGGTCCCTG 840  
 Qy 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
 Db 841 AAGAAGTCTGGGAAGCTGTGGCTGACGCGCTACCTTCACAA 882

## RESULT 25

AAAL4593  
 ID AAAL4593 standard; DNA; 1843 BP.

XX  
 AC AAAL4593;

DT 08-AUG-2000 (first entry)

XX Nucleotide sequence of a contig of a human desaturase enzyme.

XX Delta5-desaturase; poly-unsaturated long chain fatty acid; PUFA;  
 KW arachidonic acid; infant formula; dietary supplement; dietary substitute;  
 KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;  
 KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;  
 KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;  
 KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder;  
 KW blood score; platelet aggregation; vasodilatation;  
 KW gastro-intestinal bleeding; ss.

XX Homo sapiens.

XX WC2000020603-A1.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US22692.

XX 05-OCT-1998; 98US-0103109.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-Barnes JH, Das T;

XX WPI; 2000-364599/31..

XX P-PSDB; AAY84702.

XX Novel transgenic insect cell with modified delta-5-desaturase

XX production, useful for altering fatty acid biosynthesis -

XX Example 9; Page 147-148; 161pp; English.

XX AAAL4588-94 represent contigs of a human desaturase. The specification  
 CC describes a Mortierella alpina delta5-desaturase. The protein is  
 CC involved in the biosynthesis of poly-unsaturated long chain fatty  
 CC acids (PUFAs). The polynucleotide is to produce PUFAs, especially  
 CC arachidonic acid. The oils produced by the invention are used in  
 CC pharmaceutical compositions, infant formulas, dietary supplements,  
 CC dietary substitutes, and cosmetics. The nutritional compositions can be  
 CC used to treat normal individuals temporality exposed to stress, or  
 CC individuals having specialized needs due to chronic or acute diseases  
 CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or  
 CC malabsorption, and other disorders such as restenosis after angioplasty,  
 CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,

CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated  
 CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,  
 CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,  
 CC acute respiratory syndrome, hypertension, inflammatory skin disorders,  
 CC as well as reduce blood score, inhibit platelet aggregation, cause and  
 CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and  
 CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for  
 CC geriatric treatments).

XX Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

## Alignment Scores:

Fred. No.: 3,46e-171 Length: 1843  
 Score: 1646.00 Matches: 294  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 57.51% Indels: 0  
 DB: 21 Gaps: 0

US-09-719-601-5 (1-444) x AAAL4593 (1-1843)

Qy 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170  
 Db 1 GTCTTTTACCTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTGTCTTGTAC 60  
 Qy 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 Db 61 TCTAGGCCCAAGCTGGATGGCTGGCAACATGATTATGGGCACCTGTCTGTCTACAGAAA 120  
 Qy 191 ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210  
 Db 121 CCNAGTGGAAACCACTTGTCCACAATTCGTATGGCCACTTAAGGGTGCCTTGCC 180  
 Qy 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230  
 Db 181 AACTGGTGGAAATCATGCCACTTCCAGCACACGCAAGCCTAACATCTTCCAAAGGAT 240  
 Qy 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250  
 Db 241 CCGATGTGAACATGCTGGACGTGTTTGTCTGGGCAATGGCAGCCATCGAGTACGGC 300  
 Qy 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270  
 Db 301 AAGAAGAAGCTGAAATACCTGCCTCAATCACAGCACGAAATCTTCTCTGATTGGG 360  
 Qy 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMetThrMetIleValHis 290  
 Db 361 CCGCGCTGCTCATCCCATGTTATTTCCAGTACAGATCATGACCATGATCGTCCAT 420  
 Qy 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
 Db 421 AAGAAGCTGGTGGACCTGGCTGGCGCTCAGCTACTACATCCGTTCTTTCATCACCTAC 480  
 Qy 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhenIleArgPheLeuGlu 330  
 Db 481 ATCCCTTTCTACGGCATCCTGGGAGCCCTCTTTCCTCAACTCATCAGTTCCTGGAG 540  
 Qy 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350  
 Db 541 AGCCACTGGTTTGTGGTTCACACAGATGAATCACATCGTCATGGAGATTGACCAAGAG 600  
 Qy 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370  
 Db 601 GCCTACCGTGACTGTTTCAGTAGCCAGCTGACAGCCACTGCAACGCTGGAGCGTCTTC 660  
 Qy 371 PheAsnAspTrpPheSerGlyHisLeuAsnPhenIleGluHisHisLeuPheProThr 390  
 Db 661 TTCAACGAGCTGTTTCAGTGAGCACCTTAACTTCCAGATTGAGCACCACTTCTCCACC 720  
 Qy 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCGGCGACAACTTACACAGATGCGCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780

QY 411 GlyTieGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430  
 Db 781 GGCATTGAATACAGGAGAGCCGCTACTGAGGCGCCCTGCTGGACATCATCAGTCCCTG 840  
 QY 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrIleHisLys 444  
 Db 841 AAGAAGCTGGGAAGCTGTGGCGCTTACCTTACAAA 882

## RESULT 26

ABS71825

ID ABS71825 standard; DNA; 1843 BP.

XX AC ABS71825;

DT 02-DEC-2002 (first entry)

XX Human delta5-desaturase Gene #7.

XX Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

KW dihomogamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;

KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;

KW gene; ds.

XX Homo sapiens.

XX US6432684-B1.

PN 13-AUG-2002.

PD 08-JAN-1999; 99US-0227613.

XX 11-APR-1997; 97US-0833610.

PR 10-APR-1998; 98WO-US07422.

XX (ABO ) ABBOTT LAB.

FA Mukerji P, Leonard AE, Huang Y, Das T;

XX WPI; 2002-689761/74.

XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing

PT the conversion of dihomogamma-linolenic acid to arachidonic acid and

PT in the conversion of 20:4n-3 to eicosapentaenoic acid -

XX Example 1; Figure 7; 88pp; English.

XX The invention relates to an isolated human delta5-desaturase nucleotide

CC sequence (I) which desaturates polyunsaturated fatty acids at

CC carbon 5. The nucleotide sequence (I) may be used in the recombinant

CC production of vectors and host cells for the production of delta5-

CC desaturase. Delta5-desaturase may be utilised in the conversion of

CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the

CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA or

CC polyunsaturated fatty acids produced from it may be added to

CC pharmaceutical compositions, nutritional compositions, animal feeds, as

CC well as other products such as cosmetics. ABS71819-ABS71854

CC represent human delta5-desaturase coding sequences and PCR primers of

CC the invention.

XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 3,46e-171 Length: 1843

XX Score: 1646.00 Matches: 294

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 67.51% Indels: 0

XX DB: 24 Gaps: 0

XX US-09-719-601-5 (1-444) x ABS71825 (1-1843)

QY 151 ValPheTyrPheGlyAsnGlyTyrIleProThrIleuIleThrAlaPheValLeuAlaThr 170

Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTACCTCATCACGGCCCTTTGTCTCTGCTACC 60  
 QY 171 SerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190  
 Db 61 TCTCAGGCCCCAGCTGGATGGCTGCACATGATTATGGCCACCTCTCTGTCTACAGAAA 120  
 QY 191 ProLysTyrAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerIle 210  
 Db 121 CCCAAGTGGAAACCCCTTGTCCACAAATTCGTTCATTTGGCCACTTAAGGGTGCCTCTGCC 180  
 QY 211 AsnTyrTyrAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAsp 230  
 Db 181 AACTGTGGATCATGCCACTTCCAGCACCCAGCCAGCCCTAAATCTTCCACAGGAT 240  
 QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTyrGlnProlleGluTyrGly 250  
 Db 241 CCCGATGTGAACATGCTGCACCTGTGTTCCTGGGCGAATGGCAGCCCATGAGTACGGC 300  
 QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270  
 Db 301 AAGAAGAGCTGAATACCTGCCCTACATACCCAGCAGGATATCTTCTCTGATTGGG 360  
 QY 271 ProProlleuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290  
 Db 361 CCGCCCGCTGCTCATCCCATGATTTCAGTACCATCATCATCATCATCATCATCATCAT 420  
 QY 291 LysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
 Db 421 AAGAAGCTGGTGGACCTGGCCCTGCAGCTACTACATCCGCTTCTTCATCACCTAC 480  
 QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330  
 Db 481 ATCCCTTTTACGGCATCTCTGGAGCCCTCTTTTCTCTCAACTTCATCAGGTTCCTGGAG 540  
 QY 331 SerHisTyrPheValTyrValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350  
 Db 541 AGCCACTGGTGTGTGGGTGCACAGATGAATCATCATCATCATCATCATCATCATCAT 600  
 QY 351 AlaTyrArgAspTyrPheSerSerGlnLeuThrAlaThrCysAsnValGlnSerPhe 370  
 Db 601 GCCTACCGTACGTGGTTCAGTACGAGCTGAGCAGCCCTGCAAGCTGGAGGAGTCTTC 660  
 QY 371 PheAsnAspTyrPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390  
 Db 661 TTCAACGACTGGTTCAGTGGACACCTTAACCTCCAGATTGACACCACTCTTCCCCACC 720  
 QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
 Db 721 ATGCCCCGGCACAACTTACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 780  
 QY 411 GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430  
 Db 781 GGCATTGAATACAGGAGAGCCGCTACTGAGGCGCCCTGCTGGACATCATCAGTCCCTG 840  
 QY 431 LysLysSerGlyLysLeuTyrLeuAspAlaTyrIleHisLys 444  
 Db 841 AAGAAGCTGGGAAGCTGTGGCGCTTACCTTACAAA 882

## RESULT 27

ABS76712

ID ABS76712 standard; cDNA; 1843 BP.

XX AC ABS76712;

XX DT 12-DEC-2002 (first entry)

XX Human desaturase cDNA contig 2535.

XX Human; ss; delta5 desaturase; polyunsaturated fatty acid;

KW PUFAs; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;

KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;

KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;

KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;

vasodilation; cholesterol; proliferation of fibrous tissue;  
 endometriosis; myalgic encephalomyelitis; human breast milk;  
 dietary supplement; Chromosome 11q12.

Homo sapiens.

US6428990-B1.

06-AUG-2002.

12-NOV-1999; 99US-0439261.

11-APR-1997; 97US-0833610.

10-APR-1998; 98WO-US07422.

08-JAN-1999; 99US-0227613.

(ABBO) ABBOTT LAB.

Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

WPI; 2002-730518/79.

Producing a polyunsaturated fatty acid (PUFA), useful in dietary  
 supplements and in treating diseases e.g., cancer, comprises expressing  
 human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA  
 to convert to product PUFA -

Example 1; Fig 7; 104pp; English.

The invention relates to producing (M1) a polyunsaturated fatty acid  
 (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase  
 gene sequence (II); (ii) constructing a vector comprising (II); of the  
 (iii) introducing the vector into a host cell for expression of the  
 human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a  
 substrate PUFA (III) such that it is converted to a product PUFA (IV).  
 The method is useful for producing a polyunsaturated fatty acid.  
 Such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic  
 acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or  
 docosahexaenoic (DHA) acid. The PUFAs produced by the method, such  
 as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or  
 docosahexaenoic (DHA) acid, are useful for replicating the PUFA content  
 of human breast milk or to alter the presence of PUFAs normally found  
 in a non-human mammal's milk. PUFAs produced by (M1) may be added to a  
 dietary substitute or supplement, particularly an infant formula, for  
 patients undergoing intravenous feeding or for preventing or treating  
 malnutrition or other conditions or disease states. The PUFAs are  
 useful for producing nutritional compositions e.g., any food or  
 preparation for human consumption including for enteral or parenteral  
 consumption, which when taken into the body serve to nourish or build  
 up tissues or supply energy and/or maintain, restore or support  
 adequate nutritional status or metabolic function. The PUFAs are also  
 useful in animal feed supplements to alter an animal tissue or milk  
 fatty acid composition to one or more desirable for human or animal  
 consumption, in animal feed substitutes, animal vitamins or in animal  
 topical ointments. The PUFAs produced by this method are useful in  
 producing pharmaceutical compositions for treating rough or aging skin,  
 injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
 asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,  
 cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
 sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
 platelet aggregation, inducing vasodilation, reducing cholesterol  
 levels, inhibiting proliferation of fibrous tissue, treating  
 endometriosis, and myalgic encephalomyelitis. The gene for delta5  
 desaturase is located on chromosome 11q12. The present sequence  
 is a partial cDNA for a human delta5 desaturase.

SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

#### Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 3,466-171 | Length:       | 1843 |
| Score:                 | 1646.00   | Matches:      | 294  |
| Percent Similarity:    | 100.00%   | Conservative: | 0    |
| Best Local Similarity: | 100.00%   | Mismatches:   | 0    |

Query Match: 67.51% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-719-601-5 (1-444) x ABS76712 (1-1843)

|    |     |   |     |
|----|-----|---|-----|
| QY | 151 | ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr  | 170 |
| DB | 1   | GTCTTTTACTTTGGCAATGGCTGGATTCTACCCCTCATCAGCGCTTTGCTCTGTGTTACC  | 60  |
| QY | 171 | SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys  | 190 |
| DB | 61  | TCTCAGGCCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTCTACAGAAA    | 120 |
| QY | 191 | ProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla  | 210 |
| DB | 121 | CCCAAGTGGAAACCACCTTCTCCACAAATTCGTTCATTCGTCCTTAAAGGGTGCCTCTGCC | 180 |
| QY | 211 | AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp  | 230 |
| DB | 181 | AACTGGTGGATCATCGCCACTTCCAGCACACCGCCAGCCTTAACATCTTCCACAGGAT    | 240 |
| QY | 231 | ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly  | 250 |
| DB | 241 | CCCGATGTGAACATGTCTGCACGTGTTGTTCTGGCGAATGGCAGCCCATCGATACGGC    | 300 |
| QY | 251 | LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGly  | 270 |
| DB | 301 | AAGAGAGAGCTGAATACCTGCCCTACATCACCAGCACGAATACTTCTTCTGATTGGG     | 360 |
| QY | 271 | ProProLeuLeuLeuProMetTyrPheGlnTyrGlnIleLeuMetThrMetIleValHis  | 290 |
| DB | 361 | CCGCCCTGCTCATCCCAATGATTTCCAGTACCAGATCATCATGACCATGATGTCAT      | 420 |
| QY | 291 | LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr  | 310 |
| DB | 421 | ARGAAGTGGTGGACCTGGCTGGGCGCTCAGCTACTACATCCGGTCTTCTCATCCTAC     | 480 |
| QY | 311 | IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu  | 330 |
| DB | 481 | ATCCCTTTCTAGGCACTCTGGAGCCCTCTTTTCTCACTTCTCAGGTTCTCTGGAG       | 540 |
| QY | 331 | SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu  | 350 |
| DB | 541 | AGCCACTGGTTTGTGGGTCTCACAGATGATCATCGTCATGGAGATTGCCAGGAG        | 600 |
| QY | 351 | AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe  | 370 |
| DB | 601 | GCTACCTGGTGGTTCAGTACAGCCAGCTGACAGCCACCTGCAACGTGGAGAGTCTTTC    | 660 |
| QY | 371 | PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr     | 390 |
| DB | 661 | TTCAACGACTGGTTCAGTGGACACCTTAATTCAGATTGAGCACCACCTCTTCCCCACC    | 720 |
| QY | 391 | MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis  | 410 |
| DB | 721 | ATGCCCGGCAACAATTCACAAAGATCGCCCGCTGGTGGAGTCTCTATGTGCCAAGCAT    | 780 |
| QY | 411 | GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu  | 430 |
| DB | 781 | GGCATTTGAATCCAGGAGAGAGCGGTACTGAGGGGCGCTGCTGACATCATAGTTCCTTG   | 840 |
| QY | 431 | LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys                    | 444 |
| DB | 841 | AAGAAGTCTGGGAAGGTGTGGCTGGAGCGCTACCTTACAAA                     | 882 |

RESULT 28

AAF21845

ID AAF21845 standard; DNA; 1474 BP.

XX

AC AAF21845;

XX

DT 27-MAR-2001 (first entry)

XX





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FT      /*tag= a
XX      /product= CYB5RP fatty acid desaturase
XX      W0200021557-AL.
XX
XX      20-APR-2000.
XX
XX      05-OCT-1999; 99WO-US23253.
XX
XX      09-OCT-1998; 98US-0103760.
XX
XX      (MERI ) MERCK & CO INC.
XX
XX      Petrukhin K, Caskey CT;
XX      WPI; 2000-317847/27.
XX      P-P8DB; AY83229.
XX
XX      Novel cytochrome b5-related protein useful for identifying modulators
XX      useful for treating retinal dysfunction such as macular degeneration,
XX      skin diseases, diabetic complications and cardiovascular disorders
XX
XX      Claim 2; Figure 3; 44pp; English.
XX
XX      CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.
XX      Pharmaceutical compositions comprising an activator or an inhibitor of
XX      CYB5RP protein are useful for treating macular degeneration. The
XX      CYB5RP protein is useful for identifying its activators or inhibitors
XX      which are useful for treating abnormal conditions associated with
XX      CYB5RP protein activity such as skin disease, diabetic complications,
XX      inflammatory and autoimmune disorders, cardiovascular disorders and
XX      complications of viral infection. Large amounts of valuable essential
XX      fatty acids can be produced by the expression of CYB5RP protein.
XX
XX      Sequence 1700 BP; 319 A; 560 C; 480 G; 341 T; 0 other;
XX
XX      Alignment Scores:
XX      Pred. No.:      8 4e-162      Length:      1700
XX      Score:      1560.50      Matches:      278
XX      Percent Similarity: 76.23%      Conservative: 62
XX      Best Local Similarity: 62.33%      Mismatches: 103
XX      Query Match:      64.01%      Indels:      3
XX      DB:      21      Gaps:      2
XX
XX      US-09-719-601-5 (1-444) x AA293706 (1-1700)
XX
XX      1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18
XX      71 ATGGCGCGCGTGGGGAGCCGGGAGCCGGGAGGAGGAGCCCGCGAGCCGGGGGCGACCGCTG 130
XX
XX      19 ProThrPheSerTrpGluGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 38
XX      131 CCCACTTCTGCTGGAGAGAGATCCCGCGGACGACGACGACGACGACGACGACGACGACGAC 190
XX
XX      39 IleAspArgLysValTyAsnIleThrLysTrpSerIleGlnHisProGlyGlnArg 58
XX      191 ATCGAGCGCGGCTTACGACATCAGCGCTGGGACAGCGGACGACGACGACGACGACGACGAC 250
XX
XX      59 ValIleGlyHisTyAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78
XX      251 CTCATCGGCGCACCGCGCGCTGAGACCGCCAGGATGCTTCGCGGCTTCATCAAGAT 310
XX
XX      79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98
XX      311 CTCATTTTGTGCGCAAGTTCTACAGCCCTGTTGATTGGAGAGCTGGCTCCGGAGAA 370
XX
XX      99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
XX      371 CCCAGCCAGGATGGACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
XX
XX      119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuAla 138
XX      431 GCAGCGCGGAGACATGAGCTGTTGATGCCAGTCCACCTTCTTGTCTTCTTCTTCTTCTTCT 490

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QY      139 HisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp 158
DB      491 CACATCTCTGGCCATGAGGTGCTGGCTGGCTCTTATCTACTCTCTGGTCTGGCTGG 550
QY      159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
DB      551 GTGCCAGTGGCCCTGGCGGCTTCTATCTCTGGCCATCTCTCAGGCTCAGTGTGGTGTCTG 610
QY      179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHis 198
DB      611 CAGCATGACCTGGGCGCATGCTCTCATCTTCAGAAAGTCTCTGGTGGACACCATGCGCCAG 670
QY      199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218
DB      671 AAGTTCTGTATGGGCGAGCTAAAGGCTTCTCCGCCCATCTGGTGGAACTTCCGCCCATTC 730
QY      219 GlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238
DB      731 CAGCACCCAGCCCAAGCCCAACATCTTCCAAAGACCCAGAGTGCAGGTGGCGGCCGCTC 790
QY      239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLys 258
DB      791 TTCTCTCTGGGGAG---TCATCCGTCGAGTATGCAAGAGAAACGACAGTACCTACCC 847
QY      259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProPheLeuLeuIleProMetTyr 278
DB      848 TACAACCCAGCAGCACCTCTCTCTCTGATCGGCGCGCGCTCTCACCCTGGTGAC 907
QY      279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
DB      908 TTGAAGTGAANAATCGCGTACATGCTGGTGTGATGTCATGTCAGTGGCGGATTTGCTCG 967
QY      299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLysLeuGly 318
DB      968 GCCCGCAGCTTCTATGCGCGCTTCTTATCTACTCTCTCTCTCTCTCTCTCTCTCTCTGG 1027
QY      319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
DB      1028 GTGCTGCTCTTTTGTGCTGCTGAGGCTCTGGAAGCCACTGGTTCGTGTGGATCACA 1087
QY      339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358
DB      1088 CAGATGAACCATCTCCCAAGGAGATCGGCCACGAGAGACACCGGACTGGGTCACTCT 1147
QY      359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378
DB      1148 CAGCTGGCGGCGCCACTGCAACGTGGAGCCCTCATTTCACCACTGGTTCAGCGGCGAC 1207
QY      379 LeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLys 398
DB      1208 CTCACCTTCCAGATCGAGCACCATCTTCTCCCGAGATGCCGAGACACAACTACAGCCGG 1267
QY      399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418
DB      1268 GTGGCCCGCTGGTCAAGTGTGTCAGAGCAGCGGCTCAGCTACGAATGAGGCC 1327
QY      419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438
DB      1328 TTCTCTCAGCGGCTGGTGGACATCGTCAAGTCTCTGGAAGAGTCTGGTGACATCTGGCTG 1387
QY      439 AspAlaTyrLeuHisLys 444
DB      1388 GAGCGCTACCTCCATCAG 1405
XX      RESULT 30
XX      ABX93651
XX      ID ABX93651 standard; cDNA; 1717 BP.
XX      AC ABX93651;
XX      DT 09-JUN-2003 (first entry)
XX

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DE CDNA encoding human delta 6 desaturase D6DH-1, Incyte 2451043.

XX Human; ss; gene; D6DH-1; delta 6 desaturase-1; fatty acid desaturase; cardiovascular disease; angina pectoris; atheroma embolism; hypertension; atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia; hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer; mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis; aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia; basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; goiter; chronic lymphatic leukaemia; degenerative osteoarthritis; delirium; dementia; depression; dyskinesia; diabetic hyperosmolar nonketotic coma; glaucoma; hypercholesterolaemia; hypothermia; metabolic bone disease; osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome; Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma; renal amyloidosis; tuberculosis; urinary incontinence; galactosaemia; fatty acid metabolism disorder; Addison's disease; cystic fibrosis; fatty hepatocirrhosis; hyperadrenalemia; hypoadrenalemia; hyperlipaemia; hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity; lipodystrophy; phenylketonuria; cancer; Incyte 2451043.

OS Homo sapiens.

XX Key Location/Qualifiers

PH 75..1412

FT /\*tag= a

FT /\*product= "D6DH-1"

XX

PN US6492108-B1.

PD 10-DEC-2002.

XX 26-MAR-1998; 98US-0048888.

XX 26-MAR-1998; 98US-0048888.

XX (INCYTE) INCYTE GENOMICS INC.

XX Hillman JL, Guegler KJ, Corley NC, Shan P;

XX WPI; 2003-327308/31.

DR P-PSDB; ABU06788.

XX

PT New isolated polynucleotide encoding polypeptide having delta-6 desaturase activity for use in diagnosis, treatment and prevention of cardiovascular diseases, disorders of aging, disorders of fatty acid metabolism, and cancer -

XX Claim 3; Column 41-44; 39pp; English.

XX The invention relates to an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence given in the specification. The polypeptide has fatty acid desaturase activity or delta-6 desaturase activity. For use in the diagnosis, treatment and prevention of cardiovascular diseases (e.g. angina pectoris, atheroma embolism, atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension, hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene, mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis), disorders of aging (e.g. Alzheimer's disease, angioimmunoblastic lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia, diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia, hypothermia, metabolic bone disease including osteoporosis, normal pressure hydrocephalus, Parkinson's disease, Reye's syndrome, polymyalgia, rheumatism, prostatic carcinoma, renal amyloidosis, fatty hepatocirrhosis, urinary incontinence), disorders of fatty acid metabolism (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis, galactosaemia, goiter, hyperadrenalemia, hypoadrenalemia, obesity, hyperparathyroidism, hypoparathyroidism, hyperlipaemia, lipid myopathies, lipodystrophies, phenylketonuria) and cancer. The present sequence represents the cDNA encoding human delta 6 desaturase-1, D6DH-1, Incyte 2451043.

SQ Sequence 1717 BP; 330 A; 563 C; 482 G; 342 T; 0 other;

Alignment Scores: 8,52e-162 Length: 1717

Pred. No.: 1560.50 Matches: 278

Score: 76.22% Conservative: 62

Percent Similarity: 62.33% Mismatches: 103

Best Local Similarity: 64.01% Indels: 3

Query Match: 25 Gaps: 2

DB:

US-09-719-601-5 (1-444) x ABX93651 (1-1717)

Qy 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18

Db 75 ATGGGGGGGGTTCGGGAGGCGGAGCCCGCGGGAGGACCCCGCGGGGACCGCTCG 134

Qy 19 ProThrPheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38

Db 135 CCACCTTTCTGCTGGGAGCAGATCCCGCGGACGACCCCGCGGACAGTGGCTGGTC 194

Qy 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58

Db 195 ATCGAGCGCGGTCTACGACATCAGCGCTGGGACAGCGGCACCCAGGGGGACGCGC 254

Qy 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78

Db 255 CTCATCGGCCACCCAGCGGCTGAGGACGCGGATGCCCTTCGTGCTTCCATCAAGAT 314

Qy 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGlyLeuAlaProGluGlu 98

Db 315 CTCAATTTTGTGGCAAGTTCTTACAGCCCTGTGATTGGAGAGCTGGCTCGGAAGAA 374

Qy 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118

Db 375 CCAGCGCAGGATGGACCCCTGAATGGCAGCTGTGCGAGACTTTCGAGCCCTGACACG 434

Qy 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138

Db 435 GCAGCGCAGGACATGAAGCTGTTGATGCGAGTCCACCTTCTTCTTCTTCTTCTG 494

Qy 139 HisIleIleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTrp 158

Db 495 CATCTCTGCGCATGGAGGTGCTGGCTGGCTCTTATCTTCTCTCTCTCTCTCTCTG 554

Qy 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178

Db 555 GTGCCAGTCCCTGGCGGCTTCTATCTCTGCGCATCTCTCAGGCTCAGTCTGCTGTC 614

Qy 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198

Db 615 CAGCATCAGCTGGGCCATGCTCCATCTTCAAGAGTCTCTGGTGGAAACACCGTGGCC 674

Qy 199 LysPheValIleGlyHisLeuLysGlyValAsnTrpTrpAsnHisArgHisPhe 218

Db 675 AAGTTCTGTATGGGGCAGCTTAAGGGCTTCTCGCCCATCTGGTGGAACTTCGCCCA 734

Qy 219 GlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238

Db 735 CAGCACCCAGCCAGCCCAACATCTTCCAAAGACCCAGACGTGAGCGTGGCGCCGTC 794

Qy 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLys 258

Db 795 TTCCTCTCTGGGGAG---TCATCCGTCAGTATGGCAGAGAGAAACGACATACCTACC 851

Qy 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278

Db 852 TACAACAGCAGCAGCCTGTACTTCTTCTGATGGCGCGCGCTGTCTCACCTGGTGAAC 911

Qy 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298

Db 912 TTGAAGTGGAAATCTGGGTATCATGTGTGTCATGAGTGGGGGGGATTTGCTCTGG 971

Qy 299 AlaValSerTyrTyrIleArgPheIleThrTyrIleProPheTyrGlyIleLeuGly 318

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Db 972 GCGCCAGCTCTATGCCGGTCTCTTATCTACCTCCCTCTACGGGTCCTGGG 1031
Qy 319 AlalaLeuPheLeuAsnPhelIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
Db 1032 GTGCTGCTCTCTCTTTGTTGCTGTACAGGTCCTGGAAGCCACTGCTGCTGTGATCACA 1091
Qy 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSerSer 358
Db 1092 CAGATGACACCATCCCAAGAGATCGCCACGAGAGACCGGAGCTGGGTGAGTCTCT 1151
Qy 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378
Db 1152 CAGCTGGCAGCCACTGCAACGTGAGCCCTCACTTTTCAACCACTGCTTTCAGCGGCAC 1211
Qy 379 LeuAsnPheGlnIleGluHisIlePheProThrMetProArgHisAsnLeuHisLys 398
Db 1212 CTCACCTTCCAGATCAGACCACTCTTCCCGAGATGCCGAGACACATCAGCCGG 1271
Qy 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluPro 418
Db 1272 GTGGCCCGCTGCTCAAGTCGTGTGTGCCAAGCACGCGCTCAGCTACGAAGTGAAGGCC 1331
Qy 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerIleLysSerGlyLysLeuTrpLeu 438
Db 1332 TTCTCTCACCGCTGTGACATCGTCAGTCCCTGGAAGATCTGGTGACATCTGGCTG 1391
Qy 439 AspAlaTrpLeuHisLys 444
Db 1392 GAGCGCTACCTCCATCAG 1409

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## RESULT 31

AAA90954

ID AAA90954 standard; cDNA; 1757 BP.

XX AC AAA90954;

XX DT 15-JAN-2001 (first entry)

XX DE Human fatty acid desaturase 3 coding sequence.

XX KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;

XX KW liver disease; coronary artery disease; cancer; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS 134..1471

XX FT /tag= a

XX FT /product= FADS-3

XX EP1035207-AL.

XX PD 13-SEP-2000.

XX PF 09-MAR-1999; 99EP-0104664.

XX PR 09-MAR-1999; 99EP-0104664.

XX (MULT-) MULTIGENE BIOTECH GMBH.

XX PA Weber BHF, Marquardt A;

XX PI WPI; 2000-559875/52.

XX DR P-PSDB; AAY97540.

XX Novel cDNA molecules encoding three human fatty acid desaturases,

XX PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,

XX PT coronary artery disease and cancer.

XX PS Claim 2; Page 38-39; 72pp; English.

XX This sequence encodes the human fatty acid desaturase, FADS-3, of the

CC invention. An antibody directed against the 3 FADS molecule of the  
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or  
 CC therapeutic purposes. The FADS coding sequences are useful in gene  
 CC therapy. The polypeptide and antibodies are useful in screening for  
 CC modulating drugs. The polypeptides are also useful for treating liver  
 CC disease, coronary artery disease and cancer.  
 CC Note: Two copies of the sequence listing are present within this  
 CC patent, which contain different sequences. AAA90952 and AAA90955 are  
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are  
 CC stated as being SEQ ID's 7-22.

XX

SQ Sequence 1757 BP; 318 A; 580 C; 517 G; 342 T; 0 other;

## Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 8,82e-162 | Length:       | 1757 |
| Score:                 | 1560.50   | Matches:      | 278  |
| Percent Similarity:    | 76.23%    | Conservative: | 62   |
| Best Local Similarity: | 62.33%    | Mismatches:   | 103  |
| Query Match:           | 64.01%    | Indels:       | 3    |
| DB:                    | 21        | Gaps:         | 2    |

US-09-719-601-5 (1-444) x AAA90954 (1-1757)

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Qy 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18
Db 134 ATGGCGGGGCTCGGGAGCGGGAGCCCGGGAGGAGCCCGCGAGCGCGGGGGGACCGCTG 193
Qy 19 ProThrPheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38
Db 194 CCCACCTTCTGCTGGGAGCAGATCCCGCGCGCAGCACCGCCCGCGGCGACAAAGTGGCTG 253
Qy 39 IleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58
Db 254 ATCGAGCGCGCTCTACGACATCAGCCCTGGGACAGCGGCGACCGCCAGGGGGGAGCCGC 313
Qy 59 ValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78
Db 314 CTCATCGGCACACCGCGCTGAGGAGCGCCAGGATGCTTCGGTCCCTTCCATCAAGAT 373
Qy 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98
Db 374 CTCAAATTTTGGCGCAAGTTCTTACAGCCCTGTTGATTGGAGAGCTGCTCGGGAAGAA 433
Qy 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
Db 434 CCCAGCGAGATGAGACCCCTGAATGCGAGCTGTCGAGGACTTCGAGCCCTGCACCCAG 493
Qy 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138
Db 494 GCAGCGGAGGACATGAAGCTGTTGATGCGAGTCCCGACCTTCTTCTTCTTCTTCTTCT 553
Qy 139 HisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrp 158
Db 554 CACATCTGCGCCATGAGGAGTGTGGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 613
Qy 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
Db 614 GTGCCAGATGCCCTGGCGGCTTCACTCGGCCATCTCTCAGGCTCAGTCTGCTGCTGCTG 673
Qy 179 GlnHisAspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsnHisLeuValHis 198
Db 674 CAGCATGACCTGGGCCATGCTCCATCTTCAAGAGTCTCTGGTGGAAACACACGCGGCCAG 733
Qy 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218
Db 734 AAGTTCGTGATGGGCGAGCTAAAGGCTTCTCCGCCCATCTGTTGGAACTTCGCCCACTTC 793
Qy 219 GlnHisIleAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238
Db 794 CAGCACCGCCAGCCCAACATCTTCCACAAAGACCCAGACGTGACGTGGCGGCCGCTC 853
Qy 239 PheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLysLeuLysTrpLeuPro 258

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QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118
Db 1337 CCCAGCCAGGATGACCCCTGAATGCGAGCTGGTCGAGGACTTCGAGCCCTCGACAC 1278
QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuAla 138
Db 1277 GCAGCCGAGGACATGAAGCTGTTGATGCCAGTCCACCTTCCTTTCCTACTGGC 1218
QY 139 HisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheGlyAsnGlyTrp 158
Db 1217 CACATCTGGGCATGAGGTGGCTGGCTCTTATCTACTCTCTGGGTCTGGGTGG 1158
QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178
Db 1157 GTGCCAGTGGCCCTGCGCCCTTCATCTGCGCATCTCTCAGGCTCAGTCTGGTCTG 1098
QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198
Db 1097 CAGCATGACCTGGGCCATGCCCTCCATCTTCAAGAAGTCTCTGGTGAACACGCTGGCCAG 1038
QY 199 LysPheValIleGlyHisLeuLysGlyValAsnAlaAsnTrpTrpAsnHisArgHisPhe 218
Db 1037 AAGTTCGTGATGGGAGCTTAAGGCTTCTCCGCCCACTGGTGAACCTTCGCCCATTC 978
QY 219 GlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238
Db 977 CAGCACCAAGCCCAAGCCCAACATCTTCACAAAGACCCAGACGTGACGCTGGCCCGTC 918
QY 239 PheValLeuGlyGluTrpGlnProIleGlyLysLysValLysLysLysLysLysLysLys 258
Db 917 TTCCTCTCTGGGGAG---TCATCGCTGAGTATGGCAAGAAACCCAGATACCTACCC 861
QY 259 TyrAsnHisGlnHisGlyLysGlyLysLysLysLysLysLysLysLysLysLysLys 278
Db 860 TACACACAGCAGCAGCTGACTTCTCTGATCGCGCGCGCTGCTCACCTGGTGAAC 801
QY 279 PheGlnTyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298
Db 800 TTTGAAGTGGAAATCTGGCGTACATGCTGTGTCATGCGGCGGCGGATTTGCTCTGG 741
QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeuGly 318
Db 740 GCCGCCACTTCTATGCCGCTTCTTCTATCTCTACCTCCCTCTACGCGCTCCCTGGG 681
QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338
Db 680 GTGCTGCTCTTCTTGTGCTGCTGAGGTCTCTGAAAGCCCACTGCTGCTGTCGATCACA 621
QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358
Db 620 CAGATGAACCATCCCAAGAGATCGCCACAGAGACACCGGACTGGTGGTCAGTCT 561
QY 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378
Db 560 CAGCTGGCAGCACCTGCAAGTGGAGCCCTCACTTTTACCAACTGCTTTCAGCGGCAC 501
QY 379 LeuAsnPheGlnIleGluHisLysLeuPheProThrMetProArgHisAsnLeuHisLys 398
Db 500 CTCACCTTCCAGATCGACACCATCTTCCCGAGATGCGCGAGACACAACTACAGCCGG 441
QY 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418
Db 440 GTGGCCCGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 381
QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438
Db 380 TTCTTCACCGCGCTGCTGACATCTCAGTCCCTGAAAGAGTCTGGTGACATCTGCTG 321
QY 439 AspAlaTyrLeuHisLys 444
Db 320 GACGCTACCTCCATCAG 303
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RESULT 33

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ABK35347/c
ID ABK35347 standard; cDNA; 1972 BP.
XX AC ABK35347;
XX DT 08-MAY-2002 (first entry)
XX DE Human cDNA encoding secreted protein #485.
XX KW Human; secreted protein; Gene; ss; nutritional supplement; haemophilia;
XX KW viral infection; bacterial infection; fungal infection; diabetes; asthma;
XX KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
XX KW autoimmune thyroiditis; allergic reaction; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
XX KW coagulation disorder; inflammatory disorder; Crohn's disease; incision;
XX KW tissue regeneration; wound healing; burn; haematopoiesis;
XX KW myeloid cell deficiency; lymphoid cell deficiency.
XX OS Homo sapiens.
XX PN WO200177288-A2.
XX PD 18-OCT-2001.
XX PF 29-MAR-2001; 2001WO-US10224.
XX PR 06-APR-2000; 2000US-195582P.
XX PA (GEMY ) GENETICS INST INC.
XX PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
XX PI Gulukota K, Graham JR;
XX DR WPI; 2002-179321/23.
XX PT Five hundred and ninety two polynucleotides derived from a variety of
XX PT human tissue sources which encode secreted proteins, useful for
XX PT treating immune deficiencies and disorders such as autoimmune disorders
XX PS Claim 1; Page 321-322; 372pp; English.
XX CC The invention relates to 592 polynucleotides which have been derived from
XX CC a variety of human tissue sources and which encode novel secreted
XX CC proteins. The polynucleotides can be used as probes for the
XX CC identification and isolation of full length cDNA and genomic DNA. The
XX CC polynucleotides and proteins can also be used as nutritional supplements.
XX CC The proteins are useful in the treatment of various immune deficiencies
XX CC and disorders such as viral infections, bacterial infections, fungal
XX CC infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
XX CC and conditions (e.g. asthma). They are also useful for treating
XX CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
XX CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
XX CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
XX CC useful for tissue regeneration, for wound healing and in the treatment of
XX CC burns, incisions and ulcers. The proteins are also useful for regulating
XX CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
XX CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
XX SQ Sequence 1972 BP; 428 A; 523 C; 556 G; 465 T; 0 other;
Alignment Scores:
Pred. No.: 8,57e-157 Length: 1972
Score: 1516.00 Matches: 272
Percent Similarity: 76.08% Conservatives: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.18% Indels: 6
DB: 24 Gaps: 3
US-09-719-601-5 (1-444) x ABK35347 (1-1972)
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluLeuGln 27
```

1864 GCGCCGAGACCGCGCTCAGGACCTACCGCGCTACTTCCCTGGAGAGGTGGCC 1805  
 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValThr 47  
 1804 CAGCGCTCAGGTCGAGGAGCGGTGGCTAGTATGATGACCGTAAGTGTATACAAATCAGC 1745  
 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrpAlaGlyGluAsp 67  
 1744 GAGTTTCCCGCGCGGATCCAGGCGGCTCCCGGGTATCAGCCATACCGCGGCGGAT 1685  
 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 1684 GCCACGGATCCCTTTGTGGCTTCCACATCAACAGAGGCTTGTGAAGAAGTATATGAAC 1625  
 88 ProLeuLeuIleGlyLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107  
 1624 TCTCTCTGATGGAGAACTGTCTCCAGAGACGCGCCAGCTTTGAGCCCAACCAAGATAAA 1565  
 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 1564 GACCTGACAGATGAGTTCGGGAGCTCGCGGCACAGTGGAGCGGATGGGCTCATGAAG 1505  
 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 1504 GCCAACCATGCTCTTCTCTGCTGTACTCTGCTGCACATCTTGTCTGTGATGGTGAGCC 1445  
 148 TrpPheThrValPheTyrrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 1444 TGCTCACCTTTGGGTCTTGGAGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 1385  
 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrrGlyHisLeuSerVal 187  
 1384 CTCAGTCAGTTCAGGCGCCAGGCTGGCTGCTGCACATCTTGTCTGTGATGGTGAGCC 1325  
 188 TyArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 1324 TTGACGACCTCAAGTGAACCATCTGCTACATCATTTTGTGATGGCCACCTGAGGGG 1265  
 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227  
 1264 GCGCCGCGCAGTGTGGTGAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205  
 228 HisLysProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245  
 1204 CGCAAGACCCAGACATCAACATG---CATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1148  
 246 ProIleGluTyrrGlyLysLysLysLeuLysTyrrLeuProTyrrAsnHisGlnHisGlyTrp 265  
 1147 TCTGTGAGCTTGGGAACAGAGAAATAATATGCGGTACACACCCAGCAGCAAAATAC 1088  
 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrrPheGlnTyrrGlnIleIleMet 285  
 1087 TTTCTCTAATTTGGGCGCCAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1028  
 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrrIleArg 305  
 1027 TTTCTTTATCCAGCGAAGAGAGTGGTGGACTTGGCGCTGGATGATACCTTCTACGCTCCG 968  
 306 PhePheLeuThrTyrrIleProPheTyrrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325  
 967 TTTCTCTCTCTTATGTGCCACTATTGGGCTGAAAGCCCTTCTCTGGGCTTTTCTTCTATA 908  
 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345  
 907 GTGAGTTCTCTGGAAAGCAACTGTTGTGGGTGACACAGATGACCAATATTTCCCATG 848  
 346 GluIleAspGlnGluAlaTyrrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365  
 847 CACATTGATCATGACCGGAACATGGAGTGGTGTTCACCCAGCTTCCAGGCGCACATCAAT 788  
 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385

787 GTCCACAAAGTCTGCCTTCAATGACTGGTTTCAGTGGACACCTCAACTTCCAGATTGAGCAC 728  
 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405  
 727 CATCTTTTCCCAAGATGCTCGACCAATACCAAAAGTGGCTCCCTGTGGTGGAGTCC 568  
 406 LeuCysAlaLysHisGlyIleGluTyrrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425  
 567 TTGTGTGCCAAGCATGGCATAGTAGTACCAGTCCCAAGCCCTGTGTGAGCCCTTCGCGCGAC 608  
 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrrLeuHisLys 444  
 607 ATCATCCACTCACTAAAGGAGTCCAGGCGAGCTCTGGTAGATGCTATCTTCCACAA 551  
 RESULT 34  
 AAA90955  
 ID AAA90955 standard; cDNA; 4203 BP.  
 XX  
 AC AAA90955;  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human fatty acid desaturase 1 coding sequence.  
 XX  
 KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;  
 KW liver disease; coronary artery disease; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1035207-A1.  
 XX  
 PD 13-SEP-2000.  
 XX  
 PF 09-MAR-1999; 99EP-0104664.  
 XX  
 PR 09-MAR-1999; 99EP-0104664.  
 XX  
 PA (MULT-) MULTIGENE BIOTECH GMBH.  
 XX  
 PI Weber BHF, Marquardt A;  
 XX  
 DR WPI; 2000-559875/52.  
 XX  
 PT Novel cDNA molecules encoding three human fatty acid desaturases,  
 PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,  
 PT coronary artery disease and cancer -  
 XX  
 PS Claim 2; Page 12-15; 72pp; English.  
 CC  
 CC This sequence encodes the human fatty acid desaturase, FADS1, of the  
 CC invention. An antibody directed against the 3 FADS molecule of the  
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or  
 CC therapeutic purposes. The FADS coding sequences are useful in gene  
 CC therapy. The polypeptide and antibodies are useful in screening for  
 CC modulating drugs. The polypeptides are also useful for treating liver  
 CC disease, coronary artery disease and cancer.  
 CC Note: Two copies of the sequence listing are present within this  
 CC patent, which contain different sequences. AAA90952 and AAA90955 are  
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are  
 CC stated as being SEQ ID's 7-22.  
 XX  
 SQ Sequence 4203 BP; 1138 A; 1025 C; 1003 G; 1037 T; 0 other;

Alignment Scores:  
 Pred. NO.: 2.67e-156 Length: 4203  
 Score: 1516.00 Matches: 272  
 Percent Similarity: 76.08% Conservative: 62  
 Best Local Similarity: 61.96% Mismatches: 99  
 Query Match: 62.18% Indels: 6  
 DB: 21 Gaps: 3

US-09-719-601-5 (1-444) x AAA90955 (1-4203)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluIleGln 27  
 Db 97 GCGCGGAGACCGCGGCTCAGGAGACTACCCCGCCTACTTCACCTGGAGCAGGTGGCC 156  
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValThrAsnIleThr 47  
 Db 157 CAGCGCTCAGGTCGAGGCGGTGGCTAGTGTAGTACGCGTAAGGTGTACAACATCAGC 216  
 QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTrpAlaGlyGluAsp 67  
 Db 217 GAGTTTACCCCGCGGATCCAGGGGCTCCCGGGTATCAGCCATCCGCGGGCAGGAT 276  
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 Db 277 GCCCGGATCCCTTTGTGGCTTCCACATCAACAGGGCTTGTGAAGATATATGAAC 336  
 QY 88 ProLeuLeuIleGlyLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107  
 Db 337 TCTCTCCTGATTGGAGAACTGTCCAGAGACGCCGCTTTGAGCCGCCCAAGAATAAA 396  
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 Db 397 GAGCTGACAGATGAGTTCCGGAGCTCGGGCCACAGTCGAGCGGATGGGCTCATGAG 456  
 QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 Db 457 GCCAACCAATGTCTTCTCTGCTGTACTGTGTGCACATCTTCTGCTGTGTGTGTCAGCC 516  
 QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 Db 517 TGGCTACCCCTTGGGTCTTTGGGAGCTCTTTTGGCCTCTCTCTCTGCGGTGTG 576  
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187  
 Db 577 CTGAGTGCAGTTTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTGGGCACCTGTGCTC 636  
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 Db 637 TTCAGCACTCAAGTGGGAACCATCTCTACATCATTTTGTGATTGGCCACCTGAAGGG 696  
 QY 208 AlaserAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227  
 Db 697 GCCCGCGCAGTGTGTGGAACACACATGCACTTCCAGCACCATGTCAGCCCAACTGCTC 756  
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245  
 Db 757 CGCAAGAGCCAGACATCAACATG---CATCCCTCTCTTTTGGCCTTGGGAAGATCCTC 813  
 QY 246 ProIleGluTrpGlyLysLysLysLeuLysTrpLeuProTyrAsnHisGlnHisGluTrp 265  
 Db 814 TCTGTGAGCTTGGGAACAGAGAAATAATATATGCGGTACACACACAGCACAATAC 873  
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTrpGlnIleIleMet 285  
 Db 874 TTCTTCTTAATTTGGGCCCCAGCTTGTCTGCTCTCTACTTCCAGTGTATATTTCTAT 933  
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIleArg 305  
 Db 934 TTGTATTATCAGCAAGAGTGGTGGTGGCTTGGCTGTGATGATTACCTTTCACCTGCGC 993  
 QY 306 PhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325  
 Db 994 TTCTTCTCACTTATGTGCCACTATTGGGGCTGAAAGCTTCTCTGGGCTTTTCTTCATA 1053  
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345  
 Db 1054 GTTCAGTTCTGGAAGCACTGTTTGTGTGGTGCACATGACATGAACCATTTCCCATG 1113  
 QY 346 GluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365  
 Db 1114 CACATTGATCATGACCGGAACATGGACTGGTTTCCACCCAGCTCCAGGCCACATGCAAT 1173  
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385

Db 1174 GTCCAGAGTCTCCCTTCAATGACTGTTGCTGAGGACACTCACTTCAGATTGAGCAC 1233  
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405  
 Db 1234 CATCTTTTCCACAGATGCTCGACACAATTACACAAAAGTGGCTCCCTGTGTGAGTCC 1293  
 QY 406 LeuCysAlaLysHisGlyIleGluTrpGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425  
 Db 1294 TTGTGTCCCAAGCATGCATAGTAGTACCAGTCCACAGCCCTGCTGTACGCTTCGCCGAC 1353  
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTrpLeuHisLys 444  
 Db 1354 ATCATCCACTCACTAAAGGAGTCAGGCGCAGCTCTGGCTAGTACCTATCTTACCACAA 1410  
 RESULT 35  
 AAA90952 standard; cDNA; 4205 BP.  
 ID AAA90952 standard; cDNA; 4205 BP.  
 AC AAA90952;  
 DT 15-JAN-2001 (first entry)  
 XX Human fatty acid desaturase 1 coding sequence.  
 DE Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;  
 KW liver disease; coronary artery disease; cancer; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 79..1413  
 FT /\*tag= a  
 FT /product= FADS-1  
 PN EPI035207-A1.  
 XX 13-SEP-2000.  
 XX 09-MAR-1999; 99EP-0104664.  
 XX 09-MAR-1999; 99EP-0104664.  
 PA (MULT-) MULTIGENE BIOTECH GMBH.  
 PI Weber BHF, Marquardt A;  
 DR WPI; 2000-559875/52.  
 DR P-PSDB; AAY97538.  
 PT Novel cDNA molecules encoding three human fatty acid desaturases,  
 PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,  
 PT coronary artery disease and cancer -  
 XX  
 PS Claim 2; Page 34-36; 72pp; English.  
 CC This sequence encodes the human fatty acid desaturase, FADS1, of the  
 CC invention. An antibody directed against the 3 FADS molecule of the  
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or  
 CC therapeutic purposes. The FADS coding sequences are useful in gene  
 CC therapy. The polypeptide and antibodies are useful in screening for  
 CC modulating drugs. The polypeptides are also useful for treating liver  
 CC disease, coronary artery disease and cancer.  
 CC Note: Two copies of the sequence listing are present within this  
 CC patent, which contain different sequences AAA90952 and AAA90955 are  
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are  
 CC stated as being SEQ ID's 7-22.  
 XX  
 SQ Sequence 4205 BP; 1139 A; 1025 C; 1003 G; 1037 T; 1 other;  
 Alignment Scores:  
 Pred. No.: 2,68e-156 Length: 4205  
 Score: 1516.00 Matches: 272



|   |        |  |      |
|---|--------|--|------|
| Percent Similarity:                         | 76.08% | Conservative:  | 62   |
| Best Local Similarity:                      | 61.96% | Mismatches:  | 99   |
| Query Match:                                | 62.18% | Indels:  | 6    |
| DB:   | 21     | Gaps:  | 3    |
| US-09-719-601-5 (1-444) x AAA90952 (1-4205) |        |  |      |
| QY  | 11     | AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln     | 27   |
| DB  | 97     | GCAGCGGAGACCGCGGCTACGGAGCTACCCGCGCTACTTCACCTGGGAGAGGTGGCC    | 156  |
| QY  | 28     | LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr | 47   |
| DB  | 157    | CAGCGCTCAGGTGGCGAGGCGGTGGTGTAGTATCGACCGTAAAGTGTACAACATCAGC   | 216  |
| QY  | 48     | LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp | 67   |
| DB  | 217    | GAGTTTCAACCGCGGCTCCAGGGGGTCCCGGGTCCATCAGCCACTACGCCGGGCGAGAT  | 276  |
| QY  | 68     | AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys | 87   |
| DB  | 277    | GCACGGATCCCTTTGTGGCTTCCACATCAACAGGGGCTTGTGAAGATATATGAAC      | 336  |
| QY  | 88     | ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer | 107  |
| DB  | 337    | TCTCTCTGATTGGAGAACTGTCTCCAGAGACGCCGAGCTTTGAGCCCAAGAAATAAA    | 396  |
| QY  | 108    | LysIleThrGluAspPheArgAlaLeuArgLysTrpAlaGluAspMetAsnLeuPheLys | 127  |
| DB  | 397    | GAGTCAGACAGAGTTCGGGAGCTGCGGCCACAGTGGAGCGGATGGGGTCTCATGAG     | 456  |
| QY  | 128    | ThrAsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuGluSerIleAla       | 147  |
| DB  | 457    | GCCACCATGCTCTTCTGCTGTACTCTGCTGCACATCTTCTGCTGTGATGGTCGAGCC    | 516  |
| QY  | 148    | TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal | 167  |
| DB  | 517    | TGCTCACCTTTGGGTCTTTGGAGCTCTTTTCCCTTCTCTCTCTGTCGGTGTGCTG      | 576  |
| QY  | 168    | LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal | 187  |
| DB  | 577    | CTCAGTCAGTTCAGGCCCGAGGCTGGCTGCTGCAGCATGACTTTGGCCACCTGTCGTC   | 636  |
| QY  | 188    | TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly | 207  |
| DB  | 637    | TTCAGCACCTCAAAAGTGAACCATCTGCTACATCATTTTGTGATTGGCCACTGAAAGGG  | 696  |
| QY  | 208    | AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe | 227  |
| DB  | 697    | GCCCCCGCAGTTGGTGAACACATGCATCTCCAGCACCATGTCGAAGCCCACTGCTTC    | 756  |
| QY  | 228    | HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln  | 245  |
| DB  | 757    | CGCAAGACCCAGACATCAACATG---CATCCCTCTCTTTCCTTGGCGGAGATCCCTC    | 813  |
| QY  | 246    | ProIleGluTrpGlyLysLysLysLeuLysTrpLeuProTyrAsnHisGlnHisGluTyr | 265  |
| DB  | 814    | TCGTGGAGCTTGGGAACAGAGAAATATATATGCGGTACACCAACCCAGCACCAATAC    | 873  |
| QY  | 266    | PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleLeuMet | 285  |
| DB  | 874    | TTCTTCCTAAATGGGCCCCCAGCGCTTCTGCTCTCTTCTTCTCCAGTGGTATATTTCTAT | 933  |
| QY  | 286    | ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIleAsp | 305  |
| DB  | 934    | TTTGTATCCAGCGAAGAGTGGTGGATTTGGCTGGATGATTAACCTTCTACGTCCGC     | 993  |
| QY  | 306    | PhePheIleThrTrpIleProPheTyrGlyLeuGlyAlaLeuLeuPheLeuAsnPhe    | 325  |
| DB  | 994    | TTCTTCCTCACTTATGTGCCACTATTGGGCGTGAAGCCCTCTCTGGGCTTTTCTTCATA  | 1053 |
| QY  | 326    | IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet | 345  |

|           |   |  |                    |
|-----------|---|--|--------------------|
| Db        | 1054  | GTGAGTTCTCGAAAGCAACTGGTTGTGTGGGTGACACAGATGACCAATATCCCATG     | 1111               |
| Qy        | 346   | GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn | 365                |
| Db        | 1114  | CACATTGATCATGACCGGAACATGGACTGGTTTCCACCAGCTCCAGGCCACATGCAAT   | 1173               |
| Qy        | 366   | ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis | 385                |
| Db        | 1174  | GTCCACAGTCTCCCTTCAATGACTGGTTCACTGGACACCTCAACTCCAGATTGAGCAC   | 1233               |
| Qy        | 386   | HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer | 405                |
| Db        | 1234  | CATCTTTTCCCAAGATGCTCGACAAATACCAAAAGTGGTCCCTGGTGGAGTCC        | 1293               |
| Qy        | 406   | LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp | 425                |
| Db        | 1294  | TTGTGTGCCAAGATGGCATAGTACCATGTCAGGCCCTCTGTCACCTTGGCCGAC       | 1353               |
| Qy        | 426   | IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys    | 444                |
| Db        | 1354  | ATCATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCCATCTTACCACAA    | 1410               |
| RESULT 36 |   |  |                    |
| ABX93652  |   |  |                    |
| ID        | ABX93652 standard; cDNA; 1928 BP.   |  |                    |
| XX        |   |  |                    |
| AC        | ABX93652;   |  |                    |
| XX        |   |  |                    |
| DT        | 09-JUN-2003 (first entry)   |  |                    |
| XX        |   |  |                    |
| DE        | cDNA encoding human delta 6 desaturase D6DH-2, Incyte 2056310.  |  |                    |
| XX        |   |  |                    |
| KW        | Human; ss; gene; D6DH-2; delta 6 desaturase-2; fatty acid desaturase; cardiovascular disease; angina pectoris; atheroma embolism; hypertension; atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia; hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer; mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis; aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia; basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; Goiter; chronic lymphatic leukaemia; degenerative osteoarthritis; delirium; dementia; depression; dyskinesia; diabetic hyperosmolar nonketotic coma; glucocoma; hypercholesterolaemia; hypothermia; metabolic bone disease; osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome; Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma; renal amyloidosis; tuberculous; urinary incontinence; galactosaemia; fatty acid metabolism disorder; Addison's disease; cystic fibrosis; fatty hepatocirrhosis; hyperadrenalism; hypoadrenalism; hyperlipaemia; hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity; lipodystrophy; phenylketonuria; cancer; Incyte 2056310. |  |                    |
| XX        |   |  |                    |
| OS        | Homo sapiens.   |  |                    |
| XX        |   |  |                    |
| FT        | Key   | Location/Qualifiers  |                    |
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| FT        |   | /*tag= a   |                    |
| FT        |   | /product= "D6DH-2"   |                    |
| XX        |   |  |                    |
| PN        | US6492108-B1.   |  |                    |
| XX        |   |  |                    |
| PD        | 10-DEC-2002.  |  |                    |
| XX        |   |  |                    |
| PF        | 26-MAR-1998; 98US-0048888.  |  |                    |
| XX        |   |  |                    |
| PR        | 26-MAR-1998; 98US-0048888.  |  |                    |
| XX        |   |  |                    |
| PA        | (INCY-) INCYTE GENOMICS INC.  |  |                    |
| XX        |   |  |                    |
| PI        | Hillman JL,   | Guesler KJ,  | Corley NC, Shah P; |
| XX        |   |  |                    |
| DR        | WPI;  | 2003-327308/31.  |                    |
| DR        | P-PSDB;   | ABU08789.  |                    |
| XX        | New isolated polynucleotide encoding polypeptide having delta-6   |  |                    |
| PT        |   |  |                    |





OS Homo sapiens.  
 XX EP1074617-A2.  
 XX 07-FEB-2001.  
 XX 28-JUL-2000; 2000EP-0116126.  
 XX 29-JUL-1999; 99JP-0248036.  
 XX 27-AUG-1999; 99JP-0300253.  
 XX 11-JAN-2000; 2000JP-0118776.  
 XX 02-MAY-2000; 2000JP-0183767.  
 XX 09-JUN-2000; 2000JP-0241899.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX WPI; 2001-318749/34.  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX Claim 8; SEQ ID 14196; 2537pp + CD ROM; English.  
 XX The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03186 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX SQ Sequence 1856 BP; 423 A; 517 C; 496 G; 420 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2,166-156 Length: 1856  
 Score: 1512.00 Matches: 276  
 Percent Similarity: 76.07% Conservative: 61  
 Best Local Similarity: 62.30% Mismatches: 96  
 Query Match: 62.02% Indels: 10  
 DB: 22 Gaps: 5  
 US-09-719-601-5 (1-444) x AAH15766 (1-1856)  
 QY 5 GlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGlu 24  
 DB 34 GGGACCGGGCTCAGGACCTACCCCGGC-----TACTTCACCTGGGAC 78  
 QY 25 GluIleGlnLysHisAsnLeuArgThrSerGlyLeuValIleAspArgLysValTrp 44  
 DB 79 GAGGTGGCCCGCCGCTCAGGGTGCAGGCGGGTGGTGTAGTCGATCGACCGTAAGGTGTAC 138  
 QY 45 AsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrpAla 64  
 DB 1139 AACATCAGCGAGTTCCACCGCGCGCATCCAGGGGGCTCCGGGTTCATCAGCCATCAGCC 198  
 QY 65 GlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLys 84  
 DB 199 GGGCAGGATGCCAGGATCCCTTTGTGGCTTCCACATCAACAAGGGCTTTGTGAAGAAG 258  
 QY 85 PheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGly 104  
 DB 259 TATATGAACCTCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCAGCTTTGAGCCACC 318  
 QY 105 LysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsn 124  
 DB 319 AAGAATAAAGAGCTGACAGATGAGTTCGGGAGCTGCGGGCCACAGTGGAGGGATGGG 378  
 QY 125 LeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGlu 144  
 DB 379 CTCATGAAGGCCAACCACTGTCTTCTGTGTACCTGTGTCACATTTTGTGTGTGAT 438  
 QY 145 SerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThr 164  
 DB 439 GGTGAGCGCTGGCTCACCTTTGGGTCTTTGGAGCTCTTTTGGCTCTCTCTCTCTCT 498  
 QY 165 AlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHis 184  
 DB 499 GCGGTCTCTCTCAGTGCAGTTCAGGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558  
 QY 185 LeuSerValTrpArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHis 204  
 DB 559 CTGTGGTCTTCAGCAGCCTCAAGTGAACCATCTGTACATCATTTTGTGATTGGCCAC 618  
 QY 205 LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysPro 224  
 DB 619 CTGAAGGGGGCCCCCGCAGTGTGGTGAACCAACATGCTTCCAGCACCATGCCAAGGCC 678  
 QY 225 AsnIlePheHisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGly 242  
 DB 679 AACTGCTTCGCGAAGACCCACACATCAACATG---CATCCCTCTCTTTTGGCTGGG 735  
 QY 243 GluTrpGlnProIleGluTrpGlyLysLysLysLysLysLysLysLysLysLysLys 262  
 DB 736 AAGATCTCTCTCTGGAGCTTGGGAAACAGAGAGAAATAATATATATATATATATAT 795  
 QY 263 HisGluTrpPhePheLeuIleGlyProProLeuLeuIleProMetTrpPheGlnTrpGln 282  
 DB 796 CACAAATATCTTCTCTATATGGGCCCCCAGCCTTGTGCTCTCTCTCTCTCTCTCTCT 855  
 QY 283 IleIleMetMetMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTrp 302  
 DB 856 ATTTTCTATTTTGTATCCAGCGAAAGAGTGGGTGGACTTGGCTGGATGATTACCTTC 915  
 QY 303 TyrIleArgPhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAlaLeuLeuPhe 322  
 DB 916 TAGTCCGCTTCTCTCTATGTGTCATTTATGGGG---CTGAAGCCCTCTCTGGGC 972  
 QY 323 LeuAsnPheIle---ArgPheLeuGluSerHisTrpPheValTrpValTrpGlnMetAsn 341  
 DB 973 CTTTCTCTCATAGTCAGGTTCCTGGAAAGCAACTGGTTGTGGGTGCACACAGATGAAC 1032  
 QY 342 HisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSerSerGlnLeuThr 361  
 DB 1033 CATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1092  
 QY 362 AlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPhe 381  
 DB 1093 GCCACATGCAATGTCCACAGTCTGCTTCAATGATGTTGTGAGTGGACACCTCACTTC 1152  
 QY 382 GlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaPro 401  
 DB 1153 CAGATTGACACCATCTTTTCCACGATGCTCGACACAAATACCAAAATGGTCTCC 1212  
 QY 402 LeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluLysProLeuLeuArg 421  
 DB 1213 CTGGTGCATCTCTTGTGTGCGAAGCATGGCATAGATGATGATGATGATGATGATGATG 1272

QY 422 AlaLeuLeuAspIleAArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyr 441  
 DB 1273 GCCTCGCGGACATCATCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCCTAT 1332  
 QY 442 LeuHisLys 444  
 DB 1333 CTTCCACAA 1341  
 RESULT 39  
 ID AAA49932  
 XX AAA49932 standard; cDNA; 1335 BP.  
 AC AAA49932;  
 XX 10-OCT-2000 (first entry)  
 XX Human delta-5-desaturase cDNA.  
 XX Delta-5-desaturase; human; polyunsaturated fatty acid;  
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;  
 KW docosahexaenoic acid; nutrition; feedstuff; ss.  
 XX Homo sapiens.  
 XX WO2000040705-A2.  
 XX 13-JUL-2000.  
 XX 29-DEC-1999; 99WO-US31163.  
 XX 08-JAN-1999; 99US-0227613.  
 XX (ABBO ) ABBOTT LAB.  
 XX Mukerji P, Leonard AEV, Huang Y, Parker-Barnes JM;  
 DR WPI; 2000-465975/40.  
 DR P-PSDB; AAY95445.  
 XX New polypeptide useful for preparation of nutritional supplements based  
 PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids  
 PT at carbon 5 -  
 XX Claim 1; Fig 12; 127pp; English.  
 XX The present sequence is that of cDNA encoding human  
 CC delta-5-desaturase (see AAY95445), an enzyme that catalyzes the  
 CC conversion of dihomogamma-linolenic acid to arachidonic acid (AA)  
 CC and of 20:4n-3 to eicosapentaenoic acid (EPA). The cDNA was  
 CC isolated on the basis of homology to Mortierella alpina desaturase  
 CC gene sequences, involving the isolation of contigs from a database  
 CC and PCR amplifications. The isolated cDNA can be used in the  
 CC recombinant production of the delta-5-desaturase. The enzyme can  
 CC be expressed in eukaryotic or prokaryotic host cells, especially  
 CC Escherichia coli, cyanobacteria, Bacillus subtilis, yeast cells,  
 CC fungal cells, mammalian cells, plant cells or insect cells  
 CC (especially Spodoptera frugiperda) using a vector comprising the  
 CC human delta-5-desaturase nucleotide sequence. Transgenic plants  
 CC capable of producing polyunsaturated fatty acid (PUFA) in their  
 CC seeds, and transgenic mammals are also claimed. AA and EPA can be  
 CC used as substrates for the production of other PUFAs, especially  
 CC docosapentaenoic acid or docosahexaenoic acid, using additional  
 CC desaturase enzymes. The PUFA products are used in nutritional,  
 CC veterinary and pharmaceutical compositions which can be administered  
 CC to animals or humans as a dietary substitute/supplement.  
 XX Sequence 1335 BP; 282 A; 400 C; 334 G; 319 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,64e-156 Length: 1335  
 Score: 1508.00 Matches: 271  
 Percent Similarity: 75.8% Conservative: 62

Best Local Similarity: 61.73% Mismatches: 100  
 Query Match: 61.85% Indels: 6  
 DB: 21 Gaps: 3  
 US-09-719-601-5 (1-444) x AAA49932 (1-1335)  
 QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27  
 DB 19 GCAGCCGAGACCGCGGCTCAGGACCTACCCGCGCTACTTCCACCTGGACGAGGTGGC 78  
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgGlyValTrpSerIleThr 47  
 DB 79 CAGCGCTCAGGGTCGAGGAGCGGTGGCTAGTAGTCACCGTAAGGTGTACAAATCAGC 138  
 QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrpArgGluAsp 67  
 DB 139 GAGTTCAACCGCGCGCATCCAGGGGCTCCCGGTCTATCAGCCACTACGCCGCGCAGGAT 198  
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 DB 199 GCACGCGATCCCTTTGTGGCTTCCACATCAACAGGGCCTTGTGAAGAGTATATGAAC 258  
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107  
 DB 259 TCTCTCTGATTGAGACTGTCTCCAGAGCAGCCAGCTTTGAGCCCAAGAAATAAA 318  
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 DB 319 GAGCTGACAGATGATTCCGGGAGCTCGCGGCCACAGTGGAGCGGATGGGCTCATGAAG 378  
 QY 128 ThrAsnHisValPhePheLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 DB 379 GCCAACCATGTCTTCTTCCCTGCTGCTACCTGCTGCACATCTTGTGCTGGATGTGCAGCC 438  
 QY 148 TrpPheThrValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 DB 439 TGGCTCACCTTTGGGTCTTTGGAGCTCTCTTTTGGCTCTCTCTCTCTCTCTCTCTCTG 498  
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerVal 187  
 DB 499 CTCAGTCAGTTCCAGGCCCAGGCTGGCTGGCTGCAGCATGCTTTGGCACCCTTCGCTC 558  
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 DB 559 TTCAGCACCTCAAAGTGGAAACCATCTGCTACATCATTTTGTGATTTGGCCACCTGAAGGG 618  
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisIleAlaLysProAsnIlePhe 227  
 DB 619 GCCCGCCGAGTGTGGTGGAAACCATGCTTCCAGCACCATGCGCAAGCCCACTGCTTC 678  
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245  
 DB 679 CGCAAGAACCCAGACATCAACATG---CATCCCTTCTTCTTCTTGGCTTGGGGAAGATCCTC 735  
 QY 246 ProlleGluTrpGlyLysLysLysLeuLysTrpLeuProTrpAsnHisGlnHisGluTrp 265  
 DB 736 TCTGTGGAGCTTGGGAACAGAGAAATAATATATATATATATATATATATATATATATAT 795  
 QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTrpPheGlnTrpGlnIleMet 285  
 DB 796 TTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 855  
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTrpTrpIleArg 305  
 DB 856 TTTGTATATCCAGCGAAAGAGTGGGTGGACTTGGCTGGATGATTACCTTCTAGTCCGC 915  
 QY 306 PhePheIleThrTrpIleProPheTrpGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325  
 DB 916 TTCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 975  
 QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345  
 DB 976 GTCAGGTTCTCTGAAAGCAACTGGTGTGTGGGTGGACACAGATGAACATATATCCCAATG 1035

QY 346 GluileaspGlnGluAlaTyArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365  
 Db 1036 CACATTGATCATGACCGGAACATGACCTGGTTTCCACCCAGCTCTCCGGCACATGCAAT 1095  
 QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385  
 Db 1096 GTCCACAAGTCTGCCTTCAATGACTGGTTTCAGTGGACACCTCAACTTCCAGATTGAGCAC 1155  
 QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisIleAlaProLeuValLysSer 405  
 Db 1156 CATCTTTTCCACGATCCCTCGACACAAATACACAAAGTGGCTCCCTGGTGCACTCC 1215  
 QY 406 LeuCysAlaLysHisGlyIleGluTrpGlnLysProLeuLeuArgAlaLeuLeuAsp 425  
 Db 1216 TTGTGTGCCAAGCTGGCATAGTACAGTCCAGGCCCTGCTGAGCTTCGCGGAC 1275  
 QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyLeuHisLys 444  
 Db 1276 ATCATCCACTCACTAAAGGATCAGGGGAGCTCTGGCTAGATGCTATCTTCACAA 1332  
 RESULT 40  
 AAF25236  
 ID AAF25236 standard; DNA; 1335 BP.  
 XX  
 AC AAF25236;  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a human delta5 desaturase.  
 KW delta5 desaturase; desaturase gene; elongase gene; fatty acid;  
 KW eicosanoid; nutrition; infant formula; dietary supplement;  
 KW dietary substitute; animal feed; ss.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 CDS 1..1335  
 FT /\*tag= a  
 FT /product= "delta5 desaturase"  
 XX  
 FN WO200104636-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 11-JUL-2000; 2000WO-US19011.  
 XX  
 PR 12-JUL-1999; 99US-0351525.  
 XX  
 PA (UYOH-) UNIV OHIO.  
 XX  
 PI Kopchick JJ, Kelder B;  
 XX  
 DR WPI; 2001-182622/18.  
 DR P-PSDB; AAB31686.  
 XX  
 PT New compositions comprising cells that express desaturases and  
 PT elongases, for synthesizing essential fatty acids or long-chain  
 PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal  
 PT feed formulations  
 XX  
 PS Disclosure; Fig 18; 93pp; English.  
 CC  
 CC The present sequence encodes a delta5 desaturase. The desaturase  
 CC polynucleotide sequence was used to transfect mammalian cells, to  
 CC produce animal cells expressing a desaturase gene and/or an elongase  
 CC gene. Compositions comprising cells of the invention are useful for  
 CC synthesizing essential fatty acids, their derivatives or downstream  
 CC products, as well as altered levels of long-chain polyunsaturated  
 CC fatty acids and eicosanoids. The compositions are useful in nutritional  
 CC formulae, e.g. infant formula, dietary supplements or dietary  
 CC substitutes for both humans and animals. The compositions are also

CC useful in cosmetic or animal feed formulations. Furthermore, the  
 CC compositions may also be used as fat free media or as research reagents.  
 XX  
 SQ Sequence 1335 BP; 282 A; 400 C; 334 G; 319 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,64e-156 Length: 1335  
 Score: 1508.00 Matches: 271  
 Percent Similarity: 75.85% Conservative: 62  
 Best Local Similarity: 61.73% Mismatches: 100  
 Query Match: 61.85% Indels: 6  
 DB: 22 Gaps: 3

US-09-719-601-5 (1-444) x AAF25236 (1-1335)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27  
 Db 19 GCGCGCGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCACCTGGAGCGAGTGGCC 78  
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIleThr 47  
 Db 79 CAGCGCTCAGGCTGCGAGGAGCGGTGGCTAGTATCGACCGTAAAGTGTACAAATCAGC 138  
 QY 48 LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyAlaGlyGluAsp 67  
 Db 139 GAGTTCACCCCGCGCATCCAGGGGCTCCCGGGTCATCAGCCACTACCGCGGAGGAT 198  
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 Db 199 GCCAGGATCCCTTTGTGGCCTTCCACATCAACAAGGCGCTTGTGAAGAATATATGAAC 258  
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107  
 Db 259 TCTCTCTCTGATTGGAGAACTGTCTCAGAGAGCCCGAGCTTGTGAGCCACCAAGAAATAA 318  
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 Db 319 GAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGGCTCATGAAG 378  
 QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147  
 Db 379 GCCAACCATGTCTTCTCTGTCTGTACCTGTGCGACATCTTGTCTGGTGGTGGTGCAGCC 438  
 QY 148 TrpPheThrValPheTyPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 Db 439 TGGCTCACCTTGGGTCTTTGGGAGCTCTTTTGGCCCTCTCTCTCTGTGCGGTGCTG 498  
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyArgHisLeuSerVal 187  
 Db 499 CTCAGTGCAGTTTCAGGCCCGAGGCTGGCTGCGACATGACTTTGGGCACCTGTGCGTGC 558  
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 Db 559 TTCAGCACCTCAAGTGGAACTCTGTACATCATTTTGTGATTTGGCCACCTGAGGGG 618  
 QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysAlaLysProAsnIlePhe 227  
 Db 619 GCCCGCGCAGTTGGTGGAAACCATGCACTTCCAGCACCATGCCAAGCCCACTGCTTC 678  
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245  
 Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTCTCTCTTTGGCTTGGGGAGATCCTC 735  
 QY 246 ProIleGluTyArgLysLysLysLysLysTyLeuProTyAsnHisGlnHisGluTyArg 265  
 Db 736 TCTGTGGAGCTTGGGAAACAGAAAGAAAATATATGCGGTACACCAACAGCAGCAAAATAC 795  
 QY 266 PhePheLeuIleGlyProProLeuLeuLeuProMetTyArgPheGlnTyArgIleMet 285  
 Db 796 TTCTTCTTAATTGGGCGCCCGAGCCCTGTGCTCTCTACTTCCAGTGGTATATTTCTAT 855  
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyArgIleArg 305

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Db      856 TTTGTTATCCACGGAAGAGTGGGTGGACTTGGCTGGATGATTACCTTCTAGTCGCGC 915
QY      306 PhePheIleThrTyrlleProPheTyrglyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db      916 TTTCTTCTCATTATGTGCCACTATTGGGCTGAAAGCCTTCTGGGCTTTTCTTCATA 975
QY      326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db      976 GTGAGGTTCTCTGAAAGCAACTGGTTGTGGGTGACACAGATGACCATATTCCCAIG 1035
QY      346 GluIleAspGlnGluAlaTyrrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db      1036 CACATTGATCATGACCGGAACATGGACTGGTTTCCACCCAGCTCTTGCCACATGCAAT 1095
QY      366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db      1096 GTCCACAGTCTGCTTCAATGACTGGTTCACTGGACACCTCAACTCCAGATTGAGCAC 1155
QY      386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db      1156 CATCTTTTCCACAGATGCTCGACACAAATACCCAAAGTGGCTCCCTGGTGAGTCC 1215
QY      406 LeuCysAlaLysHisGlyIleGluTyrglnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db      1216 TTGTGTGCCAAGCGTGGCATAGAGTACCAGTCCAGCCCTGCTGTACGCTTGGCCGAC 1275
QY      426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrlleuHisLys 444
Db      1276 ATCATCCACTCACTAAGAGGATCAGGCGAGCTCTGGCTAGATGCCCTATCTTCACCA 1332
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Search completed: December 10, 2003, 18:36:35  
Job time : 346 secs



|                 | 1    | 2   | 3  | 4    | 5  | 6        | 7 | 8 |              |
|-----------------|------|-----|----|------|----|----------|---|---|--------------|
| oxido-reductase | 3189 | 100 | 0  | 3184 | 21 | AZ482617 |   |   | Human        |
| OXYD-OXPHOS     | 3189 | 100 | 9  | 3186 | 21 | AAC78217 |   |   | Homo sapiens |
| full-length     | 3062 | 96  | 2  | 3063 | 21 | AAG9334c |   |   | Human        |
| fatty acid d    | 2988 | 82  | 4  | 2989 | 21 | AAK90953 |   |   | Human        |
| full-length     | 2772 | 87  | 1  | 2772 | 21 | AKA93377 |   |   | Human        |
| breast cancer   | 2576 | 6   | 80 | 2521 | 22 | AST10758 |   |   | Human        |
| full-length     | 2537 | 4   | 79 | 2558 | 22 | AAK94785 |   |   | Human        |
| cDNA sequenc    | 2174 | 2   | 68 | 2190 | 22 | AAH16118 |   |   | Human        |



1681 TCCCCATAGACACCTGCTCATGGGACCTGCTCCCTCAGCGTCAGCCATCAGCCA 1740  
1681 TCCCCATAGACACCTGCTCATGGGACCTGCTCCCTCAGCGTCAGCCATCAGCCA 1740  
1741 TGGCCCTCCAGTGTCTCTAGCCCTCTCTTCCAAAGGAGCAGAGAGTGCCACCCGGGG 1800  
1741 TGGCCCTCCAGTGTCTCTAGCCCTCTCTTCCAAAGGAGCAGAGAGTGCCACCCGGGG 1800  
1801 TGGCTCTGTCTTACCTCCTCTGCTCCCTTAAAGATGGGAGGAGACAGCGGTCCATGG 1860  
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1861 GTTGGCTGTGAGTCTCCCTTGCAGGCTGGTCACTAGGCAATCACTCCCTTGGTTC 1920  
1861 GTTGGCTGTGAGTCTCCCTTGCAGGCTGGTCACTAGGCAATCACTCCCTTGGTTC 1920  
1921 TTCCAGATGCTCTTGGGGTTCATAGGGGAGGCTCTAGTGGGAGGAGGCTGACCTCC 1980  
1921 TTCCAGATGCTCTTGGGGTTCATAGGGGAGGCTCTAGTGGGAGGAGGCTGACCTCC 1980  
1981 CGGCTGTGCTTCACTCTCCCTGACGGCTGCCATTTGGTCCACCTTTTATAGAGAGGCTG 2040  
1981 CGGCTGTGCTTCACTCTCCCTGACGGCTGCCATTTGGTCCACCTTTTATAGAGAGGCTG 2040  
2041 CTTTGTAAAGCTCGGCTCTCCCTCTGAGCTCGTAAAGTACCGAGGCTCTCTT 2100  
2041 CTTTGTAAAGCTCGGCTCTCCCTCTGAGCTCGTAAAGTACCGAGGCTCTCTT 2100  
2101 AAGATGTCCAGGGCCCGAGGCGCGGCGCAGAGCCAGCCAAACCTTGGGCGCTGGAAGA 2160  
2101 AAGATGTCCAGGGCCCGAGGCGCGGCGCAGAGCCAGCCAAACCTTGGGCGCTGGAAGA 2160  
2161 GTCTCCACCCCATCACTAGAGTGTCTGACCTTGGGCTTTACGGGCGCCCAITTCACCG 2220  
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2221 CCTCCCAACTTGAAGCTGTGACCTTGGGAGCCAAAGGGGAGTCCCTGCTCTTGTGAC 2280  
2221 CCTCCCAACTTGAAGCTGTGACCTTGGGAGCCAAAGGGGAGTCCCTGCTCTTGTGAC 2280  
2281 TCAGCAGAGGAGTGCCACGCTTCAGGAGGGGCGGCTGCGCTGGAGGCTCAGCCCAACC 2340  
2281 TCAGCAGAGGAGTGCCACGCTTCAGGAGGGGCGGCTGCGCTGGAGGCTCAGCCCAACC 2340  
2341 CTCAGCTTTTCTCAGAGTGTCTGAGTCCAGATTCAGAGATTCAGAGATTCAGAGATTC 2400  
2341 CTCAGCTTTTCTCAGAGTGTCTGAGTCCAGATTCAGAGATTCAGAGATTCAGAGATTC 2400  
2401 CAAAGGCTCTGTATCAGCTGGGAGTCCAGCCCAATCCCTGGCCATTTGGCCCGCAGGGG 2460  
2401 CAAAGGCTCTGTATCAGCTGGGAGTCCAGCCCAATCCCTGGCCATTTGGCCCGCAGGGG 2460  
2461 GACGTGGGCGCTGAGGCTGAGAGGAGCAGTGGAGTCTGCTGCCAGCCCTC 2520  
2461 GACGTGGGCGCTGAGGCTGAGAGGAGCAGTGGAGTCTGCTGCCAGCCCTC 2520  
2521 CCCATCTCGGCGCTGCTGTGTGGAGCGGCTGCTCAGGCACTCTCTGCTGAACTGTC 2580  
2521 CCCATCTCGGCGCTGCTGTGTGGAGCGGCTGCTCAGGCACTCTCTGCTGAACTGTC 2580  
2581 CTTTACTGTGTTTAACTGCTCCAGGATGCAATTCATGATAGAGGGGCGGCGAGGCT 2640  
2581 CTTTACTGTGTTTAACTGCTCCAGGATGCAATTCATGATAGAGGGGCGGCGAGGCT 2640  
2641 GGGCCCTCTGCAATCTGCTTCCACATGGGCTGCTCGGTGGCCCTGACTGTGAC 2700  
2641 GGGCCCTCTGCAATCTGCTTCCACATGGGCTGCTCGGTGGCCCTGACTGTGAC 2700  
2701 GGAGGGCCAGGAGGAGCAGAGGGGAGGAGTCTCAGGAGGAGGCTGCGCTCAGGGGCTGG 2760  
2701 GGAGGGCCAGGAGGAGCAGAGGGGAGGAGTCTCAGGAGGAGGCTGCGCTCAGGGGCTGG 2760  
2761 GGAGGGGTAACCTCATGAGGACCGGCTGAGCTGAGAGGAGGAGGCTGGGGCTGGA 2820

2761 GGAGGGGTAACCTCATGAGGACCGGCTGAGAGGAGGAGGCTGGGGCTGGA 2820  
2821 GGTGCTGTAGCTGAGGGGACCGGCAAGTGAAGGGGAGGAGGAGTCTCTGGAGGAT 2880  
2821 GGTGCTGTAGCTGAGGGGACCGGCAAGTGAAGGGGAGGAGGAGTCTCTGGAGGAT 2880  
2881 CTTGAGCTCTGTTGAGTCTAACCACTAACTCAGTCTTTAGATTTCAGGGGAGGGCAGG 2940  
2881 CTTGAGCTCTGTTGAGTCTAACCACTAACTCAGTCTTTAGATTTCAGGGGAGGGCAGG 2940  
2941 CACCAACAACCTCAGAAATGGGGCTTTTCGGGGAGGGGCTAGTCCCTCCAGCTCTAAGCA 3000  
2941 CACCAACAACCTCAGAAATGGGGCTTTTCGGGGAGGGGCTAGTCCCTCCAGCTCTAAGCA 3000  
3001 GCCAGAGGAGCTGCTGATCTAAGCATCTGGGTTCATGCGCAATGGCATGCCATGCCAGCT 3060  
3001 GCCAGAGGAGCTGCTGATCTAAGCATCTGGGTTCATGCGCAATGGCATGCCATGCCAGCT 3060  
3061 ACTGTATGCCCGGACCCCGCAGAGGAGCAATGAACCATAGGAGTGTATGTAATGT 3120  
3061 ACTGTATGCCCGGACCCCGCAGAGGAGCAATGAACCATAGGAGTGTATGTAATGT 3120  
3121 TTATCATGTACTTCCCGACCCCTACATTTTGAATAAATAAGGAATTTTAAAAA 3180  
3121 TTATCATGTACTTCCCGACCCCTACATTTTGAATAAATAAGGAATTTTAAAAA 3180  
3181 AAAAA 3184  
3181 AAAAA 3184  
RESULT 2  
AAC76019  
ID AAC76019 standard; cDNA; 3106 BP.  
XX AAC76019;  
XX AC AAC76019;  
XX AC AAC76019;  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF1574 polynucleotide sequence SEQ ID NO:3147.  
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
XX vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
XX hypotensive; dermatological; immunosuppressive; antiinflammatory;  
XX antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;  
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
XX cholesterol ester storage; systemic lupus erythematosus; infection;  
XX severe combined immunodeficiency; diabetes mellitus; hypothyroidism; SCID; AIDS;  
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;  
XX thrombosis; contraceptive; ss.  
OS Homo sapiens.  
XX  
XX WO200058473-A2.  
PN  
XX  
XX 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US08621.  
XX  
XX 31-MAR-1999; 99US-0127607.  
XX 02-APR-1999; 99US-0127636.  
XX 05-APR-1999; 99US-0127728.  
XX 30-MAR-2000; 2000US-0540763.  
XX  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M; PI



QY 1713 CCTCCCTCAGCGCTCAGCCATCAGCCATGCGCCCTCCAGTCTCCTAGCCCTCTTCTC 1772  
Db 1821 CCTCCCTCAGCGCTCAGCCATCAGCCATGCGCCCTCCAGTCTCCTAGCCCTCTTCTC 1880  
QY 1773 CAAGGACAGAGAGTGGCCACCGGGGGTGGCTCTGCTTCTACCTCCACTCTCTGCCCCA 1832  
Db 1681 CAAGGACAGAGAGTGGCCACCGGGGGTGGCTCTGCTTCTACCTCCACTCTCTGCCCCA 1740  
QY 1833 AAGATGGAGGAGACACAGCGTCCATGCGTCTGCGCTGTGAGTCTCCCTTTGAGCGCTGG 1892  
Db 1741 AAGATGGAGGAGACACAGCGTCCATGCGTCTGCGCTGTGAGTCTCCCTTTGAGCGCTGG 1800  
QY 1893 TCACTAGGATACACCCCGCTTTGGTCTTCTAGATGCTCTTGGGGTTTCATAGGGCAGGT 1952  
Db 1801 TCACTAGGATACACCCCGCTTTGGTCTTCTAGATGCTCTTGGGGTTTCATAGGGCAGGT 1860  
QY 1953 CCTAGTCGGGACGAGCGCCCTGACCCCTCCGCGCTGCGCTTCACTCTCCCTGACCGCTGCCA 2012  
Db 1861 CCTAGTCGGGACGAGCGCCCTGACCCCTCCGCGCTGCGCTTCACTCTCCCTGACCGCTGCCA 1920  
QY 2013 TTGGTCCACCCCTTTTCATAGAGAGCCCTGCTTTGTTTACAAAGCTCGGGTCTCCCTCTGCA 2072  
Db 1921 TTGGTCCACCCCTTTTCATAGAGAGCCCTGCTTTGTTTACAAAGCTCGGGTCTCCCTCTGCA 1980  
QY 2073 GCTCGGTTAGTACCGAGCGCTCTCTTAGATGCTCCAGGGCCCCAGGCCCCGGGACACA 2132  
Db 1981 GCTCGGTTAGTACCGAGCGCTCTCTTAGATGCTCCAGGGCCCCAGGCCCCGGGACACA 2040  
QY 2133 GCCAGCCCAACCTTTGGGCGCTTGAAGAGTCTCTCCACCCCACTCACTAGAGTGTCTTGACC 2192  
Db 2041 GCCAGCCCAACCTTTGGGCGCTTGAAGAGTCTCTCCACCCCACTCACTAGAGTGTCTTGACC 2100  
QY 2193 CTGGGCTTTACGGGCGCCATTCACCGCTCTCCCACTTTGAGGCTGTGACCTTGGGACC 2252  
Db 2101 CTGGGCTTTACGGGCGCCATTCACCGCTCTCCCACTTTGAGGCTGTGACCTTGGGACC 2160  
QY 2253 AAAGGGGAGTCCCTGCTCTCTGCTGCTCAGCAGAGGAGTGGCCACGTTTCAGGAGGG 2312  
Db 2161 AAAGGGGAGTCCCTGCTCTCTGCTGCTCAGCAGAGGAGTGGCCACGTTTCAGGAGGG 2220  
QY 2313 GCCGGCTGGCTGAGGCTCAGCCACCTCTCAGCTTTTCTCAGGCTGTCTGAGTCC 2372  
Db 2221 GCCGGCTGGCTGAGGCTCAGCCACCTCTCAGCTTTTCTCAGGCTGTCTGAGTCC 2280  
QY 2373 AAGATTCGAGCAATCTGACCTTTCTCAAGGCTCTGTTATCAGCTGGGCGAGTGCAG 2432  
Db 2281 AAGATTCGAGCAATCTGACCTTTCTCAAGGCTCTGTTATCAGCTGGGCGAGTGCAG 2340  
QY 2433 CCAATCCCTGGCCATTTGGCCCCAGGGGACGTCGGGCCCTGCAAGGCTGCAGAGGGCACT 2492  
Db 2341 CCAATCCCTGGCCATTTGGCCCCA-GGGGACGTCGGGCCCTGCAAGGCTGCAGAGGGCACT 2399  
QY 2493 GGAGCTGGAGGTCTCGTCCAGCCCTCCCATCTCGGGCTGTGTGTGAGCGGCGCTG 2552  
Db 2400 GGAGCTGGAGGTCTCGTCCAGCCCTCCCATCTCGGGCTGTGTGTGAGCGGCGCTG 2459  
QY 2553 CCTCAGGCACTCTCTCTGCTGAACCTGCCCCCTTACTGTGTTAACTGTGCTCCAGGATG 2612  
Db 2460 CCTCAGGCACTCTCTCTGCTGAACCTGCCCCCTTACTGTGTTAACTGTGCTCCAGGATG 2519  
QY 2613 CATTCGTAGAGGGGGCGGAGGGCTGGGCCCTGTGACATCTGCTTTTCCACCATG 2672  
Db 2520 CATTCGTAGAGGGGGCGGAGGGCTGGGCCCTGTGACATCTGCTTTTCCACCATG 2579  
QY 2673 GCCTTGCCTCGGCTGCGCTTCTGCTGAGGAGGCGCCAGGAGGCGAGCGGGGAGTC 2732  
Db 2580 GCCTTGCCTCGGCTGCGCTTCTGCTGAGGAGGCGCCAGGAGGCGAGCGGGGAGTC 2639  
QY 2733 TCAGAGAGAGGCTGCGCTGAGGGCTGGGAGGGGGTACCTCATAGACAACAGGGTGGAG 2792  
Db 2640 TCAGAGAGAGGCTGCGCTGAGGGCTGGGAGGGGGTACCTCATAGAGAACAGGGTGGAG 2699  
QY 2793 CTGAGAACAGGAGGAGGTGGGGCTGGAGGTGCTGGTGGAGGCGGCGCAAGTGAG 2852

Db 2700 CTGAGAACAGGAGGAGGTGGGGCTGGAGGTGCTGGTAGCTGAGGGAACGGCAAGTGAG 2759  
QY 2853 AGGGAGGAGGAGGAGTCTCTCGGAGGATCTCGAGTCTGTGTGAGTCTAACCCACTAAT 2912  
Db 2760 AGGGAGGAGGAGGAGTCTCTCGGAGGATCTCGAGTCTGTGTGAGTCTAACCCACTAAT 2819  
QY 2913 CAGTTCCTTAGATTACAGGGAAGGGCAGGCACCAACTCAGAATGGGGGCTTTTCGGGGA 2972  
Db 2820 CAGTTCCTTAGATTACAGGGAAGGGCAGGCACCAACTCAGAATGGGGGCTTTTCGGGGA 2879  
QY 2973 GGGCGCCCTAGTCCCCCAGCTCTTAAGCAGCAGAGGAGACCTGATCTAAGCATCTGGGT 3032  
Db 2880 GGGCGCCCTAGTCCCCCAGCTCTTAAGCAGCAGAGGAGACCTGATCTAAGCATCTGGGT 2939  
QY 3033 TGCCATGCAATGGCATGCCGCCAGCTGATGTATGCCGCCGACCCCGCAGAGGACAGAA 3092  
Db 2940 TGCCATGCAATGGCATGCCGCCAGCTGATGTATGCCGCCGACCCCGCAGAGGACAGAA 2999  
QY 3093 TGAACCCATAGGAGCTGATGTAATGTTATCATGTTACTTCCCAACCCCTACATTTT 3152  
Db 3000 TGAACCCATAGGAGCTGATGTAATGTTATCATGTTACTTCCCAACCCCTACATTTT 3059  
QY 3153 TGAATAAATAAGGAATTTTAAAAA 3184  
Db 3060 TGAATAAATAAGGAATTTTATCTCAAAA 3091

RESULT 3  
AAK94346  
ID AAK94346 standard; cDNA; 3083 BP.  
XX AAK94346;  
AC AAK94346;  
XX DT 06-NOV-2001 (first entry)  
XX Human full-length cDNA, SEQ ID NO: 3049.  
DE Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX Homo sapiens.  
XX EP1130094-A2.  
XX 05-SEP-2001.  
XX 07-JUL-2000; 2000EP-0114089.  
XX 08-JUL-1999; 99JP-0194486.  
PR 11-JAN-2000; 2000JP-0118774.  
PR 02-MAY-2000; 2000JP-0183765.  
XX (HELI-) HELIX RES INST.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
DR P-PSDB; AAM93425.  
XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their  
PT use in genetic manipulation -  
XX  
PS Claim 8; SEQ ID NO 3049; 1380pp + sequence listing; English.  
XX  
CC The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
CC molecules have been determined. Primers for synthesizing the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesised by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily

CC without any special methods. The present sequence is a full length  
 CC human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX  
 SQ Sequence 3083 BP; 615 A; 937 C; 884 G; 647 T; 0 other;

Query Match 96.2%; Score 3064; DB 22; Length 3083;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 3078; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 90 GCACACCGCTGGAGCGAGCGCTCTGTGACGACGACCGCGCGGGAGCGCGCA 149  
 DB 1 GCACACACCGCTGGAGCGAGCGCTCTGTGACGACGACCGCGCGGGAGCGCGCA 60

QY 150 GTGACGCGGGCGTCACTGCGGAGGAGCGATGGGGAAGGAGGAGGAGGCGGG 209  
 DB 61 GTGACGCGGGCGTCACTGCGGAGGAGCGATGGGGAAGGAGGAGGAGGCGGG 120

QY 210 GCGCGGAGCGGAGGCTGCGGTGCCACCTTCAGCTGGGAGGAGATTCAGAGCATAAC 269  
 DB 121 GCGCGGAGCGGAGGCTGCGGTGCCACCTTCAGCTGGGAGGAGATTCAGAGCATAAC 180

QY 270 CTGCGACCGACGAGTGGGCTGTCTATTGACCGCAAGGTTTACACATCACCAATGTCTC 329  
 DB 181 CTGCGACCGACGAGTGGGCTGTCTATTGACCGCAAGGTTTACACATCACCAATGTCTC 240

QY 330 ATCCAGACCGCGGGGCGAGCGGTCTATCGGGCACTACGCTGGAGAGATTCAGAGCAGAT 389  
 DB 241 ATCCAGACCGCGGGGCGAGCGGTCTATCGGGCACTACGCTGGAGAGATTCAGAGCAGAT 300

QY 390 GCCTTCGCGCCCTTCACCTGACCTGGAATTCGTGGGCAAGTCTTGAACCCCTGTCTG 449  
 DB 301 GCCTTCGCGCCCTTCACCTGACCTGGAATTCGTGGGCAAGTCTTGAACCCCTGTCTG 360

QY 450 ATGTGTGACTGCGCGGAGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 509  
 DB 361 ATGTGTGACTGCGCGGAGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 420

QY 510 GAGGACTTCGCGGCGCTGAGGAGAGCGGCTGAGGACATGAACCTGTTCAAGACCAACCAC 569  
 DB 421 GAGGACTTCGCGGCGCTGAGGAGAGCGGCTGAGGACATGAACCTGTTCAAGACCAACCAC 480

QY 570 GTGTTCT 629  
 DB 481 GTGTTCT 540

QY 630 GTCTTTCTACTTTGGCAATGGCTGGATTCCTATCCCTCATCAGCGCCCTTTGCTCTCTACC 689  
 DB 541 GTCTTTCTACTTTGGCAATGGCTGGATTCCTATCCCTCATCAGCGCCCTTTGCTCTCTACC 600

QY 690 TCTCAGGCGCAAGCTGGATGGCGAACAATGATATGGCGACCTGTCTGTCTACAGAAA 749  
 DB 601 TCTCAGGCGCAAGCTGGATGGCGAACAATGATATGGCGACCTGTCTGTCTACAGAAA 660

QY 750 CCCAAGTGGAAACACCTTTGCCCAATTCGTCATTGGGCACTTTAAAGGCTGCTCTGCC 809  
 DB 661 CCCAAGTGGAAACACCTTTGCCCAATTCGTCATTGGGCACTTTAAAGGCTGCTCTGCC 720

QY 810 AACTGTGGAAATCATGCCACTTCCAGACCAAGCGCTTAACATCTTCCACAGGAT 869  
 DB 721 AACTGTGGAAATCATGCCACTTCCAGACCAAGCGCTTAACATCTTCCACAGGAT 780

QY 870 CCGATGTGAACATGTGACGCTGTTTGTCTGGGGAATGGAGCGCCATTCAGTACGCG 929  
 DB 781 CCGATGTGAACATGTGACGCTGTTTGTCTGGGGAATGGAGCGCCATTCAGTACGCG 840

QY 930 AAGAAGAGCTGAAATACCTTCCGCTCAATCAACAGCAAGATCTTCTCTGTGGTGG 989  
 DB 841 AAGAAGAGCTGAAATACCTTCCGCTCAATCAACAGCAAGATCTTCTCTGTGGTGG 900

QY 990 CCGCGGCTGCTATCCCGCTGATTTCCAGTACAGATCATCATGACCATGATCGTCCAT 1049

DB 901 CCGCGCTGCTCATCCCATGTAATTTCCAGTACCAGATCATCATGACCATGATGCTCCAT 960  
 QY 1050 AAGAAGTGGTGGACTGGCGCTGGCGCTGAGCTACTACATCCGCTTCTTATCACCTAC 1109  
 DB 961 AAGAAGTGGTGGACTGGCGCTGGCGCTGAGCTACTACATCCGCTTCTTATCACCTAC 1020

QY 1110 ATCCCTTTCTACGGCATCTCTGGGAGCCCTCTCTTCTCAACTTCATCAGGTTCCTGAG 1169  
 DB 1021 ATCCCTTTCTACGGCATCTCTGGGAGCCCTCTCTTCTCAACTTCATCAGGTTCCTGAG 1080

QY 1170 AGCACTGTTTGTGTGGTTCACAGATGATACATGATGATGATGATGATGATGATGATGATGAT 1229  
 DB 1081 AGCACTGTTTGTGTGGTTCACAGATGATACATGATGATGATGATGATGATGATGATGATGAT 1140

QY 1230 GCTACCGTGACTGGTTCACTAGCAGCAGCTGACAGCAGCCTGCAACGCTGGAGCAGTCTTC 1289  
 DB 1141 GCTACCGTGACTGGTTCACTAGCAGCAGCTGACAGCAGCCTGCAACGCTGGAGCAGTCTTC 1200

QY 1290 TTCAACGACTGGTTCAGTGGACACCTTAACCTTCCAGATTCAGCAGCAGTCTTCCCGACC 1349  
 DB 1201 TTCAACGACTGGTTCAGTGGACACCTTAACCTTCCAGATTCAGCAGCAGTCTTCCCGACC 1260

QY 1350 ATGCCCGGCAACAACCTTACCAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 1409  
 DB 1261 ATGCCCGGCAACAACCTTACCAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT 1320

QY 1410 GGCAATTGAATCAAGGAGAGCGCTACTAGAGGCGCTCTGAGCATCATCAGGTCCCTG 1469  
 DB 1321 GGCAATTGAATCAAGGAGAGCGCTACTAGAGGCGCTCTGAGCATCATCAGGTCCCTG 1380

QY 1470 AAGAAGTCTGGGAAGCTGTGGTGGAGCGCTTACCTTCAAAATGAAGCCACAGCCCGCG 1529  
 DB 1381 AAGAAGTCTGGGAAGCTGTGGTGGAGCGCTTACCTTCAAAATGAAGCCACAGCCCGCG 1440

QY 1530 GACACCTCTGGGAAGCGGTGCAAGTGGGTGATGCGCAGAGGAATGATGGGCTTTTGTTC 1589  
 DB 1441 GACACCTCTGGGAAGCGGTGCAAGTGGGTGATGCGCAGAGGAATGATGGGCTTTTGTTC 1500

QY 1590 TGAGGCGTGTCCAGAGGCTGGTGTATGACATGCTCAGCAGCAGCAGTGTGATGATGATGATGAT 1649  
 DB 1501 TGAGGCGTGTCCAGAGGCTGGTGTATGACATGCTCAGCAGCAGCAGTGTGATGATGATGATGAT 1560

QY 1650 CCCTTTCT 1709  
 DB 1561 CCCTTTCT 1620

QY 1710 CTGCGCT 1769  
 DB 1621 CTGCGCT 1680

QY 1770 TTCCAAGGAGCAGAGAGTGGCCCAAGGCGGTGGCTCTGTCCTTACCTTCTCTCTCTCT 1829  
 DB 1681 TTCCAAGGAGCAGAGAGTGGCCCAAGGCGGTGGCTCTGTCCTTACCTTCTCTCTCTCT 1740

QY 1830 CTAAGAATGGAGAGACAGCGGTCCATGGGTCTGCGCTCTGAGTCTCTCTCTCTCTCTCT 1889  
 DB 1741 CTAAGAATGGAGAGACAGCGGTCCATGGGTCTGCGCTCTGAGTCTCTCTCTCTCTCTCT 1800

QY 1890 TGGTCACTAGGACATCAACCCCGCTTGGTCTCTTCTGATGCTCTTGGGTTTCAAGGGCA 1949  
 DB 1801 TGGTCACTAGGACATCAACCCCGCTTGGTCTCTTCTGATGCTCTTGGGTTTCAAGGGCA 1860

QY 1950 GGTCTAGTGGGAGGCGCCCTGACCCCTCCGCGCTGGCTTCTCTCTCTCTCTCTCTCTCT 2009  
 DB 1861 GGTCTAGTGGGAGGCGCCCTGACCCCTCCGCGCTGGCTTCTCTCTCTCTCTCTCTCTCT 1920

QY 2010 CCATTGGTCCACCTTTTCATAGAGGCGCTCTTGTATCAAAAGCTCGGCTCTCTCTCTCT 2069  
 DB 1921 CCATTGGTCCACCTTTTCATAGAGGCGCTCTTGTATCAAAAGCTCGGCTCTCTCTCTCT 1980

QY 2070 GCAGCTCGTTAAGTACCGGAGGCTCTCTTAAAGATGTCAGGCGCCCGAGCCCGCGGCG 2129  
 DB 1981 GCAGCTCGTTAAGTACCGGAGGCTCTCTTAAAGATGTCAGGCGCCCGAGCCCGCGGCG 2040



QY 2130 ACAGCCAGCCCAACCTTGGCCCTGGAGAGTCTCTCCAGCCCATCACTAGATGCTCTG 2189  
Db 2041 ACAGCCAGCCCAACCTTGGCCCTGGAGAGTCTCTCCAGCCCATCACTAGATGCTCTG 2100  
QY 2190 ACCCTGGGCTTTACAGCGGCCCAATTCACACGCGCTCCCAACTTGGAGCTGTGACCTTGGG 2249  
Db 2101 ACCCTGGGCTTTACAGCGGCCCAATTCACACGCGCTCCCAACTTGGAGCTGTGACCTTGGG 2160  
QY 2250 ACCAAAGGGAGTCCCTGCTCTTGTGACTAGCAGAGCAGTGGCCACGTTACAGGA 2309  
Db 2161 ACCAAAGGGAGTCCCTGCTCTTGTGACTAGCAGAGCAGTGGCCACGTTACAGGA 2220  
QY 2310 GGGCGCGCTGCGCTGGAGGCTCAGCCACCCCTCCAGCTTTCTCAGGGTGTCTGAGG 2369  
Db 2221 GGGCGCGCTGCGCTGGAGGCTCAGCCACCCCTCCAGCTTTCTCAGGGTGTCTGAGG 2280  
QY 2370 TCCAAAGTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTATCAGCTGGGCACTGC 2429  
Db 2281 TCCAAAGTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTATCAGCTGGGCACTGC 2340  
QY 2430 CAGCCAAATCCCTGGCCATTTGGCCCCAGGGGAGCTGGCCCTGCAGGCTGCAGGAGGGC 2489  
Db 2341 CAGCCAAATCCCTGGCCATTTGGCCCCAGGGGAGCTGGCCCTGCAGGCTGCAGGAGGGC 2399  
QY 2490 ACTGAGCTGGAGGCTCTGCTCCAGGCTCCCATCTCGGGGCTGTGTGTGAGCGGG 2549  
Db 2400 ACTGAGCTGGAGGCTCTGCTCCAGGCTCCCATCTCGGGGCTGTGTGTGAGCGGG 2459  
QY 2550 CTGCTCAGGCACTCTCTGCTCAACTGCGCTTACTGTGTAACTGCTTCTCAGG 2609  
Db 2460 CTGCTCAGGCACTCTCTGCTCAACTGCGCTTACTGTGTAACTGCTTCTCAGG 2519  
QY 2610 ATGCATTTCTGATAGGAGGGGCGCAGGGCTGGGCTTTGTGACAACTGTGCTTTTACCAC 2669  
Db 2520 ATGCATTTCTGATAGGAGGGGCGCAGGGCTGGGCTTTGTGACAACTGTGCTTTTACCAC 2579  
QY 2670 ATGGCTTGTCTCGTGGCTCTGCTGCTCAGGAGGCGCAGGAGGCGAGCGGGAGGA 2729  
Db 2580 ATGGCTTGTCTCGTGGCTCTGCTGCTCAGGAGGCGCAGGAGGCGAGCGGGAGGA 2639  
QY 2730 GTCTCAGGAGGAGGCTGCTCCTGAGGGGCTGGGGAGGGGTACCTCATGAGGACACAGGGTG 2789  
Db 2640 GTCTCAGGAGGAGGCTGCTCCTGAGGGGCTGGGGAGGGGTACCTCATGAGGACACAGGGTG 2699  
QY 2790 GAGCTGAGAGAGAGGAGTGGGGCTGGAGGTGCTGTGAGCTGAGGGAGCGGGCAAGT 2849  
Db 2700 GAGCTGAGAGAGAGGAGTGGGGCTGGAGGTGCTGTGAGCTGAGGGAGCGGGCAAGT 2759  
QY 2850 GAGAGGGAGGAGGAGTCTCTGGAGGATCTCTGAGCTGCTGTGTGAGCTTAACCCACT 2909  
Db 2760 GAGAGGGAGGAGGAGTCTCTGGAGGATCTCTGAGCTGCTGTGTGAGCTTAACCCACT 2819  
QY 2910 AATCAGTTCTTAGATTACAGGGAAGGGCAGGACCAACAACTCAGATGAGGGGCTTTCCG 2969  
Db 2820 AATCAGTTCTTAGATTACAGGGAAGGGCAGGACCAACAACTCAGATGAGGGGCTTTCCG 2879  
QY 2970 GAGGGGCTAGTCCCTCCAGCTTAAGCAGGCGCAGGAGGAGCTGATCTTAAGCATCTG 3029  
Db 2880 GAGGGGCTAGTCCCTCCAGCTTAAGCAGGCGCAGGAGGAGCTGATCTTAAGCATCTG 2939  
QY 3030 GGTGGCCATGCAATGGCATCCCCCAGCTACTGTATGCCCCCGACCCCCCGCAGAGGCA 3089  
Db 2940 GGTGGCCATGCAATGGCATCCCCCAGCTACTGTATGCCCCCGACCCCCCGCAGAGGCA 2999  
QY 3090 GAATGAACCCATAGGAGCTATGTAATGTTTATCATGTTACTTCCCAACCCCTACATT 3149  
Db 3000 GAATGAACCCATAGGAGCTATGTAATGTTTATCATGTTACTTCCCAACCCCTACATT 3059  
QY 3150 TTTTGAATAAATAAGGAATTTT 3173  
Db 3060 TTTTGAATAAATAAGGAATTTT 3083

RESULT 4  
ID AAA90953 standard; cDNA; 4089 BP.  
XX  
AC AAA90953;  
XX  
DT 15-JAN-2001 (first entry)  
XX  
DE Human fatty acid desaturase 2 coding sequence.  
XX  
KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;  
KW liver disease; coronary artery disease; cancer; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 21..1355  
FT /tag= a  
FT /product= FADS-2  
XX  
PN EP1035207-A1.  
XX  
PD 13-SEP-2000.  
XX  
PF 09-MAR-1999; 99EP-0104664.  
XX  
PR 09-MAR-1999; 99EP-0104664.  
XX  
(MULT-) MULTIGENE BIOTECH GMBH.  
XX  
PI Weber BHF, Marquardt A;  
XX  
DR WPI; 2000-559875/52.  
DR P-PSDB; AAY97539.  
XX  
PT Novel cDNA molecules encoding three human fatty acid desaturases,  
PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,  
PT coronary artery disease and cancer -  
XX  
PS Claim 2; Page 36-38; 72pp; English.  
XX  
CC This sequence encodes the human fatty acid desaturase, FADS2, of the  
CC invention. An antibody directed against the 3 FADS molecule of the  
CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or  
CC therapeutic purposes. The FADS coding sequences are useful in gene  
CC therapy. The polypeptide and antibodies are useful in screening for  
CC modulating drugs. The polypeptides are also useful for treating liver  
CC disease, coronary artery disease and cancer.  
CC Note: Two copies of the sequence listing are present within this  
CC patent, which contain different sequences. AAA90952 and AAA90955 are  
CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are  
CC stated as being SEQ ID's 7-22.  
XX  
SQ Sequence 4089 BP; 875 A; 1230 C; 1136 G; 848 T; 0 other;  
Query Match 94.2%; Score 2998.2; DB 21; Length 4089;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3011; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 160 CGTCACAGTCGCGCAGCAGCATGGGGAAGGAGGAAACGAGGCGAGGGGCGCGGAGC 219  
Db 1 CGTCACAGTCGCGCAGCAGCATGGGGAAGGAGGAAACGAGGCGAGGGGCGCGGAGC 60  
QY 220 GCGAGGTGCTGGTGCCACCTTCAGCTGGGAGGAGATTTCAGAGCATACCTTCGCGCAGC 279  
Db 61 GCGAGGTGCTGGTGCCACCTTCAGCTGGGAGGAGATTTCAGAGCATACCTTCGCGCAGC 120  
QY 280 ACAGTGGGCTGTGCTATGACCGCAAGGTTTCAACATCACCAAAATGCTTCACAGCACC 339  
Db 121 ACAGTGGGCTGTGCTATGACCGCAAGGTTTCAACATCACCAAAATGCTTCACAGCACC 180  
QY 340 CGGGGGCGCCAGCGGGTTCATCGGCGACTACGCTGGAGAGATGCAACGAGTGCCTTCCGCG 399



Db 181 CGGGGGCCAGGGGTATCGGGCTACTGAGAGAGATGCAACGATGCCCTTCGCG 240  
 QY 400 CTTTCCACCTGACCTGGAATTCGTGGCAAGTTCCTGAAACCCCTGCTGATTCGTGAAC 459  
 Db 241 CTTTCCACCTGACCTGGAATTCGTGGCAAGTTCCTGAAACCCCTGCTGATTCGTGAAC 300  
 QY 450 TGGCCCGGAGGAGCCAGCCAGGACGAGCCAGGACCAAGATCAAGATCACTGAGGACTTC 519  
 Db 301 TGGCCCGGAGGAGCCAGCCAGGACGAGCCAGGACCAAGATCAAGATCACTGAGGACTTC 360  
 QY 520 GGGCCCTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCAACACACCTGTTCTTC 579  
 Db 361 GGGCCCTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCAACACACCTGTTCTTC 420  
 QY 580 TCTCTCTCTGCGCCACATFATCGCCCTGGAGAGATTCGATGTTCTACTTCTACT 639  
 Db 421 TCTCTCTCTGCGCCACATFATCGCCCTGGAGAGATTCGATGTTCTACTTCTACT 480  
 QY 640 TTGGCAATGGCTGGATTCCTACCTCATCAGCGCTTTGTCTTCTGCTACCTCTCAGGCC 699  
 Db 481 TTGGCAATGGCTGGATTCCTACCTCATCAGCGCTTTGTCTTCTGCTACCTCTCAGGCC 540  
 QY 700 AAGCTGGATGGTGCAACATGATTAATGAGCCACTGTCTGTCTGTCACAGAAAACCAAGTGA 759  
 Db 541 AAGCTGGATGGTGCAACATGATTAATGAGCCACTGTCTGTCTGTCACAGAAAACCAAGTGA 600  
 QY 760 ACCACCTTCTCCAAATTCGTTCATGGCCACTTAAAGGGTCCCTCTGCAACTGGTGA 819  
 Db 601 ACCACCTTCTCCAAATTCGTTCATGGCCACTTAAAGGGTCCCTCTGCAACTGGTGA 660  
 QY 820 ATCATCGCACTTCCAGCACCAGCCAACTTCAATCTTCCAAAGATCCCGATGTA 879  
 Db 661 ATCATCGCACTTCCAGCACCAGCCAACTTCAATCTTCCAAAGATCCCGATGTA 720  
 QY 880 ACATGTGACGTTTGTCTGGGCAATGAGCCCATGAGTACGCGCAGAGAGAGAGC 939  
 Db 721 ACATGTGACGTTTGTCTGGGCAATGAGCCCATGAGTACGCGCAGAGAGAGAGC 780  
 QY 940 TGAATACCTTGCCTCAATCACCAGCAGCAATCTTCTCTGATTTGGGCGCGCTGC 999  
 Db 781 TGAATACCTTGCCTCAATCACCAGCAGCAATCTTCTCTGATTTGGGCGCGCTGC 840  
 QY 1000 TCATCCCATGATTTCCAGTACCATCATGACCATGATTCCTCATAGAGTGG 1059  
 Db 841 TCATCCCATGATTTCCAGTACCATCATGACCATGATTCCTCATAGAGTGG 900  
 QY 1060 TGGACCTGGCTGGGCGCTCAGCTACTACATCCGTTTCTTCATCACTACCTCCCTTCT 1119  
 Db 901 TGGACCTGGCTGGGCGCTCAGCTACTACATCCGTTTCTTCATCACTACCTCCCTTCT 960  
 QY 1120 ACGGCATCTGGGAGCCCTCTTTCTGTCATCTCATAGGTTCTGGAGAGCCACTG 1179  
 Db 961 ACGGCATCTGGGAGCCCTCTTTCTGTCATCTCATAGGTTCTGGAGAGCCACTG 1020  
 QY 1180 TTGTGTGGTGCACAGATGAATCAATCGTCATGAGATTGACACGAGGCGCTACCGTG 1239  
 Db 1021 TTGTGTGGTGCACAGATGAATCAATCGTCATGAGATTGACACGAGGCGCTACCGTG 1080  
 QY 1240 ACTGGTTTCACTAGCTGACAGCCACCTGCAACCTGAGAGTCTCTTCTTCAAGACT 1299  
 Db 1081 ACTGGTTTCACTAGCTGACAGCCACCTGCAACCTGAGAGTCTCTTCTTCAAGACT 1140  
 QY 1300 GGTTCAGTGACCTTAACTTCAGATTGAGACACACCTTCTCCACCATGCGCCGCG 1359  
 Db 1141 GGTTCAGTGACCTTAACTTCAGATTGAGACACACCTTCTCCACCATGCGCCGCG 1200  
 QY 1360 ACAACTTACCAAGATCGCCCGCTGGTGAAGTCTCTATGTGCAAGATGCGATTGAAT 1419  
 Db 1201 ACAACTTACCAAGATCGCCCGCTGGTGAAGTCTCTATGTGCAAGATGCGATTGAAT 1260  
 QY 1420 ACCGAGAGAGCCGCTACTGAGGCGCTGCTGACATCATCAGTCCCTGAGAGTCTG 1479

Db 1261 ACCAGGAGAGCCGCTACTGAGGGCCCTGTGACATCATCAGGTCCTGAAGAAGTCTG 1320  
 QY 1480 GGAAGCTGTGGTGAAGCCCTTCACTTCAAAATGAAGCCACAGCCCGGAGCACCGTGG 1539  
 Db 1321 GGAAGCTGTGGTGAAGCCCTTCACTTCAAAATGAAGCCACAGCCCGGAGCACCGTGG 1380  
 QY 1540 GGAAGGGTGCAGGTGGGTGATGGCCAGAGAAATGATGGGCTTTTGTCTGAGGGGTGT 1599  
 Db 1381 GGAAGGGTGCAGGTGGGTGATGGCCAGAGAAATGATGGGCTTTTGTCTGAGGGGTGT 1440  
 QY 1600 CGAGAGGTGTGTGATGACCTGCTCAAGAGCCCATGTTGGATCTTCTCTCTCTCTCC 1659  
 Db 1441 CGAGAGGTGTGTGATGACCTGCTCAAGAGCCCATGTTGGATCTTCTCTCTCTCTCC 1500  
 QY 1660 TCTCTCTTCTCTCTTCACTCTCCCATAGACACCTGCCCCTCATGGGACCTGCCCCTCC 1719  
 Db 1501 TCTCTCTTCTCTCTTCACTCTCCCATAGACACCTGCCCCTCATGGGACCTGCCCCTCC 1560  
 QY 1720 TCAGCCGTGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAG 1779  
 Db 1561 TCAGCCGTGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAG 1620  
 QY 1780 CAGAGAGGTGGCCACCGGGGTGGTCTGCTTCACTTCACTTCACTTCACTTCACTTCACT 1839  
 Db 1621 CAGAGAGGTGGCCACCGGGGTGGTCTGCTTCACTTCACTTCACTTCACTTCACTTCACT 1680  
 QY 1840 GAGGAGACCAAGCGTCCATGGGTCTGGCTGTGAGTCTCCCTTGCAGGCTGGTCACTAG 1899  
 Db 1681 GAGGAGACCAAGCGTCCATGGGTCTGGCTGTGAGTCTCCCTTGCAGGCTGGTCACTAG 1740  
 QY 1900 GCATACCCCGCTTTGGTCTTTCAGATGCTTTGGGTTTCATAGGGGAGGTCCTAGTTC 1959  
 Db 1741 GCATACCCCGCTTTGGTCTTTCAGATGCTTTGGGTTTCATAGGGGAGGTCCTAGTTC 1800  
 QY 1960 GGGCAGGCGCCCTGACCCCTCCCGCTGGCTTCACTTCCCTGACCGCTGCCATTTGGTTC 2019  
 Db 1801 GGGCAGGCGCCCTGACCCCTCCCGCTGGCTTCACTTCCCTGACCGCTGCCATTTGGTTC 1860  
 QY 2020 ACCCTTTCATAGAGGCTGCTTTGTTTCAAGAGTCCGGTCTCCCTCTGAGGTCGGT 2079  
 Db 1861 ACCCTTTCATAGAGGCTGCTTTGTTTCAAGAGTCCGGTCTCCCTCTGAGGTCGGT 1920  
 QY 2080 TAAGTACCCGAGGCTCTCTTAAAGATGTCCAGGGCCCGGCGGCGGAGCAGCCAGCC 2139  
 Db 1921 TAAGTACCCGAGGCTCTCTTAAAGATGTCCAGGGCCCGGCGGCGGAGCAGCCAGCC 1980  
 QY 2140 CAAACCTTGGGCGCTGGAAGAGTCTCCACCCCATCACTAGAGTCTCTGACCTGGCT 2199  
 Db 1981 CAAACCTTGGGCGCTGGAAGAGTCTCCACCCCATCACTAGAGTCTCTGACCTGGCT 2040  
 QY 2200 TTCACGGGCGCCCATTCACACCGCTTCCCAACTTTGAGCTTTGGGACCAAGGGG 2259  
 Db 2041 TTCACGGGCGCCCATTCACACCGCTTCCCAACTTTGAGCTTTGGGACCAAGGGG 2100  
 QY 2260 GAGTCCCTGCTCTTGTGATCAGAGAGGAGTGGCCAGCTTTCAGGGAGGGGCGGCT 2319  
 Db 2101 GAGTCCCTGCTCTTGTGATCAGAGAGGAGTGGCCAGCTTTCAGGGAGGGGCGGCT 2160  
 QY 2320 GGCCTGAGGCTCAGCCACCCCTCCAGCTTTTCTCAGGGGTGCTTGGGATTCAGAGTTC 2379  
 Db 2161 GGCCTGAGGCTCAGCCACCCCTCCAGCTTTTCTCAGGGGTGCTTGGGATTCAGAGTTC 2220  
 QY 2380 TGGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCGGCAATTC 2439  
 Db 2221 TGGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCGGCAATTC 2280  
 QY 2440 CTGGCCATTTGGCCCGGAGGAGTGGCCCTGAGGCTGAGGAGGAGGAGTGGAGCTG 2499  
 Db 2281 CTGGCCATTTGGCCCGGAGGAGTGGCCCTGAGGCTGAGGAGGAGGAGTGGAGCTG 2339  
 QY 2500 GAGGCTCTCGTCCAGGCTTCCCATCTCGGGGCTGCTGTGTGAGAGGCGCTGCTCAGG 2559  
 Db 2340 GAGGCTCTCGTCCAGGCTTCCCATCTCGGGGCTGCTGTGTGAGAGGCGCTGCTCAGG 2399

QY 2560 CACTCTCTCTGTGAACCTGCTTACTGTGTTTAACTGTTTGTCTCCAGGATGCAATCTG 2619  
Db 2400 CACTCTCTCTGTGAACCTGCTTACTGTGTTTAACTGTTTGTCTCCAGGATGCAATCTG 2459  
QY 2620 ATAGGAGGGGGGCGAGGCTGGGCTTGTGCAATCTGCTCTTCCACACATGGCTTGC 2679  
Db 2460 ATAGGAGGGGGGCGAGGCTGGGCTTGTGCAATCTGCTCTTCCACACATGGCTTGC 2519  
QY 2680 CTCGGTGGCCCTGACTGTCTAGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2739  
Db 2520 CTCGGTGGCCCTGACTGTCTAGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2579  
QY 2740 GAGGCTGCCCTGAGGGGCTGGGAGGGGTACTCTCATGAGGACCAAGGTGAGCTGAGAA 2799  
Db 2580 GAGGCTGCCCTGAGGGGCTGGGAGGGGTACTCTCATGAGGACCAAGGTGAGCTGAGAA 2639  
QY 2800 GAGGAGGAGTGGGCTGGAGGTCTGTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGG 2859  
Db 2640 GAGGAGGAGTGGGCTGGAGGTCTGTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGG 2699  
QY 2860 GAGGAGGAGTCTGGGAGGATCTGAGCTGCTGTGCTGCTAAACCTAACTCAATCAATCT 2919  
Db 2700 GAGGAGGAGTCTGGGAGGATCTGAGCTGCTGTGCTAAACCTAACTCAATCAATCT 2759  
QY 2920 TAGATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2979  
Db 2760 TAGATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2819  
QY 2980 TAGTCCCTCCCTGCTTAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3039  
Db 2820 TAGTCCCTCCCTGCTTAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2879  
QY 3040 GCAATGGCATGCCCCCAGCTACTGTATGCCCCCGACCCCGAGGAGGAGGAGGAGGAGG 3099  
Db 2880 GCAATGGCATGCCCCCAGCTACTGTATGCCCCCGACCCCGAGGAGGAGGAGGAGGAGG 2939  
QY 3100 ATAGGAGGCTGATCGTAATGTTTATCATCTTACTTCCACCCCTACATTTTTCGAATA 3159  
Db 2940 ATAGGAGGCTGATCGTAATGTTTATCATCTTACTTCCACCCCTACATTTTTCGAATA 2999  
QY 3160 AATAAGGAATTTTA 3174  
Db 3000 AATAAGGAATTTTA 3014

## RESULT 5

AAK94377 ID AAK94377 standard; cDNA; 2825 BP.  
XX AC AAK94377;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human full-length cDNA, SEQ ID NO: 3111.  
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX OS Homo sapiens.  
XX PN EF1130094-A2.  
XX PD 05-SEP-2001.  
XX PF 07-JUL-2000; 2000EP-0114089.  
XX PR 08-JUL-1999; 99JP-0194486.  
XX PR 11-JAN-2000; 2000JP-0118774.  
XX PR 02-MAY-2000; 2000JP-0183765.  
XX PA (HELI-) HELIX RES INST.  
XX PI Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;  
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
WPI; 2001-524255/58.  
P-PSDB; AAMP3456.  
830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -  
Claim 8; SEQ ID NO 3111; 1380pp + sequence listing; English.  
The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.  
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.  
XX  
SQ Sequence 2825 BP; 562 A; 868 C; 778 G; 617 T; 0 other;  
Query Match 87.1%; Score 2772.2; DB 22; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2785; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 386 GGATGCCCTTCGGGCGCTTCCACCTGACCTGGAAATTCGTGGGCAAGTTCCTTGAACCCCT 445  
Db 33 GGATGCCCTTCGGGCGCTTCCACCTGACCTGGAAATTCGTGGGCAAGTTCCTTGAACCCCT 92  
QY 446 GCTGATGGTGAATGCTGCCCGGAGGAGCCAGCCAGGACCAAGCAAGCACTCAAGAT 505  
Db 93 GCTGATGGTGAATGCTGCCCGGAGGAGCCAGCCAGGACCAAGCAAGCACTCAAGAT 152  
QY 506 CACTGAGGACTTCGGGCGCTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCA 565  
Db 153 CACTGAGGACTTCGGGCGCTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCA 212  
QY 566 CCAGTGTCTTCT 625  
Db 213 CCAGTGTCTTCT 272  
QY 626 CACTGTCTTCT 685  
Db 273 CACTGTCTTCT 332  
QY 686 TACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAG 745  
Db 333 TACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAG 392  
QY 746 AAAACCCAGTGGAAACCACTTGTCCAAAATTCGTCAATTTGGCCACTTAAAGGTGCTC 805  
Db 393 AAAACCCAGTGGAAACCACTTGTCCAAAATTCGTCAATTTGGCCACTTAAAGGTGCTC 452  
QY 806 TGCCAACTGGTGGAAATCATCGCACTTCCAGCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 865  
Db 453 TGCCAACTGGTGGAAATCATCGCACTTCCAGCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 512  
QY 866 GGATCCCGATGTGAACATGCTGCAAGTGTGTTTGTCTGGGCGAATGGCAGCCATCGAGTA 925  
Db 513 GGATCCCGATGTGAACATGCTGCAAGTGTGTTTGTCTGGGCGAATGGCAGCCATCGAGTA 572  
QY 926 CGCAAGAAGAGCTGAAATACCTGCCCTACATCACCAGCAGAACTACTTCTTCCTGAT 985  
Db 573 CGCAAGAAGAGCTGAAATACCTGCCCTACATCACCAGCAGAACTACTTCTTCCTGAT 632  
QY 986 TGGGCCCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATCATCATGACCAATGATCGT 1045  
Db 633 TGGGCCCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATCATCATGACCAATGATCGT 692

1046 CCATAGAACTGGGTGACCTGGCTGGGCGCTCAGCTACTACATCGGTTCTTCATCAC 1105  
693 CCATAGAACTGGGTGACCTGGCTGGGCGCTCAGCTACTACATCGGTTCTTCATCAC 752  
1106 CTACATCCCTTTCTACGGCACTCTGGAGCCCTCCCTTTCTCCTCAATCTCATCAGGTTCT 1165  
753 CTACATCCCTTTCTACGGCACTCTGGAGCCCTCCCTTTCTCCTCAATCTCATCAGGTTCT 812  
1166 GGAGAGCACTGGTTCTGTGGGTGCACACAGATGAATCAGTCGTATGAGATTGAACA 1225  
813 GGAGAGCACTGGTTCTGTGGGTGCACACAGATGAATCAGTCGTATGAGATTGAACA 872  
1226 GGAGGCTACCGTCACTGGTTCTAGTAGCCAGCTGCAGCCACTGCAACGTGGAGCAGTC 1285  
873 GGAGGCTACCGTCACTGGTTCTAGTAGCCAGCTGCAGCCACTGCAACGTGGAGCAGTC 932  
1286 CTTCTTCAACGACTGGTTCTAGTAGCCAGCTGCAGCCACTGCAACGTGGAGCAGTC 1345  
933 CTTCTTCAACGACTGGTTCTAGTAGCCAGCTGCAGCCACTGCAACGTGGAGCAGTC 992  
1346 CACCATGCCCGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAA 1405  
993 CACCATGCCCGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAA 1052  
1406 GCATGGCAATTGAATACACAGAGAGCCGCTACTGAGGCGCTCTGGACATCATCAGTTC 1465  
1053 GCATGGCAATTGAATACACAGAGAGCCGCTACTGAGGCGCTCTGGACATCATCAGTTC 1112  
1466 CTTGAAGAACTCTGGGAAGCTGGTCTGAGCGCTACTCTTCAAAATGAAGCCACAGCC 1525  
1113 CTTGAAGAACTCTGGGAAGCTGGTCTGAGCGCTACTCTTCAAAATGAAGCCACAGCC 1172  
1526 CCGGACACCGTGGGGAAGGGTGCAGTGGGTGATGGCCAGAGGAATGATGGGTTT 1585  
1173 CCGGACACCGTGGGGAAGGGTGCAGTGGGTGATGGCCAGAGGAATGATGGGTTT 1232  
1586 GTTCTGAGGGGTGTCAGAGAGCTGGTGTATGCACTGCTCAGCGACCCCATGTGGATCT 1645  
1233 GTTCTGAGGGGTGTCAGAGAGCTGGTGTATGCACTGCTCAGCGACCCCATGTGGATCT 1292  
1646 TTTCTCCCTTTCT 1705  
1293 TTTCTCCCTTTCT 1352  
1706 GGACTGCGCTCTCAGCGCTCAGCCATCAGCCATGGCCCTCCAGTGGCTCTCAGCC 1765  
1353 GGAAGTCCCTCTCAGCGCTCAGCCATCAGCCATGGCCCTCCAGTGGCTCTCAGCC 1412  
1766 CTTCTTCCAGAGCAGAGAGTGGCCACCGGGGTGGCTGTGCTTCTCTCTCTCTCTCTCT 1825  
1413 CTTCTTCCAGAGCAGAGAGTGGCCACCGGGGTGGCTGTGCTTCTCTCTCTCTCTCTCT 1472  
1826 GCGCTAAGATGGAGAGACCGGCTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 1885  
1473 GCGCTAAGATGGAGAGACCGGCTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 1532  
1886 AGCTGTGCTACTAGGCACTACCCCGCTTTGGTTCTTTCAGATGCTCTTGGGTTCTAGG 1945  
1533 AGCTGTGCTACTAGGCACTACCCCGCTTTGGTTCTTTCAGATGCTCTTGGGTTCTAGG 1592  
1946 GGCAGTCTAGTGGGAGGGCCCTGACCCCTCCGCGCTGGCTTCACTCTCCCTGACG 2005  
1593 GGCAGTCTAGTGGGAGGGCCCTGACCCCTCCGCGCTGGCTTCACTCTCCCTGACG 1652  
2006 GCTGCCATTGGTCCACCCCTTTTCATAGAGAGCCCTGCTTTGTTACAAAGCTCGGGTCTCC 2065  
1653 GCTGCCATTGGTCCACCCCTTTTCATAGAGAGCCCTGCTTTGTTACAAAGCTCGGGTCTCC 1712  
2066 TCCTCAGCTGGTTAAGTACCGAGGCTCTCTTAAGATGTCAGGGCCCGGCGCCG 2125  
1713 TCCTCAGCTGGTTAAGTACCGAGGCTCTCTTAAGATGTCAGGGCCCGGCGCCG 1772  
2126 GGGCACAGCCCAAACTTGGGCCCTGGAGAGTCTCTCCACCCCATCACTAGATGC 2185

RESULT 6

1773 GGGCACAGCCCAAACTTGGGCCCTGGAGAGTCTCTCCACCCCATCACTAGATGC 1832  
2186 TCTGACCTGGCTTTTCACGGGCCCAATTCACCGCTCCCAACTTTGAGCCTGTGACCT 2245  
1833 TCTGACCTGGCTTTTCACGGGCCCAATTCACCGCTCCCAACTTTGAGCCTGTGACCT 1892  
2246 TGGACCAAAAGGGGAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2305  
1893 TGGACCAAAAGGGGAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1952  
2306 GGGAGGGCCCGCTGGCTGAGGCTCAGCCACCTCTCAGCTTTTCTCCTCAGGCTGCTCT 2365  
1953 GGGAGGGCCCGCTGGCTGAGGCTCAGCCACCTCTCAGCTTTTCTCCTCAGGCTGCTCT 2012  
2366 GAGTCCAAAGATTCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATTACAGCTGGCA 2425  
2013 GAGTCCAAAGATTCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATTACAGCTGGCA 2072  
2426 GTGCCAGCAATCTCTGGCCATTTGGCCCGCAGGGGACGTGGCCCTGCGAGCTGACGA 2485  
2073 GTGCCAGCAATCTCTGGCCATTTGGCCCGCAGGGGACGTGGCCCTGCGAGCTGACGA 2131  
2486 GGGCACTGGAGCTGGGAGTCTCTCTCCAGCCCTCCCACTCTCGGGGCTGCTGTGTGAC 2545  
2132 GGGCACTGGAGCTGGGAGTCTCTCTCCAGCCCTCCCACTCTCGGGGCTGCTGTGTGAC 2191  
2546 GGGCTGGCTCAGGCACT 2605  
2192 GGGCTGGCTCAGGCACT 2251  
2606 CAGGATGCTATCTGATAGGAGGGGCGCAGGGCTGGGCTTTGTGACAACTCTGCTTTCA 2665  
2252 CAGGATGCTATCTGATAGGAGGGGCGCAGGGCTGGGCTTTGTGACAACTCTGCTTTCA 2311  
2666 CCACATGCCCTTGGCTCGGTGGCCCTGACTGTCTAGGAGGGCCAGGAGGAGCAGAGCGGA 2725  
2312 CCACATGCCCTTGGCTCGGTGGCCCTGACTGTCTAGGAGGGCCAGGAGGAGCAGAGCGGA 2371  
2726 GGGAGTCTCAGAGAGGCTCCCTGAGGGGCTGGGAGGGGTACCTCATAGAGACAG 2785  
2372 GGGAGTCTCAGAGAGGCTCCCTGAGGGCTGGGAGGGGTACCTCATAGAGACAG 2431  
2786 GGTGAGCTGAGAAGAGAGAGTGGGGCTGAGGTGTGGTGTGAGTGGGAGCAGGCG 2845  
2432 GGTGAGCTGAGAAGAGAGAGTGGGGCTGAGGTGTGGTGTGAGTGGGAGCAGGCG 2491  
2846 AAGTGAAGGGGAGGAGGAGTCCCTGGAGGATCTGAGTCTCTGTTCAGTCTTAACC 2905  
2492 AAGTGAAGGGGAGGAGGAGTCCCTGGAGGATCTGAGTCTCTGTTCAGTCTTAACC 2551  
2906 CACTAATCAGTCTTAGATTTCAGGGAGGGCAGGCAACAACTCAGAAATGGGGCTT 2965  
2552 CACTAATCAGTCTTAGATTTCAGGGAGGGCAGGCAACAACTCAGAAATGGGGCTT 2611  
2966 TCGGGAGGGGCTGAGTCCCGCCAGCTTAAGCAGCCAGGAGGACCTGCATTAAGCA 3025  
2612 TCGGGAGGGGCTGAGTCCCGCCAGCTTAAGCAGCCAGGAGGACCTGCATTAAGCA 2671  
3026 TCTGGTTCATGGAATGGCATGGCCCGCCAGCTTACTGTATGCCCGCCGAG 3085  
2672 TCTGGTTCATGGAATGGCATGGCCCGCCAGCTTACTGTATGCCCGCCGAG 2731  
3086 GGCAGATGAACCCATAGGAGCTGATCGTAAATGTTTATCATGTACTTCCCGCCACCCCTA 3145  
2732 GGCAGATGAACCCATAGGAGCTGATCGTAAATGTTTATCATGTACTTCCCGCCACCCCTA 2791  
3146 CATTTTTGAATAAATAAGGAATTTTA 3174  
2792 CATTTTTGAATAAATAAGGAATTTTA 2820





|    |      |  |      |
|----|------|--|------|
| Db | 1    | ATTGATGGTTCACGTCTTTTACCTTTGGCAATGCTGGATTCCTACCTCATCAAGGCC      | 60   |
| Qy | 675  | TTTGTCTTGTCTACTCTTCAGGCCCAAGCTGTGATGGCTGCAACATGATATGGCCACCTG   | 734  |
| Db | 61   | TTTGTCTTGTCTACTCTTCAGGCCCAAGCTGTGATGGCTGCAACATGATATGGCCACCTG   | 120  |
| Qy | 735  | TCGTCTACAGAAAACCCCAAGTGGAAACCACTTGTCCCAAAATTCGTCAATTTGGCCACCTA | 794  |
| Db | 121  | TCGTCTACAGAAAACCCCAAGTGGAAACCACTTGTCCCAAAATTCGTCAATTTGGCCACCTA | 180  |
| Qy | 795  | AAGGTGCTCTGCCAACTGTGTGAATCATTCGCCACTTCCAGCAACACGCCAAAGCCTAAC   | 854  |
| Db | 181  | AAGGTGCTCTGCCAACTGTGTGAATCATTCGCCACTTCCAGCAACACGCCAAAGCCTAAC   | 240  |
| Qy | 855  | ATCTTCCACAGGATCCCGATGTGAACATGCTGCAGCTGTGTGTCTGGGGAATGGCAG      | 914  |
| Db | 241  | ATCTTCCACAGGATCCCGATGTGAACATGCTGCAGCTGTGTGTCTGGGGAATGGCAG      | 300  |
| Qy | 915  | CCCATCGAGTAGCGCAAGAGAGCTGAAATACCTGCCCTCAAAATCAACACAGCAGCAATAC  | 974  |
| Db | 301  | CCCATCGAGTAGCGCAAGAGAGCTGAAATACCTGCCCTCAAAATCAACACAGCAGCAATAC  | 360  |
| Qy | 975  | TTCTTCTGATTTGGGCGCGCTGTCTCATCCCATGTATTTCCAGTACCAAGATCATATG     | 1034 |
| Db | 361  | TTCTTCTGATTTGGGCGCGCTGTCTCATCCCATGTATTTCCAGTACCAAGATCATATG     | 420  |
| Qy | 1035 | ACCATGATCGTCATAGAAGCTGGGTGGACCTGGCTGGCGCTGAGCTACTACATCCGG      | 1094 |
| Db | 421  | ACCATGATCGTCATAGAAGCTGGGTGGACCTGGCTGGCGCTGAGCTACTACATCCGG      | 480  |
| Qy | 1095 | TTCTTCTGATTTGGGCGCGCTGTCTCATCCCATGTATTTCCAGTACCAAGATCATATG     | 1154 |
| Db | 481  | TTCTTCTGATTTGGGCGCGCTGTCTCATCCCATGTATTTCCAGTACCAAGATCATATG     | 540  |
| Qy | 1155 | ATCAGGTTCCTGAGAGCCACTGGTTGTGTGGTGCACACAGATGAATCACATCGTCATG     | 1214 |
| Db | 541  | ATCAGGTTCCTGAGAGCCACTGGTTGTGTGGTGCACACAGATGAATCACATCGTCATG     | 600  |
| Qy | 1215 | GAGATTGACAGAGGCTTACCTGTACTGTTCAGTAGCAGTGAAGCCACCTGCGAAC        | 1274 |
| Db | 601  | GAGATTGACAGAGGCTTACCTGTACTGTTCAGTAGCAGTGAAGCCACCTGCGAAC        | 660  |
| Qy | 1275 | GTGAGCAGTCTTCTTCAACGACTGGTTCAGTGGACACTTAACTTCCAGATTTGAGCAC     | 1334 |
| Db | 661  | GTGAGCAGTCTTCTTCAACGACTGGTTCAGTGGACACTTAACTTCCAGATTTGAGCAC     | 720  |
| Qy | 1335 | CACCTCTTCCCAACCATGCCCCGGCACAACTTACAAAGATCGCCCCGCTGGTGAAGTCT    | 1394 |
| Db | 721  | CACCTCTTCCCAACCATGCCCCGGCACAACTTACAAAGATCGCCCCGCTGGTGAAGTCT    | 780  |
| Qy | 1395 | CTATGTCCCAAGCATGGCATTTGAATACCAAGAGAGCCCTACTGAGGGCCCTGCTGGAC    | 1454 |
| Db | 781  | CTATGTCCCAAGCATGGCATTTGAATACCAAGAGAGCCCTACTGAGGGCCCTGCTGGAC    | 840  |
| Qy | 1455 | ATCATCAGTTCCTTGAAGAGTCTGGGAAGCTGTGGCTGAGCCCTACCTTCAAAATGA      | 1514 |
| Db | 841  | ATCATCAGTTCCTTGAAGAGTCTGGGAAGCTGTGGCTGAGCCCTACCTTCAAAATGA      | 900  |
| Qy | 1515 | AGCCACAGCCCCCGGACACCTGTGGGAAGGGGTGAGGTGGGGTGAATGGCCAGAGGAAT    | 1574 |
| Db | 901  | AGCCACAGCCCCCGGACACCTGTGGGAAGGGGTGAGGTGGGGTGAATGGCCAGAGGAAT    | 960  |
| Qy | 1575 | GATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGGTGTATCACTGTCTACGGACCCC      | 1634 |
| Db | 961  | GATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGGTGTATCACTGTCTACGGACCCC      | 1020 |
| Qy | 1635 | ATGTTGGAATTTTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 1694 |
| Db | 1021 | ATGTTGGAATTTTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 1080 |
| Qy | 1695 | CTGCCCTCATGGGACCTGCTCTCTCAGCCGCTCAGCCATCAGCCATGCTCCCTCAGTG     | 1754 |
| Db | 1081 | CTGCCCTCATGGGACCTGCTCTCTCAGCCGCTCAGCCATCAGCCATGCTCCCTCAGTG     | 1140 |
| Qy | 1755 | CCTCTTAGCCCTCTTTCGAAGAGCAGAGAGTGGCCACCCGGGGTCTCTGTCTCTAC       | 1814 |
| Db | 1141 | CCTCTTAGCCCTCTTTCGAAGAGCAGAGAGTGGCCACCCGGGGTCTCTGTCTCTAC       | 1200 |
| Qy | 1815 | CTCCACTCTCTGCCCTTAAAGATGGGAGGAGACACAGCGTCCATGGGTCTGGCTGTGAG    | 1874 |
| Db | 1201 | CTCCACTCTCTGCCCTTAAAGATGGGAGGAGACACAGCGTCCATGGGTCTGGCTGTGAG    | 1260 |
| Qy | 1875 | TCCTCCCTTCAGCCTGGTCTACTAGGCATCACCCCGCTTTGGTCTTCAGATGCTCTTG     | 1934 |
| Db | 1261 | TCCTCCCTTCAGCCTGGTCTACTAGGCATCACCCCGCTTTGGTCTTCAGATGCTCTTG     | 1320 |
| Qy | 1935 | GGGTTCATAGGGCAGGTCTTAGTGGGAGGGCCCTGACCCCTCCCGGCTGGCTTCAC       | 1994 |
| Db | 1321 | GGGTTCATAGGGCAGGTCTTAGTGGGAGGGCCCTGACCCCTCCCGGCTGGCTTCAC       | 1380 |
| Qy | 1995 | TCCTCCCTGACGGTGCATTTGGTCCACCCCTTCATAGAGGGCTCTCTTTGTTACAAAGC    | 2054 |
| Db | 1381 | TCCTCCCTGACGGTGCATTTGGTCCACCCCTTCATAGAGGGCTCTCTTTGTTACAAAGC    | 1440 |
| Qy | 2055 | TCGGGTCTCTCTCTGAGCTCGGTAAAGTACCCGAGGGCTCTCTTAAGATGTCAGGGC      | 2114 |
| Db | 1441 | TCGGGTCTCTCTCTGAGCTCGGTAAAGTACCCGAGGGCTCTCTTAAGATGTCAGGGC      | 1500 |
| Qy | 2115 | CCAGGCCCGGGGACACAGCCAGCCAAACCTTTGGGCTCTGGAAGAGTCTCCACCCCAT     | 2174 |
| Db | 1501 | CCAGGCCCGGGGACACAGCCAGCCAAACCTTTGGGCTCTGGAAGAGTCTCCACCCCAT     | 1560 |
| Qy | 2175 | CACCTAGAGTCTCTGACCCCTGGGCTTTACGGGCCCATTTCCACCGCTCTCCCACTTGA    | 2234 |
| Db | 1561 | CACCTAGAGTCTCTGACCCCTGGGCTTTACGGGCCCATTTCCACCGCTCTCCCACTTGA    | 1620 |
| Qy | 2235 | GCCTGTGACCTTGGGACCCAAAGGGGAGTCCCTGCTCTTTGTGACTCAGCAGAGGAGT     | 2294 |
| Db | 1621 | GCCTGTGACCTTGGGACCCAAAGGGGAGTCCCTGCTCTTTGTGACTCAGCAGAGGAGT     | 1680 |
| Qy | 2295 | GGCCACCTTCAGGGAGGGCGGCTGGCTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCT     | 2354 |
| Db | 1681 | GGCCACCTTCAGGGAGGGCGGCTGGCTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCT     | 1740 |
| Qy | 2355 | CAGGTGTCTGAGGTCCAAAGATTTCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTA   | 2414 |
| Db | 1741 | CAGGTGTCTGAGGTCCAAAGATTTCTGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTA   | 1800 |
| Qy | 2415 | TCAGCTGGCAGTCCAGCCAAATCCCTGGCGATTTGGCCCCCAGGGGACCTGGGCCCTGC    | 2474 |
| Db | 1801 | TCAGCTGGCAGTCCAGCCAAATCCCTGGCGATTTGGCCCCCAGGGGACCTGGGCCCTGC    | 1859 |
| Qy | 2475 | AGGCTGCAGAGGAGCACTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCACTCTCGGGGCT    | 2534 |
| Db | 1860 | AGGCTGCAGAGGAGCACTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCACTCTCGGGGCT    | 1919 |
| Qy | 2535 | GCTGTGTGAGCGGCTGCTCAGGCACTCTCTGTGTGAACCTGCCCCCTTACTGTGTTA      | 2594 |
| Db | 1920 | GCTGTGTGAGCGGCTGCTCAGGCACTCTCTGTGTGAACCTGCCCCCTTACTGTGTTA      | 1979 |
| Qy | 2595 | ACCTGTTGCTCCAGATGATTTCTGATAGAGGGGGGGCAGGGCTGGGCTCTGTGACAA      | 2654 |
| Db | 1980 | ACCTGTTGCTCCAGATGATTTCTGATAGAGGGGGGGCAGGGCTGGGCTCTGTGACAA      | 2039 |
| Qy | 2655 | TCCTGCTTTCACCATGCTTCCCTCGGTGGCCCTGACTGTCTGAGGAGGGCCAGGGAG      | 2714 |
| Db | 2040 | TCCTGCTTTCACCATGCTTCCCTCGGTGGCCCTGACTGTCTGAGGAGGGCCAGGGAG      | 2099 |
| Qy | 2715 | GCAGGCGGAGGAGGCTCAGAGAGGCTGCTCCCTCAGGGGCTGGGAGGGGTACTCTC       | 2774 |
| Db | 2100 | GCAGGCGGAGGAGGCTCAGAGAGGAGCTGCTCCCTCAGGGGCTGGGAGGGGTACTCTC     | 2159 |
| Qy | 2775 | ATGAGGACACAGGCTGAGAGTCTGAGAGGAGGAGGCTGGGGCTGGAGGCTGCTGAGCTG    | 2834 |
| Db | 2160 | ATGAGGACACAGGCTGAGAGTCTGAGAGGAGGAGGCTGGGGCTGGAGGCTGCTGAGCTG    | 2219 |









CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

XX SQ Sequence 2165 BP; 410 A; 655 C; 629 G; 471 T; 0 other;

Query Match 67.3%; Score 2144.4; DB 22; Length 2165;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2159; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

|    |      |   |      |
|----|------|---|------|
| QY | 1008 | ATGATTTCCAGTACAGATCATGACCATGATGCTCCATAGAACTGGGTGGACCTG  | 1067 |
| DB | 1    | ATGATTTCCAGTACAGATCATGACCATGATGCTCCATAGAACTGGGTGGACCTG  | 60   |
| QY | 1068 | GCTGGGCGTCAGTACTACATGCGGTTCCTTCATCAGCATCCCTTTCTACGGCATC | 1127 |
| DB | 61   | GCTGGGCGTCAGTACTACATGCGGTTCCTTCATCAGCATCCCTTTCTACGGCATC | 120  |
| QY | 1128 | CTGGGAGCCCTCTTTCTCACTTTCATCAGGTTCTGGAGAGCAGTGGTTGTGG    | 1187 |
| DB | 121  | CTGGGAGCCCTCTTTCTCACTTTCATCAGGTTCTGGAGAGCAGTGGTTGTGG    | 180  |
| QY | 1188 | GTACACAGATGAATCACATCGTATGGAGATGACAGAGGCTTACGTGACGTGTC   | 1247 |
| DB | 181  | GTACACAGATGAATCACATCGTATGGAGATGACAGAGGCTTACGTGACGTGTC   | 240  |
| QY | 1248 | AGTAGCCAGCTGACGCCACCTGCACGTTGAGGAGTCTCTTCAAGACGTGTTCA   | 1307 |
| DB | 241  | AGTAGCCAGCTGACGCCACCTGCACGTTGAGGAGTCTCTTCAAGACGTGTTCA   | 300  |
| QY | 1308 | GGACACCTTAACCTTCAGATTGAGCACCACCTCTTCCACCACATGCCCCGGCACA | 1367 |
| DB | 301  | GGACACCTTAACCTTCAGATTGAGCACCACCTCTTCCACCACATGCCCCGGCACA | 360  |
| QY | 1368 | CACAGATGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATAC    | 1427 |
| DB | 361  | CACAGATGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATAC    | 420  |
| QY | 1428 | AAGCCGCTACTGAGGGCCCTGCTGGACATCATCAGGTCCCTGAAGAAGTCTGG   | 1487 |
| DB | 421  | AAGCCGCTACTGAGGGCCCTGCTGGACATCATCAGGTCCCTGAAGAAGTCTGG   | 480  |
| QY | 1488 | TGGCTGACCCCTTACCTTCAAAATGAGCCAGCCCCCGGGACACCTGGGGAGGG   | 1547 |
| DB | 481  | TGGCTGACCCCTTACCTTCAAAATGAGCCAGCCCCCGGGACACCTGGGGAGGG   | 540  |
| QY | 1548 | TGCAGGTGGGCTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTC    | 1607 |
| DB | 541  | TGCAGGTGGGCTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTC    | 600  |
| QY | 1608 | CTGGTGTATGCACTGCTCAAGGACCCCATGTTGGATCTTCTCCCTTCTCTCT    | 1667 |
| DB | 601  | CTGGTGTATGCACTGCTCAAGGACCCCATGTTGGATCTTCTCCCTTCTCTCT    | 660  |
| QY | 1668 | TTCTCTTCACTCTCCCCATAGCACCTTCCCTCATGGAGCTGCCCTCCCTCAG    | 1727 |
| DB | 661  | TTCTCTTCACTCTCCCCATAGCACCTTCCCTCATGGAGCTGCCCTCCCTCAG    | 720  |
| QY | 1728 | CAGCCATCAGCATGGCCCTCCAGTGCCTCTTAGGCCCTTCTTCCAAAGAGCAG   | 1787 |
| DB | 721  | CAGCCATCAGCATGGCCCTCCAGTGCCTCTTAGGCCCTTCTTCCAAAGAGCAG   | 780  |

|    |      |   |      |
|----|------|---|------|
| QY | 1788 | TGCCCCACCGGGGGTGGCTCTGTCTTACCTCCACATCTCTGCCCTTAAAGATGGAGGAGAC | 1847 |
| DB | 781  | TGCCCCACCGGGGGTGGCTCTGTCTTACCTCCACATCTCTGCCCTTAAAGATGGAGGAGAC | 840  |
| QY | 1848 | CAGCGGTCCATGGGTCTGGCCCTGAGTCTCCCTTGCAGCTGGTCTACTAGGCAATCACC   | 1907 |
| DB | 841  | CAGCGGTCCATGGGTCTGGCCCTGAGTCTCCCTTGCAGCTGGTCTACTAGGCAATCACC   | 900  |
| QY | 1908 | CCCGCTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGGACAGTCTTAGTCCGGCAGGG  | 1967 |
| DB | 901  | CCCGCTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGGACAGTCTTAGTCCGGCAGGG  | 960  |
| QY | 1968 | CCCTGACCCCTCCGGCCTGGCTTCACTCTCCCTGACGGCTGCCATTTGGTCCACCTTTC   | 2027 |
| DB | 961  | CCCTGACCCCTCCGGCCTGGCTTCACTCTCCCTGACGGCTGCCATTTGGTCCACCTTTC   | 1020 |
| QY | 2028 | ATAGAGAGCCCTGCTTTGTATACAAAGCTCGGTCTCCCTCTCTGCAGCTCGTAAAGTACC  | 2087 |
| DB | 1021 | ATAGAGAGCCCTGCTTTGTATACAAAGCTCGGTCTCCCTCTCTGCAGCTCGTAAAGTACC  | 1080 |
| QY | 2088 | CGAGGCTCTCTTAAAGATGTCAGGGCCCCAGGGCCCGGGGACAGCCAGCCCAACCTT     | 2147 |
| DB | 1081 | CGAGGCTCTCTTAAAGATGTCAGGGCCCCAGGGCCCGGGGACAGCCAGCCCAACCTT     | 1140 |
| QY | 2148 | GGCCCTTGAAGAGTCTCCACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTACGGG    | 2207 |
| DB | 1141 | GGCCCTTGAAGAGTCTCCACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTACGGG    | 1200 |
| QY | 2208 | CCCATTCACACCCCTCCCAACTTGGGCTGTGAGCTTTGGGACCAAGAGGGGAGTCCCT    | 2267 |
| DB | 1201 | CCCATTCACACCCCTCCCAACTTGGGCTGTGAGCTTTGGGACCAAGAGGGGAGTCCCT    | 1260 |
| QY | 2268 | CGTCTCTGTGAGTCTCAGCAGAGGACAGTGGCCAGCTTTCAGGGGGGCGGCTGGAG      | 2327 |
| DB | 1261 | CGTCTCTGTGAGTCTCAGCAGAGGACAGTGGCCAGCTTTCAGGGGGGCGGCTGGAG      | 1320 |
| QY | 2328 | GGCTCAGCCACCCCTCCAGCTTTTCTCAGGGGTCTCTGAGGTCCAAAGATTCTGAGCAA   | 2387 |
| DB | 1321 | GGCTCAGCCACCCCTCCAGCTTTTCTCAGGGGTCTCTGAGGTCCAAAGATTCTGAGCAA   | 1380 |
| QY | 2388 | TCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGAGTGGCCAGGCAATCCCTGGCCAT   | 2447 |
| DB | 1381 | TCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGAGTGGCCAGGCAATCCCTGGCCAT   | 1440 |
| QY | 2448 | TTGGCCCCAGGGGAGACGTGGGCCCCCTGCAGGCTCAGAGGGGCACTGGAGTGGAGTCT   | 2507 |
| DB | 1441 | TTGGCCCCCA - GGGAGCGTGGGCCCTGCAGGCTCAGAGGGGCACTGGAGTGGAGTCT   | 1499 |
| QY | 2508 | CGTCCAGCCCTCCCAATCTCGGGGCTGTGTGTGGACGGCGCTGCTCAGGCACTCTCC     | 2567 |
| DB | 1500 | CGTCCAGCCCTCCCAATCTCGGGGCTGTGTGTGGACGGCGCTGCTCAGGCACTCTCC     | 1559 |
| QY | 2568 | TGTCTGAACCTGCCCCCTTACTGTGTAACTGTTTCTTCCAGGATGCAATCTGATAGAGG   | 2627 |
| DB | 1560 | TGTCTGAACCTGCCCCCTTACTGTGTAACTGTTTCTTCCAGGATGCAATCTGATAGAGG   | 1619 |
| QY | 2628 | GGGCGGAGGGCTGGGCTTGTGACATCTGCCCTTTTCCACATGSCCTTGGCTGGGG       | 2687 |
| DB | 1620 | GGGCGGAGGGCTGGGCTTGTGACATCTGCCCTTTTCCACATGSCCTTGGCTGGGG       | 1679 |
| QY | 2688 | CCCTGAGTGTGAGGAGGGGCGGAGGAGGAGGAGGAGGAGTCTCAGGAGGAGGCTGC      | 2747 |
| DB | 1680 | CCCTGAGTGTGAGGAGGGGCGGAGGAGGAGGAGGAGGAGTCTCAGGAGGAGGCTGC      | 1739 |
| QY | 2748 | CCTGAGGGCTGGGAGGGGGTACTCTATGAGGACAGGGTGGAGTCTGAGAGGAGGAGGA    | 2807 |
| DB | 1740 | CCTGAGGGCTGGGAGGGGGTACTCTATGAGGACAGGGTGGAGTCTGAGAGGAGGAGGA    | 1799 |
| QY | 2808 | GGTGGGGCTGAGTGTCTGTAGTCTGAGGGGAGCGGCAAGTGTAGAGGGAGGAGGAGGAA   | 2867 |
| DB | 1800 | GGTGGGGCTGAGTGTCTGTAGTCTGAGGGGAGCGGCAAGTGTAGAGGGAGGAGGAGGAA   | 1859 |
| QY | 2868 | GTCTGGGAGGATCCTGAGCTGTGTGTCAGTCTAAACCCACTAATCATAGTCTTAGATTCA  | 2927 |

1860 GTCTGGGAGGATCTCTGAGCTGCTGTTGCACTCTAAACCCACTAATCACTTCTTAGATTCA 1919  
2928 GGGGAAGGCGAGGACCAACAACTCAGATGGGGGCTTTTGGGGAGGGCGCTAGTCCCC 2987  
1920 GGGGAAGGCGAGGACCAACAACTCAGATGGGGGCTTTTGGGGAGGGCGCTAGTCCCC 1979  
2988 CCAGCTCTAAGCAGCAGGAGGAGCTTCAATCTAAGCATCTGGGTTCCTCATGGCAATGGC 3047  
1980 CCAGCTCTAAGCAGCAGGAGGAGCTTCAATCTAAGCATCTGGGTTCCTCATGGCAATGGC 2039  
3048 ATGCCCCCGAGCTACTGTATGCCCGGACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 3107  
2040 ATGCCCCCGAGCTACTGTATGCCCGGACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 2099  
3108 CTGATCGTAAATGTTTATCATGCTTACTTCCCGACCCCTACATTTTTCGAATAAAATAAGG 3167  
2100 CTGATCGTAAATGTTTATCATGCTTACTTCCCGACCCCTACATTTTTCGAATAAAATAAGG 2159  
3168 AATTTT 3173  
2160 AATTTT 2165

RESULT 10  
AAH15815  
ID AAH15815 standard; cDNA; 2146 BP.  
XX  
AC AAH15815;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human cDNA sequence SEQ ID NO:14291.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
PR 27-AUG-1999; 99JP-0300253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183767.  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX  
WPI; 2001-318749/34.  
XX  
PR Primer sets for synthesizing polynucleotides, particularly the 5602  
PT full-length cDNAs defined in the specification, and for the detection  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
PT full-length cDNAs -  
XX  
PS Claim 8; SEQ ID 14291; 2537pp + CD ROM; English.  
XX  
CC The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
XX of the present invention.  
SQ Sequence 2146 BP; 403 A; 651 C; 626 G; 466 T; 0 other;  
Query Match 66.9%; Score 2130.2; DB 22; Length 2146;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2143; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1027 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCGCGCTCAGCTACT 1086  
DB 1 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCCCGCGCTCAGCTACT 60  
QY 1087 ACATCGGTTCTTCATCACTACATCCCTTTCTACGGCATCTCTGGAGCCCTCTCTTTCC 1146  
DB 61 ACATCGGTTCTTCATCACTACATCCCTTTCTACGGCATCTCTGGAGCCCTCTCTTTCC 120  
QY 1147 TCAACTTTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTTCACACAGATGAATCACA 1206  
DB 121 TCAACTTTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTTCACACAGATGAATCACA 180  
QY 1207 TGTCTATGGAGATTACACAGAGGCGCTACCGTACTGGTTTCTAGTACGACGTGACAGCCA 1266  
DB 181 TGTCTATGGAGATTACACAGAGGCGCTACCGTACTGGTTTCTAGTACGACGTGACAGCCA 240  
QY 1267 CTGCAACGCTGAGCAGTCTCTTCTTCAACGACTGGTTCTAGTGGACACCTTAACTTCCAGA 1326  
DB 241 CTGCAACGCTGAGCAGTCTCTTCTTCAACGACTGGTTCTAGTGGACACCTTAACTTCCAGA 300  
QY 1327 TTGAGCACCACTCTTCCCAACATGCCCCGCGCAAACTTACAAAGATCGCCCCGCTGG 1386  
DB 301 TTGAGCACCACTCTTCCCAACATGCCCCGCGCAAACTTACAAAGATCGCCCCGCTGG 360  
QY 1387 TGAAGTCTCTATGTCGCAAGCATGCAATTAATACAGAGAGCGCTTACTGAGGGCC 1446  
DB 361 TGAAGTCTCTATGTCGCAAGCATGCAATTAATACAGAGAGCGCTTACTGAGGGCC 420  
QY 1447 TGCTGGACATCATCAGTCCCTGAAGAAAGTCTGGGAAGCTGTGGTGGACGCTTACCTTC 1506  
DB 421 TGCTGGACATCATCAGTCCCTGAAGAAAGTCTGGGAAGCTGTGGTGGACGCTTACCTTC 480  
QY 1507 ACAATGAAGCCACAGCCCCCGGGACACCGTGGGAGGGGTGCGAGTGGGTGATGGCC 1566  
DB 481 ACAATGAAGCCACAGCCCCCGGGACACCGTGGGAGGGGTGCGAGTGGGTGATGGCC 540  
QY 1567 AGAGGAATCATGGGCTTTTGTCTGAGGGGTCTCCGAGAGGCTGGTGTATGACCTGCTCA 1626  
DB 541 AGAGGAATCATGGGCTTTTGTCTGAGGGGTCTCCGAGAGGCTGGTGTATGACCTGCTCA 600  
QY 1627 CGGACCCCATGTTGATCTTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686  
DB 601 CGGACCCCATGTTGATCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660  
QY 1687 ATAGCACCTCGCCTCATGGGACCTTCCCTCCCTCAGCCGCTCAGCATCAGCATCAGCATG 1746  
DB 661 ATAGCACCTCGCCTCATGGGACCTTCCCTCCCTCAGCCGCTCAGCATCAGCATCAGCATG 720  
QY 1747 TCCAGTGTGCTCTAGCCCTTCTTCCAAAGAGCGAGAGGTGGCCACCGGGGGTGGCTC 1806  
DB 721 TCCAGTGTGCTCTAGCCCTTCTTCCAAAGAGCGAGAGGTGGCCACCGGGGGTGGCTC 780  
QY 1807 TGTCTTACCTCCACTCTCTGCCCCCTTAAAGATGGAGGAGACCAGCGGTCTCATGGGTCTGG 1866

Db 781 TGTCTACTCTCACTCTCTGCCCCTAAGATGGGAGGAGACAGGGTCCATGGTCTGG 840  
QY 1867 COTGTGAGTTCCTCCCTTGAGCGCTGGTCACTAGGCAATCACCCCGCGCTTGGTCTTTCAGA 1926  
Db 841 COTGTGAGTCTCCCTTGAGCGCTGGTCACTAGGCAATCACCCCGCGCTTGGTCTTTCAGA 900  
QY 1927 TGTCTTGGGTTTCATAGGGGAGGTCTAGTCGGGAGGGCCCTGACCCCTCCCGGCT 1986  
Db 901 TGTCTTGGGTTTCATAGGGGAGGTCTAGTCGGGAGGGCCCTGACCCCTCCCGGCT 960  
QY 1987 GGTCTCACTCTCCCTTGAGCGGTGCCATTTGGTCCACCCCTTCATAGAGGGCTGCTTGT 2046  
Db 961 GGTCTCACTCTCCCTTGAGCGGTGCCATTTGGTCCACCCCTTCATAGAGGGCTGCTTGT 1020  
QY 2047 TACAAGGTCGGGTCTCCCTCTGAGCTCGGTTAAGTACCGGAGGCTCTCTTAAAGATG 2106  
Db 1021 TACAAGGTCGGGTCTCCCTCTGAGCTCGGTTAAGTACCGGAGGCTCTCTTAAAGATG 1080  
QY 2107 TCCAGGGCCCAAGCGCGGSCACAGCCAGCCAAACCTTTGGGCCCTTGGAGAGTCTTC 2166  
Db 1081 TCCAGGGCCCAAGCGCGGSCACAGCCAGCCAAACCTTTGGGCCCTTGGAGAGTCTTC 1140  
QY 2167 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCAGGGGCCCATTCACCCCTCC 2226  
Db 1141 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCAGGGGCCCATTCACCCCTCC 1200  
QY 2227 CAACCTGAGCCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCA 2286  
Db 1201 CAACCTGAGCCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCA 1260  
QY 2287 GAGGAGTGGCCAGTTCAGGAGGGGCGGCTGGAGGCTGAGGCTCAGCCACCCCTCCAG 2346  
Db 1261 GAGGAGTGGCCAGTTCAGGAGGGGCGGCTGGAGGCTGAGGCTCAGCCACCCCTCCAG 1320  
QY 2347 CTTTTCCTCAGGCTGCTCAGGTCAGATTCAGGACCAATCTGACCCCTCTCCAAAGG 2406  
Db 1321 CTTTTCCTCAGGCTGCTCAGGTCAGATTCAGGACCAATCTGACCCCTCTCCAAAGG 1380  
QY 2407 CTTCTGTATCAGTGGGAGTGCACAGCCAAATCCCTTGGCCATTTGGCCCGCAGGGGACGTG 2466  
Db 1381 CTTCTGTATCAGTGGGAGTGCACAGCCAAATCCCTTGGCCATTTGGCCCGCACA-GGGGACGTG 1439  
QY 2467 GGCCTTCAGGCTCAGGAGGACCTGAGCTGGAGGTCCTGCTCCAGCCCTCCCCATC 2526  
Db 1440 GGCCTTCAGGCTCAGGAGGACCTGAGCTGGAGGTCCTGCTCCAGCCCTCCCCATC 1499  
QY 2527 TCGGGGCTGTGTGTGGAGGGGCTGCTCAGGCACTCTCTCTGTCTGAACCTGCGCTTAC 2586  
Db 1500 TCGGGGCTGTGTGTGGAGGGGCTGCTCAGGCACTCTCTCTGTCTGAACCTGCGCTTAC 1559  
QY 2587 TGTGTTTAACTTGTCTCAGGATGCTCTGATAGGAGGGGCGGAGGGCTGGGCT 2646  
Db 1560 TGTGTTTAACTTGTCTCAGGATGCTCTGATAGGAGGGGCGGAGGGCTGGGCT 1619  
QY 2647 TGTGACAACTGCTCTTTCACCAATGGCTTGCCTCGTGGCCCTGACTGTTCAGGAGGG 2706  
Db 1620 TGTGACAACTGCTCTTTCACCAATGGCTTGCCTCGTGGCCCTGACTGTTCAGGAGGG 1679  
QY 2707 CAGGGAGGAGAGGGAGGAGTCTCAGGAGGAGGCTGCCCTGAGGGGCTGGGAGGG 2766  
Db 1680 CAGGGAGGAGAGGGAGGAGTCTCAGGAGGAGGCTGCCCTGAGGGGCTGGGAGGG 1739  
QY 2767 GGTACCTCATGAGGACAGGGTGGAGCTGAGAGAGGAGGAGTGGGGCTGGAGGTCT 2826  
Db 1740 GGTACCTCATGAGGACAGGGTGGAGCTGAGAGAGGAGGAGTGGGGCTGGAGGTCT 1799  
QY 2827 GGTAGCTGAGGGACGGGCAAGTGTAGAGGGAGGAGGAGTCTCTGGAGAGATCTTGAG 2886  
Db 1800 GGTAGCTGAGGGACGGGCAAGTGTAGAGGGAGGAGGAGTCTCTGGAGAGATCTTGAG 1859  
QY 2887 CTGCTGTGAGTCTACCCCACTAATCAGTTCCTTAGATTACAGGGAGGGAGGACCAAA 2946

Db 1860 CTGCTGTTGCACTTAACCCCACTAATCACTTCTTAGATTTCAGGGAGGGCAGGCACAA 1919  
QY 2947 CAACTCAGAAATGGGGCTTTTCGGGAGGGCGCTAGTCCCGCCAGCTCTAAGCAGCCAGG 3006  
Db 1920 CAACTCAGAAATGGGGCTTTTCGGGAGGGCGCTAGTCCCGCCAGCTCTAAGCAGCCAGG 1979  
QY 3007 AGGAGCTCCTCACTAAGCAATCTGGGTTCGCAATGGCAATGGCCCGCCAGCTACTGTA 3066  
Db 1980 AGGAGCTCCTCACTAAGCAATCTGGGTTCGCAATGGCAATGGCCCGCCAGCTACTGTA 2039  
QY 3067 TGCCTCCGACCCCGGAGGAGGAGCAATGAACCATAGGAGCTGATCGTAATGTTTATCA 3126  
Db 2040 TGCCTCCGACCCCGGAGGAGGAGCAATGAACCATAGGAGCTGATCGTAATGTTTATCA 2099  
QY 3127 TGTACTTCCCAACCCCTACATTTTGAATAAAATAGGAATTTT 3173  
Db 2100 TGTACTTCCCAACCCCTACATTTTGAATAAAATAGGAATTTT 2146

RESULT 11  
AAV63643

ID AAV63643 standard; cDNA; 2257 BP.

XX AAV63643;

XX AC AAV63643;

XX 15-FEB-1999 (first entry)

XX Contig 253538a encoding a human desaturase enzyme.

Fatty acid; desaturase; polyunsaturated fatty acid;  
malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
cancer; diabetes; eczema; platelet aggregation; vasodilation;  
cholesterol level; endometriosis; premenstrual syndrome; human;  
myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

XX Homo sapiens.

XX WO9846763-A1.

XX 22-OCT-1998.

XX 10-APR-1998; 98WO-US07126.

XX 11-APR-1997; 97US-0834655.

XX (ABBO ) ABBOTT LAB.  
XX (CALJ ) CALGENE LLC.XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
XX Thurmond J;

XX WPI; 1998-594582/50.

XX P-PSDB; AAW84156.

New isolated fatty acid desaturase enzymes - used for the production  
of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
compositions, nutritional compositions, cosmetics or animal feed

XX Example 12; Pages 117-118; 165pp; English.

XX The present sequence encodes a human desaturase enzyme. The sequence was  
XX identified based on homology between human cDNA sequences and Mortierella  
XX alpina desaturase gene sequences. The specification describes methods for  
XX desaturating a fatty acid and for producing a desaturated fatty acid by  
XX expressing increased levels of a desaturase. The enzyme can be used for  
XX desaturating fatty acids. The enzyme can be used to produce  
XX polyunsaturated fatty acids, which can be used for treating malnutrition,  
XX in pharmaceutical compositions, in cosmetics or in animal feed. The  
XX polyunsaturated fatty acids can be used for treating e.g. restenosis  
XX after angioplasty, inflammation, rheumatoid arthritis, asthma,  
XX psoriasis, cancer, diabetes or eczema or reduce blood pressure. They  
XX can also be used to inhibit platelet aggregation, cause vasodilation,

CC lower cholesterol levels, inhibit proliferation of vessel wall smooth  
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding  
CC and other side effects caused by non-steroidal anti-inflammatory drugs,  
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic  
CC encephalomyelitis and chronic fatigue after viral infections, treat  
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and  
CC inflammatory skin disorders.  
XX  
SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Query Match 60.9%; Score 1937.6; DB 19; Length 2257;  
Best Local Similarity 92.1%; Pred. No. 0;  
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

QY 233 GCCACCTTCAGCTGGGAGAGATTGAGAGATACCTGCGCAGCAGTGGGGTGT 292  
DB 15 GCGTACTTCACCTGGGAGAGGTGGCCAGCGCTCAGGGTGGAGAGCGGTGCTAGT 74

QY 293 CATTCAGCGCAAGTTTACAACTATCCAAATGGTCCATCCAGCACCCGGGGGCGAGCG 352  
DB 75 GATCGACCGTAAGGTGTACAACTATCCAGAGTTTCAACCGCGGCATCCAGGGGGTCCCG 134

QY 353 GGTTCATCGGCACTAGCTCGGAGAGATGCAACGGATGCTTCGGCGCTTCCACCTGA 412  
DB 135 GTTCATCAGCCATACCGCCGGCAGATGCCAGATCCCTTTGGGCTTCCACATCA 194

QY 413 CTTGGAAATTCGTGGGCAAGTTCTTGAAACCCCTGCTGATGTGAACTGGCCCGGAGGA 472  
DB 195 CAAGGGCTTTGTAAGAGTATATGAATCTCTCTGATGGAGAACTGTCTCCAGAGCA 254

QY 473 GCCAGCCAGGACACCGGCAAGTCTTCAAGAACCCCTGCTGATGTGAACTGGCCCGGAGGA 532  
DB 255 GCCAGCTTTGAGCCCAACCAAGATTAAGAGCTGACAGATGATTCGGGAGCTGGGGC 314

QY 533 GACGGCTGAGGACATGAACCTGTTCAGAACCAACCCAGTGTCTCTCTCTCTCTCTGGC 592  
DB 315 CACAGTGGAGCGGATGGGCTCATGAAGCCCAACCATGTCTTCTCTGTGTACCTGCT 374

QY 593 CCACATCATCGCCCTGAGAGCAATTGCATGGTTTCACTGTCTTACTTTGGCAATGGCTG 652  
DB 375 GCACATCTTGTGTGATGGTGGAGCTGGCTGACCCCTTGGGTCTTTGGGACGTCCTT 434

QY 653 GATTCCTACCTCATC---ACGGCTTTGCTTGTCTTGTACCTCTCAGGCCCAAGCTGGATG 709  
DB 435 TTTGGCCCTTCTCTCTGTGGGTGTGTCTCAGTGAGTTCAGAGGCCCAAGCTGGATG 494

QY 710 GTTGCAACATGATTAATGGCCACTGTGTCTGTCTACAGAAACCCCAAGTGAACCACTTGT 769  
DB 495 GCTGCAACATGATTAATGGCCACTGTGTCTACAGAAACCCCAAGTGAACCACTTGT 554

QY 770 CCACAAATTCGTATTCGGCCACTTAAAGGTGTCTGTGCCAATGGTGAATCATCGCCA 829  
DB 555 CCACAAATTCGTATTCGGCCACTTAAAGGTGTCTGTGCCAATGGTGAATCATCGCCA 614

QY 830 CTTCCAGCACACGCCAAGCTTAACATCTTCCAAAGGATCCCGATGTGAACATGCTGCA 889  
DB 615 CTTCCAGCACACGCCAAGCTTAACATCTTCCAAAGGATCCCGATGTGAACATGCTGCA 674

QY 890 GGTGTTTGTTCGGGCAATGGCCATCGATCGAGTACGGCAAGAGCTGAATACCT 949  
DB 675 CGTGTGTTGTTCGGGCAATGGCCATCGAGTACGGCAAGAGCTGAATACCT 734

QY 950 GCCCTACAAATCACCAGCACGAATACTTCTTCTGATTTGGGCGCGCGTGTCTATCCCCAT 1009  
DB 735 GCCCTACAAATCACCAGCACGAATACTTCTTCTGATTTGGGCGCGCGTGTCTATCCCCAT 794

QY 1010 GTATTTCCAGTACAGATCATATGACCATGATGCTCCATTAAGAACTGGGTGACCTGGC 1069  
DB 795 GTATTTCCAGTACAGATCATATGACCATGATGCTCCATTAAGAACTGGGTGACCTGGC 854

QY 1070 CTGGGCGGTGAGCTACTACATCCGGTTCTTTCATCACCTACATCCCTTTCTACGGCATCT 1129  
DB 855 CTGGGCGGTGAGCTACTACATCCGGTTCTTTCATCACCTACATCCCTTTCTACGGCATCT 914

QY 1130 GGGAGCCCTCCTTTTCTCAACTTTCATCAGTTCCTTGAGAGCCACTGGTTGTGGGT 1189  
DB 915 GGGAGCCCTCCTTTTCTCAACTTTCATCAGTTCCTTGAGAGCCACTGGTTGTGGGT 974

QY 1190 CACACAGATGAATCACATCGTCATGGAGATTGACAGAGCCCTTACGTAAGTTCAG 1249  
DB 975 CACACAGATGAATCACATCGTCATGGAGATTGACAGAGCCCTTACGTAAGTTCAG 1034

QY 1250 TAGCAGCTGACAGCCACCTGACAGTGGAGAGTCTTCTTCAACAGCTGGTTCACTGG 1309  
DB 1035 TAGCAGCTGACAGCCACCTGACAGTGGAGAGTCTTCTTCAACAGCTGGTTCACTGG 1094

QY 1310 ACACCTTAACCTTCAGATTGAGCACACCTCTTCTCCACCATGCCCCGGCACTTACA 1369  
DB 1095 ACACCTTAACCTTCAGATTGAGCACACCTCTTCTCCACCATGCCCCGGCACTTACA 1154

QY 1370 CAAGATGCCCGCGTGTGAAGTCTCTATGTGCCAAGCATGGCATTAAGTACAGAGAA 1429  
DB 1155 CAAGATGCCCGCGTGTGAAGTCTCTATGTGCCAAGCATGGCATTAAGTACAGAGAA 1214

QY 1430 CCGCTACTGAGGGCCCTGTCTGGACATCATCAGTCCCTGAAGAACTCTGGAAAGCTGTG 1489  
DB 1215 GCGCTACTGAGGGCCCTGTCTGGACATCATCAGTCCCTGAAGAACTCTGGAAAGCTGTG 1274

QY 1490 GCTGGAAGCTTACCTTCAAAATGAAGCAGAGCCCGGGGACACCGTGGGAAAGGGGTG 1549  
DB 1275 GCTGGAAGCTTACCTTCAAAATGAAGCAGAGCCCGGGGACACCGTGGGAAAGGGGTG 1334

QY 1550 CAGTGGGGTTCATGGCCAGAGGAATGATGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT 1609  
DB 1335 CAGTGGGGTTCATGGCCAGAGGAATGATGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT 1394

QY 1610 GGTGTATGCACTGTCTACGAGCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTTTT 1669  
DB 1395 GGTGTATGCACTGTCTACGAGCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTTTT 1454

QY 1670 CTCCTTCATCTCCCCCATAGCACCTGCTCATGGAGCTGCTCCCTCCCTCAGCCGTCA 1729  
DB 1455 CTCCTTCATCTCCCCCATAGCACCTGCTCATGGAGCTGCTCCCTCCCTCAGCCGTCA 1514

QY 1730 GCCATCAGCCATGCGCCCTCCAGTGCCTCTTAGGCCCTTTTTCAGAGAGCAGAGAGTG 1789  
DB 1515 GCCATCAGCCATGCGCCCTCCAGTGCCTCTTAGGCCCTTTTTCAGAGAGCAGAGAGTG 1574

QY 1790 GCCACCGGGGTGCTGTCTCTACCTCCACTCTGCCCTTAAGATGGAGAGAGCA 1849  
DB 1575 GCCACCGGGGTGCTGTCTCTACCTCCACTCTGCCCTTAAGATGGAGAGAGCA 1634

QY 1850 GCGGTCCATGCGCTGTGGCTCTGCCCTTTCAGCCCTGGTCACTTAGGCATCACCCC 1909  
DB 1635 GCGGTCCATGCGCTGTGGCTCTGCCCTTTCAGCCCTGGTCACTTAGGCATCACCCC 1694

QY 1910 GCTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGGAGGTCCTAGTCCGGCAGGGCC 1969  
DB 1695 GCTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGGAGGTCCTAGTCCGGCAGGGCC 1754

QY 1970 CTTGACCTCTCCCGCTGCTTCACTCTCCCTGAGCGTGCATTTGGTCCACCTTTTCAT 2029  
DB 1755 CTTGACCTCTCCCGCTGCTTCACTCTCCCTGAGCGTGCATTTGGTCCACCTTTTCAT 1814

QY 2030 AGAGAGGCTCTTTGTTTACAAAGCTCGGGTCTCCCTCTGAGCTCGGTTAAGTACCGG 2089  
DB 1815 AGAGAGGCTCTTTGTTTACAAAGCTCGGGTCTCCCTCTGAGCTCGGTTAAGTACCGG 1874

QY 2090 AGGCTCTCTTTAAGATGCCAGGGCCCGAGCCCGGGGACAGCCAGCCCAACCTTGG 2149  
DB 1875 AGGCTCTCTTTAAGATGCCAGGGCCCGAGCCCGGGGACAGCCAGCCCAACCTTGG 1934

QY 2150 GCGCTGGAAGAGTCTTCCACCCCATCACTAGAGTGTCTGTACCTTGGGCTTTCAGGGCC 2209  
DB 1935 GCGCTGGAAGAGTCTTCCACCCCATCACTAGAGTGTCTGTACCTTGGGCTTTCAGGGCC 1994

QY 2210 CCATTCACGCGCTCCCAACTTGGAGCTGTGACCTTGGACCAACAAAGGGGAGTCCCTCG 2269  
 Db |||||  
 QY 1995 CCATTCACGCGCTCCCAACTTGGAGCTGTGACCTTGGACCAACAAAGGGGAGTCCCTCG 2054  
 Db |||||  
 QY 2270 TCTTTGTGACTCAGCAGAGGCGAGTGCCACGTTTCAGGAGGCGCGGTGGCTGGAGG 2329  
 Db |||||  
 QY 2055 TCTTTGTGACTCAGCAGAGGCGAGTGCCACGTTTCAGGAGGCGCGGTGGCTGGAGG 2114  
 Db |||||  
 QY 2330 CTCAGCCACCCCTCCAGCTTTTCTCAGGCTGTGCTGAGGTCCAGATTCTGGAGCAATC 2389  
 Db |||||  
 QY 2115 CTCAGCCACCCCTCCAGCTTTTCTCAGGCTGTGCTGAGGTCCAGATTCTGGAGCAATC 2174  
 Db |||||  
 QY 2390 TGACCTTTCTCCAAAGGCTCTGTATCAGCTGGGCGAGTGCACCAATCCTGGCCATTT 2449  
 Db |||||  
 QY 2175 TGACCTTTCTCCAAAGGCTCTGTATCAGCTGGGCGAGTGCACCAATCCTGGCCATTT 2234  
 Db |||||  
 QY 2450 GGGCCCGAGGGGAGCTGGGCGCTG 2473  
 Db |||||  
 QY 2235 GGGCCCA-GGGGAGCTGGGCGCTG 2257  
 Db |||||

RESULT 12

AXX00910  
 ID AAX00910 standard; DNA; 2257 BP.  
 AC AAX00910;  
 XX  
 DT 26-MAR-1999 (first entry)  
 XX  
 DE Human desaturase gene contig 253538a.  
 XX  
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;  
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;  
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;  
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;  
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;  
 KW diabetes; cosmetic; animal feed; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Location/Qualifiers  
 FT 1..2256  
 FT CDS  
 FT /\*tag= a  
 FT /note= "contains internal stop codons"

WO9846764-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 10-APR-1998; 98MO-US07421.  
 XX  
 PR 24-OCT-1997; 97US-0956985.  
 PR 11-APR-1997; 97US-0833610.  
 PR 11-APR-1997; 97US-0834033.  
 PR 11-APR-1997; 97US-0834655.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX  
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 XX  
 DR WPI; 1999-080739/07.  
 DR P-PSDB; AAW95514.  
 XX  
 PT Nucleic acid construct able to express fatty acid desaturase in  
 PT plants - useful in human or animal nutrition, as cosmetics and  
 PT therapeutically, e.g. for restenosis, cancer and diabetes  
 XX  
 PS Claim 48; Page 161-162; 210pp; English.  
 XX  
 CC The invention relates to a nucleic acid construct that contains at least  
 CC one of the nucleotide sequences (AAX00989 to AAX00891) encoding

CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to  
 CC AAW95506) respectively, coupled to an expression control sequence  
 CC functional in plants. Recombinant plant cells containing at least one DNA  
 CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the  
 CC production of polyunsaturated fatty acid (PUFA). These recombinant cells  
 CC or plants containing them are used to produce oils such as linoleic  
 CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic  
 CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils  
 CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas; or  
 CC dietary supplements or substitutes, for use in humans or animals; (iii)  
 CC for treating disorders associated with inadequate consumption or  
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.  
 CC restenosis after angioplasty, inflammation; AIDS, rheumatoid arthritis,  
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,  
 CC and (v) as animal feeds. Fragments of the DNA are used as probes to  
 CC isolate related coding sequences. Recombinant plants can produce high  
 CC yields of PUFA, since new pathways can be created and unwanted ones  
 CC suppressed. Plants can be engineered to express oils of particular PUFA  
 CC composition, e.g. one similar to that in human milk, and product recovery  
 CC is simpler than with e.g. fish. Sequences AAX00904-910 represent DNA  
 CC sequences of various contigs of human desaturase genes which are similar  
 CC to the M. alpina desaturase sequences.  
 XX  
 SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;  
 Query Match 60.9%; Score 1937.6; DB 20; Length 2257;  
 Best Local Similarity 92.1%; Pred. No. 0;  
 Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;  
 QY 233 GCCACCTTTACGCTGGGAGGAGTTCAGAGCATTAACCTGCGCACCGACAGTGGGTGCT 292  
 Db 15 GCGTACTTTCACCTGGGACGAGTGGCCGCGCTCAGGGTCCGAGGAGCGGTGGCTAGT 74  
 QY 293 CATTGACCGCAGGTTTCAACATCACCAGTGGTCCATCCAGCACCGCGGGGCGGACGC 352  
 Db 75 GATCAGCCGTAAGGTGTACACATCAGCGAGTTCACCGCGCGGATCCAGGGGGCTCCCG 134  
 QY 353 GGTCTATCGGGGCACTACGCTGGGAGAGATGCAACGGATGCTTCGCGGCTTCCACCTGA 412  
 Db 135 GGTCTATCAGCCACTACGCGGGGAGGATGCCAGGATGCTTCGCGGCTTCCACATCAA 194  
 QY 413 CTGGAATTCGTGGGCAAGTCTTGAACCCCTGCTGATTTGGTGAACCTGGCGGAGGA 472  
 Db 195 CAAGGGCCTTGTGAAGAAGTATATGAACCTCTCTCTGATTGGAGAACTGTCTCCAGACA 254  
 QY 473 GCCCAGCAGGACCAACCGCAAGAACTCAAGAGTCACTGAGGACTTCCGGGCGCTGAGGAA 532  
 Db 255 GCCCAGCTTTGAGCCCAACCAAGATTAAGAGCTGACAGATGATTCGGGAGCTCGGGC 314  
 QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACCAAGTGTCTTCTCTCTCTCTCTGCG 592  
 Db 315 CACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTCTCTCTCTCTCTCT 374  
 QY 593 CCACATCATCGCCCTGGAGCAGCATTCATGTTCTCACTGTTCTTCTTCTTCTTCTTCTTCT 652  
 Db 375 GCACATCTGCTGCTGGATGGTGGCCTGGCTGGCTGACCTTTCCTTGGGCTTGGGACGCT 434  
 QY 653 GATTCTCTACCTCATC---ACGGCCTTGTCTTGTCTGCTCTGAGGCCCAAGCTGGATG 709  
 Db 435 TTTGGCCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494  
 QY 710 GCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGGAAACCACTTGT 769  
 Db 495 GCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAACCAAGTGGAAACCACTTGT 554  
 QY 770 CCACAAATTCGTCATTGGCCACTTAAAGGGTGGCTCTGCCAATCTGTTGGAATCATGCCA 829  
 Db 555 CCACAAATTCGTCATTGGCCACTTAAAGGGTGGCTCTGCCAATCTGTTGGAATCATGCCA 614  
 QY 830 CTTCCAGCACCGCCCAAGCTTAACATCTTCCACAGGATCCGAGTCAACATGCTGCA 889  
 Db 615 CTTCCAGCACCGCCCAAGCTTAACATCTTCCACAGGATCCGAGTCAACATGCTGCA 674



949 890 CGTGTGTTGTTCTGGCGAATGCGAGCCATCGAGTACGGCAAGAAAGCTGAATACCT 949  
Db 675 CGTGTGTTGTTCTGGCGAATGCGAGCCATCGAGTACGGCAAGAAAGCTGAATACCT 734  
Qy 950 GCCCTACAAATCACAGACGAAATACCTTCTCTGATTTGGGCGCGCTGCTCATCCCAT 1009  
Db 735 GCCCTACAAATCACAGACGAAATACCTTCTCTGATTTGGGCGCGCTGCTCATCCCAT 794  
Qy 1010 GTATTTCCAGTACAGATCATCATGATCGTCCATAAGAACTGGGTGGACCTGGC 1069  
Db 795 GTATTTCCAGTACAGATCATCATGATCGTCCATAAGAACTGGGTGGACCTGGC 884  
Qy 1070 CTGGGCGGTAGCTACATCCGCTTCTTCAATCACCTATACCTTCTTCAAGCAATCCT 1129  
Db 855 CTGGGCGGTAGCTACATCCGCTTCTTCAATCACCTATACCTTCTTCAAGCAATCCT 914  
Qy 1130 GGGAGCCCTCTTTCTCTCAATTCATCAGGTTCTCTGGAGAGCCACCTGTTGTTGGGT 1189  
Db 915 GGGAGCCCTCTTTCTCTCAATTCATCAGGTTCTCTGGAGAGCCACCTGTTGTTGGGT 974  
Qy 1190 CACACAGATGAATCACATCGTATGAGATTCACAGAGGCTTACCGTGAATGTTTCAAG 1249  
Db 975 CACACAGATGAATCACATCGTATGAGATTCACAGAGGCTTACCGTGAATGTTTCAAG 1034  
Qy 1250 TAGCCAGCTGACGACCTGACAGCTGGAGCTGCTTCTTCAAGCAATGTTTCAAGTGG 1309  
Db 1035 TAGCCAGCTGACGACCTGACAGCTGGAGCTGCTTCTTCAAGCAATGTTTCAAGTGG 1094  
Qy 1310 ACACCTTAACTTCAGAGTTGAGACCACTCTTCCCAACATGCCCCGACCACTTACA 1369  
Db 1095 ACACCTTAACTTCAGAGTTGAGACCACTCTTCCCAACATGCCCCGACCACTTACA 1154  
Qy 1370 CAAGATGCCCGCTGTTGAGTCTTATGTCACAGCTGAGTGAATACAGAGGAA 1429  
Db 1155 CAAGATGCCCGCTGTTGAGTCTTATGTCACAGCTGAGTGAATACAGAGGAA 1214  
Qy 1430 CCGGCTACTGAGGCGCTGCTGGACATCATCAGTCTCTGAAAGTCTGGGAGCTGTG 1489  
Db 1215 CCGGCTACTGAGGCGCTGCTGGACATCATCAGTCTCTGAAAGTCTGGGAGCTGTG 1274  
Qy 1490 GCTGAGCCCTTACCTTCAAAATGAGCCACAGCCCCCGGGACACCGTGGGAGAGGGTG 1549  
Db 1275 GCTGAGCCCTTACCTTCAAAATGAGCCACAGCCCCCGGGACACCGTGGGAGAGGGTG 1334  
Qy 1550 CAGGTGGGCTGATGGCCAGAGAAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCT 1609  
Db 1335 CAGGTGGGCTGATGGCCAGAGAAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGGCT 1394  
Qy 1610 GGTGATGCACTGCTACGAGCCCATGTTGGATCTTTTCTCCCTTCTCTCTCTCTTTT 1669  
Db 1395 GGTGATGCACTGCTACGAGCCCATGTTGGATCTTTTCTCCCTTCTCTCTCTCTTTT 1454  
Qy 1670 CTCTTACATCTCCCCATAGCACCTGCGCTCATGGAGCTGCTCCCTCCCTCAGCCGTCA 1729  
Db 1455 CTCTTACATCTCCCCATAGCACCTGCGCTCATGGAGCTGCTCCCTCCCTCAGCCGTCA 1514  
Qy 1730 GCCATACGCCATGGCCCTCCAGTGCCTTCTAGCCCTTCTTCCAGGAGCAGAGAGGTG 1789  
Db 1515 GCCATACGCCATGGCCCTCCAGTGCCTTCTAGCCCTTCTTCCAGGAGCAGAGAGGTG 1574  
Qy 1750 GCCACGGGGGTGGCTGCTCTACCTACCTCTGCGCCCTTAAGATGGGAGAGACCA 1849  
Db 1575 GCCACGGGGGTGGCTGCTCTACCTACCTCTGCGCCCTTAAGATGGGAGAGACCA 1634  
Qy 1850 GCGGTCCATGGGTCTGGGCTGTGAGTCTCCCTTCTGAGCCTGGTCACTAGGCAATCACCCC 1909  
Db 1635 GCGGTCCATGGGTCTGGGCTGTGAGTCTCCCTTCTGAGCCTGGTCACTAGGCAATCACCCC 1694  
Qy 1910 GCGTTTGGTCTTTCAGATGCTCTTGGGTTTATAGGGGAGGTCCTAGTGGGAGGGCC 1969  
Db 1695 GCGTTTGGTCTTTCAGATGCTCTTGGGTTTATAGGGGAGGTCCTAGTGGGAGGGCC 1754  
Qy 1970 CTGAGCCCTCCGGGCTGGCTTCACTCTCCCTGACGGCTGCCATTTGGTCCACCCCTTTTCA 2029

1755 CCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCAATTTGTCACCCCTTTTCA 1814  
Qy 2030 AGAGAGGCTGCTTTGTTTACAAAGCTCGGCTCTCCCTCTCGAGCTCGGTTAAGTACCGG 2089  
Db 1815 AGAGAGGCTGCTTTGTTTACAAAGCTCGGCTCTCCCTCTCGAGCTCGGTTAAGTACCGG 1874  
Qy 2090 AGGCTCTCTTTAAGATGTCAGGGGCCCCAGGCCCCCGGGGACAGCCAGCCAAACCTTTGG 2149  
Db 1875 AGGCTCTCTTTAAGATGTCAGGGGCCCCAGGCCCCCGGGGACAGCCAGCCAAACCTTTGG 1934  
Qy 2150 GGCCTGGAAGAGTCTCTCAACCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAAGGGCC 2209  
Db 1935 GGCCTGGAAGAGTCTCTCAACCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAAGGGCC 1994  
Qy 2210 CCATTTCCACCGCTCTCCCAACTTGACCTTGACCTTGGACCTTGGACCTTGGACCTTGG 2269  
Db 1995 CCATTTCCACCGCTCTCCCAACTTGACCTTGGACCTTGGACCTTGGACCTTGGACCTTGG 2054  
Qy 2270 TCTTTGTGACTCAGACAGAGGAGTGGCCACGTTTTCAGGGAGGGGCGGCTGGGAGG 2329  
Db 2055 TCTTTGTGACTCAGACAGAGGAGTGGCCACGTTTTCAGGGAGGGGCGGCTGGGAGG 2114  
Qy 2330 CTCAGCCACCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTTCTGGAGCAATC 2389  
Db 2115 CTCAGCCACCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTTCTGGAGCAATC 2174  
Qy 2390 TCACCTTTCTCAAAGGCTTGTATCAGCTGGGAGTGCAGCCAAATCCCTTGGCAATTT 2449  
Db 2175 TCACCTTTCTCAAAGGCTTGTATCAGCTGGGAGTGCAGCCAAATCCCTTGGCAATTT 2234  
Qy 2450 GSCCCACAGGGGAGCTGGGCGCTG 2473  
Db 2235 GSCCCCA-GGGGAGCTGGGCGCTG 2257

RESULT 13  
AAV82642  
ID AAV82642 standard; DNA; 2257 BP.  
XX AAV82642;  
XX DT 11-FEB-1999 (first entry)  
XX Contig 253538a encoding a desaturase enzyme.  
XX Fatty acid; desaturase; polyunsaturated fatty acid;  
XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
XX cancer; diabetes; eczema; platelet aggregation; vasodilation;  
XX cholesterol level; endometriosis; premenstrual syndrome;  
XX myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
XX acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
XX Homo sapiens.  
XX MO9846765-A1.  
XX 22-OCT-1998.  
XX 10-APR-1998; 98MO-US07422.  
XX 11-APR-1997; 97US-0833610.  
XX (ABBO ) ABBOTT LAB.  
XX (CALJ ) CALGENE LLC.  
XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;  
XX Thurmond J;  
XX WPI; 1999-009334/01.  
XX P-PSDB; AAW85135.  
XX New nucleic acid encoding delta5 and other desaturase enzymes -



PT useful in production of oils of increased arachidonic acid content,  
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics  
XX  
XX  
PS Claim 86; Pages 111-112; 153pp; English.  
XX  
CC The present sequence encodes a human desaturase enzyme. The enzyme  
CC sequence is used in the methods of the invention. The specification  
CC describes methods for desaturating a fatty acid and for producing a  
CC desaturated fatty acid by expressing increased levels of a desaturase.  
CC The enzyme can be used for desaturating fatty acids. The enzyme can be  
CC used to produce polyunsaturated fatty acids, which can be used for  
CC treating malnutrition, in pharmaceutical compositions, in cosmetics or  
CC in animal feed. The polyunsaturated fatty acids can be used for treating  
CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,  
CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.  
CC They can also be used to inhibit platelet aggregation, cause  
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel  
CC wall smooth muscle and fibrous tissue, reduce or prevent  
CC gastro-intestinal bleeding and other side effects caused by non-steroidal  
CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual  
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after  
CC viral infections, treat AIDS, multiple sclerosis, acute respiratory  
CC syndrome, hypertension and inflammatory skin disorders.  
XX  
SQ Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;

Query Match 60.9%; Score 1937.6; DB 20; Length 2257;  
Best Local Similarity 92.1%; Pred. No. 0;  
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;

QY 233 GCCACCTTCAGCTGGGAGAGATTGAGAGATACCTCGGACGACGAGAGTGGGCTGT 292  
DB 15 GCGTACTTCACTGGGACGAGGTGGCCGCGCTCAGGTCGAGGACGGTGGCTAGT 74  
QY 293 CATGACCGCAAGTTTACAAATACCAATGGTCCATCCAGACCCGCGGGGCGAGCG 352  
DB 75 GATCGACCGTAAGTGTATCAACATCAGCGAGTTTCAACCGCGGCAATCCAGGGGGTCCCG 134  
QY 353 GGTTCATCGGCACTAGCTGGGAGAGATGCAAGGATGCTTCCGCGCTTCCACCTGA 412  
DB 135 GGTTCATCGGCACTAGCTGGGAGAGATGCAAGGATGCTTCCGCGCTTCCACCTGA 194  
QY 413 CTTGGAAATCTGGGCAAGTTCTTTGAAACCCCTGCTGATTGGTGAATCGGCCCGGAGGA 472  
DB 195 CAAAGGCGCTTGTGAAGATATATGAATCTCTCTGATTGGAGAACTGTCTCCAGAGCA 254  
QY 473 GCCCAGCCAGCAACCGCAAGACTCAAGATCACTGAGGACTTCCGGGCGCTGAGGAA 532  
DB 255 GCCCAGCTTTGAGCCCAACCAAGATTAAGAGCTGACAGATAGTTCCGGAGGTGGGCG 314  
QY 533 GAGCGCTGAGGACATGAACCTGTTCAAGACCAACCGTGTCTTCTCTCTCTCTCTGCT 592  
DB 315 CACAGTGGAGCGGATGGGCTCATGAAGGCCAACCATGTCTTCTCTCTCTCTCTCTCT 374  
QY 593 CCACATCATCGCCCTGGAGAGCAATGATGTTGATGTTGATGTTGATGTTGATGTTGATG 652  
DB 375 GCACATCTTGTCTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 434  
QY 653 GATTCTTACCTCATC---ACGGCGCTTTGCTTGTGATCTCTCAGCGCCCAAGCTGGATG 709  
DB 435 TTTGGCCCTTCTCTCTGTGGGTGCTGCTCAGTGAGTTTCAGAGGCCCAAGCTGGATG 494  
QY 710 GCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAACCAAGTGGAACCACTTGT 769  
DB 495 GCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAACCAAGTGGAACCACTTGT 554  
QY 770 CCACAAATTCGTCAATGGCCACTTAAAGGGTGGCTCTGCCAATGTTGGAATCATGCCCA 829  
DB 555 CCACAAATTCGTCAATGGCCACTTAAAGGGTGGCTCTGCCAATGTTGGAATCATGCCCA 614  
QY 830 CTTCCAGACCAACGCCAAGCTTAACATCTTCCAAAGGATCCCGAGTGAACATGTGCA 889  
DB 615 CTTCCAGACCAACGCCAAGCTTAACATCTTCCAAAGGATCCCGAGTGAACATGTGCA 674

QY 890 CGTGTGTTGTTCTGGGCAATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCT 949  
DB 675 CGTGTGTTGTTCTGGGCAATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAAATACCT 734  
QY 950 GCCTACATCACAGCAGCAATACCTTCTCTGATTGGGCGCGCTCTCATCCCCAT 1009  
DB 735 GCCTACATCACAGCAGCAATACCTTCTCTGATTGGGCGCGCTCTCATCCCCAT 794  
QY 1010 GTATTTCAGTACAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGC 1069  
DB 795 GTATTTCAGTACAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGC 854  
QY 1070 CTGGGCGCTGAGTACATCATCGGTTCTTCATCAGTACATCATCTTCTACGGATCCT 1129  
DB 855 CTGGGCGCTGAGTACATCATCGGTTCTTCATCAGTACATCATCTTCTACGGATCCT 914  
QY 1130 GGGAGCGCTCTCTTCTCACTTTCATCAGTTCCTGGAGAGCACTGGTTTGTGGGT 1189  
DB 915 GGGAGCGCTCTCTTCTCACTTTCATCAGTTCCTGGAGAGCACTGGTTTGTGGGT 974  
QY 1190 CACAGATGAATCAGATCATGATGAGATGACAGAGAGGCTACCGTACCTGTTTACG 1249  
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DB 1095 ACACCTTAATTCAGATTGAGCACCACCTCTTCCACCACCATCCCGCGGACCACTTACA 1154  
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DB 1215 GCCGCTACTGAGGCGCTCTGTCGACATCATCAGTCCCTGAAAGAGTCTGGAGAGTGT 1274  
QY 1490 GCTGGAGCGCTTACCTTCCAAATGAGCCACAGCCCGGGGACACCTGGGGAGGGGTG 1549  
DB 1275 GCTGGAGCGCTTACCTTCCAAATGAGCCACAGCCCGGGGACACCTGGGGAGGGGTG 1334  
QY 1550 CAGTGGGGTGAATGGCCAGAGGAATGATGGGCTTTTCTGAGGGGTGTCCGAGAGCT 1609  
DB 1335 CAGTGGGGTGAATGGCCAGAGGAATGATGGGCTTTTCTGAGGGGTGTCCGAGAGCT 1394  
QY 1610 GGTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTTTT 1669  
DB 1395 GGTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTTTT 1454  
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DB 1635 CGGTCATAGGGTCTGGGCTGTGAGTCTCCCTTTCAGAGCTGTGTCATAGGATCACTCC 1694  
QY 1910 CGCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1969  
DB 1695 CGCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1754



Db 675 CGTGTGTTGTTCTGGCGGAATGCGACCCATCGAGTACGGCAGAGAGCTGAATACCT 734  
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 Db 1155 CAAGATCGCCCGCTGGTGAAGTCTATGTCGACGATGCGATGAATACAGAGAA 1214  
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 Db 1635 GCGGTTCATGGGTCTGGGCTGTGAGTCTCCCTTGCAGCGCTGTCTACTAGGCATCACCC 1694  
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 Db 1695 CGCTTTGGTTCATGATGCTTGGGTTCTAGGGGCGAGTCTCTAGTGGGCGGCGC 1754  
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QY 2030 AGAGAGCGCTGCTTTGTTTAAAGCTCGGGTCTCCTCTCTGAGCTCGGTTAAGTACCCG 2089  
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 Db 1875 AGGCTCTCTTAAAGTCTCAGGGGCCAGGCCCCGGGCGACAGCCGAAACCTTGG 1934  
 QY 2150 GCGCTGGAAGTCTCCACCCCATCACTAGAGTGTCTGACCTGGGGTCTTTCAGGGGCG 2209  
 Db 1935 GCGCTGGAAGTCTCTCCACCCCATCACTAGAGTGTCTGACCTGGGGTCTTTCAGGGGCG 1994  
 QY 2210 CCATTCCACCGCTCTCCCACTTTGACCTGTGACCTTGGGACCAAGGGGGAGTCCCTCG 2269  
 Db 1995 CCATTCCACCGCTCTCCCACTTTGACCTGTGACCTTGGGACCAAGGGGGAGTCCCTCG 2054  
 QY 2270 TCTCTTGTGACTCAGCAGAGGAGTGGCCACCTTCAAGGAGGGGCGGCTGCGCTGGAG 2329  
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 QY 2330 CTGAGCCGACCTTCCAGCTTTTCTCAGGGTGTCTGAGTCTCAAGATTCTGGAGCAATC 2389  
 Db 2115 CTGAGCCGACCTTCCAGCTTTTCTCAGGGTGTCTGAGTCTCAAGATTCTGGAGCAATC 2174  
 QY 2390 TGACCTTCTCCAAAGCTCTGTATCAGCTGGGAGTGGCCCAATCCCTGGCCATTT 2449  
 Db 2175 TGACCTTCTCCAAAGCTCTGTATCAGCTGGGAGTGGCCCAATCCCTGGCCATTT 2234  
 QY 2450 GGGCCGAGGGGAGCTGGGCGCTG 2473  
 Db 2235 GGGCCCA-GGGAGCTGGGCGCTG 2257

RESULT 15  
 AAA09453  
 ID AAA09453 standard; DNA; 2257 BP.  
 XX  
 AC AAA09453;  
 DT 10-AUG-2000 (first entry)  
 XX  
 Human contig 2535 DNA encoding desaturase homologue.  
 DE delta-6 desaturase; gamma-linolenic acid; biosynthesis;  
 KW transgenic insect cell; polyunsaturated long chain fatty acid;  
 KW antiinflammatory; antirheumatic; antiaesthetic; antipsoriatic;  
 KW osteopathic; cytosolic; antidiabetic; dermatological; gynecological;  
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;  
 KW antiaggregant; vasotropic; ss.  
 XX  
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 XX  
 FH Key Location/Qualifiers  
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 FT /transl\_except= (pos:1963..1965, aa:Xaa)  
 FT /transl\_except= (pos:2017..2019, aa:Xaa)  
 FT /transl\_except= (pos:2062..2064, aa:Xaa)  
 FT /note= "Xaa not defined"  
 XX  
 PN WO200020602-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 29-SEP-1999; 99WO-US22686.  
 XX  
 PR 05-OCT-1998; 98US-0103110.  
 XX









PD 13-AUG-2002.  
XX 08-JAN-1999; 99US-0227613.  
XX 11-APR-1997; 97US-0833610.  
PR 10-APR-1998; 98WO-US07422.  
XX (ABBO ) ABBOTT LAB.  
XX Mukerji P, Leonard AE, Huang Y, Das T;  
XX WPI; 2002-689761/74.  
XX  
XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing  
PT the conversion of dihomogamma-linolenic acid to arachidonic acid and  
PT in the conversion of 20:4n-3 to eicosapentaenoic acid -  
XX  
XX Example 1; Figure 8; 88pp; English.  
XX  
XX The invention relates to an isolated human delta5-desaturase nucleotide  
CC sequence (I) which desaturates polyunsaturated fatty acids at  
CC carbon 5. The nucleotide sequence (I) may be used in the recombinant  
CC production of vectors and host cells for the production of delta5-  
CC desaturase. Delta5-desaturase may be utilised in the conversion of  
CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the  
CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or  
CC polyunsaturated fatty acids produced from it may be added to  
CC pharmaceutical compositions, nutritional compositions, animal feeds, as  
CC well as other products such as cosmetics. AB571819-AB571854  
CC represent human delta5-desaturase coding sequences and PCR primers of  
CC the invention.  
XX  
XX Sequence 2257 BP; 438 A; 719 C; 596 G; 504 T; 0 other;  
SQ  
Query Match 60.9%; Score 1937.6; DB 24; Length 2257;  
Best Local Similarity 92.1%; Pred. No. 0;  
Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;  
QY 233 GCCACCTTCAGTGGGAGAGATTGAGAGATACCTGCGCAGCAGTGGGTGTGT 292  
DB 15 GCGTACTTCCTGCGGACGAGTGGCGCCAGCGCTCAGGGTGGAGAGCGGTGGTGT 74  
QY 293 CATGACCGCAAGTTTACAAATACCAATGGTCCATCCAGCACCCGGGGGGCAGCG 352  
DB 75 GATCGACCGTAAGGTGTACAAATACGAGGTTCACCGCGCGGATCCAGGGGGTCCCG 134  
QY 353 GGTTCATCGGCACTACCTGGAGAGATGCAACGGATGCTTCCGGCGCTTCCACCTGA 412  
DB 135 GGTTCATCGGCACTACCGCGGGGAGGATGCCAGGATCCCTTGTGGCGCTTCCACATCA 194  
QY 413 CCTGGAATTCGTGGGCAAGTTCTTTGAAACCCCTGCTGATGTGAATCGGCCCGGAGGA 472  
DB 195 CAAGGGCTTGTGAAGAGTATATGAATCTCTCTGATTGGAGAACTGTCTCCAGAGCA 254  
QY 473 GCCCAGCAGGACACCGCAAGACTCAAGATCACTGAGACTTCGGGCGCTGAGAA 532  
DB 255 GCCCAGCTTTGAGCCCAACCAAGATAAAGAGCTGACAGATGAGTTCGGGAGCTGGGGC 314  
QY 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACCACTGCTTCTCTCTCTCTCTGGC 592  
DB 315 CACAGTGGAGCGATGGGCTCATGAAGGCCAACCACTGTCTTCTCTGCTGTGCTGCT 374  
QY 593 CCACATCATCGCCCTGGAGAGCATTTGATGTTTCACTGTTTCTTCTTGGCAATGGCTG 652  
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QY 653 GATTCCTACCTCATC---ACGGGCTTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 709  
DB 435 TTTGCGCTTCTCTCTGTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494  
QY 710 GCTGCAACATGATTATGCGCACTGTCTGTCTACAGAAACCCCAAGTGGAAACCACTTGT 769  
DB 495 GCTGCAACATGATTATGCGCACTGTCTGTCTACAGAAACCCCAAGTGGAAACCACTTGT 554

QY 770 CCACAAATTCGTCATGGCCACTTAAAGGGTGCCTTCGCAAACTGGTGAATCATCGCA 829  
DB 555 CCACAAATTCGTCATGGCCACTTAAAGGGTGCCTTCGCAAACTGGTGAATCATCGCA 614  
QY 830 CTTCCAGCAGCAGCCCAAGCCTAAACATCTTCCACAGGATCCCGATGTGAACATCTGCA 889  
DB 615 CTTCCAGCAGCAGCCCAAGCCTAAACATCTTCCACAGGATCCCGATGTGAACATCTGCA 674  
QY 890 CGTGTTTGTCTGGCGAATGGCAGCCCATCGAGTACGGCAAGAGAACTGAAATACCT 949  
DB 675 CGTGTTTGTCTGGCGAATGGCAGCCCATCGAGTACGGCAAGAGAACTGAAATACCT 734  
QY 950 GCCTTCAATCAGCAGCAGCAATATCTTCTGATTTGGCGCGCGCTCTCATCCCAT 1009  
DB 735 GCCTTCAATCAGCAGCAGCAATATCTTCTGATTTGGCGCGCGCTCTCATCCCAT 794  
QY 1010 GTATTTCCAGTACAGATCATCATGACCATGCTGCTCAAGAACTGGGTGGACCTGGC 1069  
DB 795 GTATTTCCAGTACAGATCATCATGACCATGCTGCTCAAGAACTGGGTGGACCTGGC 854  
QY 1070 CTGGGCGGTGAGTATACATCCGGTCTTTCATCAGTACATCCCTTTCTACGGCATCT 1129  
DB 855 CTGGGCGGTGAGTATACATCCGGTCTTTCATCAGTACATCCCTTTCTACGGCATCT 914  
QY 1130 GGGAGCCCTCTTTTCTCAACTTCATCAGTTCTGGAGAGCACTGTTGTGTGGGT 1189  
DB 915 GGGAGCCCTCTTTTCTCAACTTCATCAGTTCTGGAGAGCACTGTTGTGTGGGT 974  
QY 1190 CACACAGATGAATCAGATCATCATGATGAGATGACAGAGGCTTACCGTACGTGTTAG 1249  
DB 975 CACACAGATGAATCAGATCATCATGATGAGATGACAGAGGCTTACCGTACGTGTTAG 1034  
QY 1250 TAGCCAGTGCAGCAGCAGCTGCAACGTGGAGAGTCTCTTCAACGACTGGTTCAGTGG 1309  
DB 1035 TAGCCAGTGCAGCAGCAGCTGCAACGTGGAGAGTCTCTTCTCAAGACTGGTTCAGTGG 1094  
QY 1310 ACACCTTAACTTCAGATTGAGCAGCAGCAGCTCTTCCCAACATGCCCGGCAACATTA 1369  
DB 1095 ACACCTTAACTTCAGATTGAGCAGCAGCAGCTCTTCCCAACATGCCCGGCAACATTA 1154  
QY 1370 CAAGATGCCCGCGTGTGAAGTCTCTATGTGCAAGACTGGCATTTGAATACCAAGAGAA 1429  
DB 1155 CAAGATGCCCGCGTGTGAAGTCTCTATGTGCAAGACTGGCATTTGAATACCAAGAGAA 1214  
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DB 1515 GCCATGAGCCAGTGGCCCTCCAGTGGCTCTTAGGCCCTTCTTCCAGAGAGAGAGAGTG 1574  
QY 1790 GCCACCGGGGTGGCTGTCTTACCTCCACTCTCTGCCCCCTAAAGATGGAGAGAGCA 1849  
DB 1575 GCCACCGGGGTGGCTGTCTTACCTCCACTCTCTGCCCCCTAAAGATGGAGAGAGCA 1634





195 CAAGGCGCTGTGAAGAGTATGAACTCTCTCTCTGATTGAGAACTGTCTCAGAGCA 254  
 473 GCCACGACGAGCAACGCGCAAGAACTCAAGATCACTAGAGACTTCCGGGCCCTGAGGAA 532  
 255 GCCAGCTTTGAGCCCAACCAAGATTAAGAGAGTGCACATGATGTTCCGGGAGCTGCGGCG 314  
 533 GACGGCTGAGGACATGAACCTGTTCAAGACCAACACAGTGTCTTCTCTCTCTCTCTCTG 592  
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 593 CCACATCATGCGCCCTGGAGAGCAATGCAATGATGATGATGATGATGATGATGATGATG 652  
 375 GCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 434  
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RESULT 19  
 AAV63642  
 ID AAV63642 standard; cDNA; 1843 BP.  
 XX  
 AC AAV63642;  
 XX

DT 15-FEB-1999 (first entry)  
 XX Contig 2535 encoding a human desaturase enzyme.  
 DE Fatty acid; desaturase; polyunsaturated fatty acid;  
 XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome; human;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
 XX Homo sapiens.  
 OS WO9846763-A1.  
 FN 22-OCT-1998.  
 XX 10-APR-1998; 98WO-US07126.  
 XX 11-APR-1997; 97US-0834655.  
 PR (ABBO) ABBOTT LAB.  
 XX (CALJ) CALGENE LLC.  
 PA Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 XX WPI; 1998-594582/50.  
 DR P-PSDB; AAW84155.  
 XX New isolated fatty acid desaturase enzymes - used for the production  
 of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
 compositions, nutritional compositions, cosmetics or animal feed  
 XX Example 12; Pages 116-117; 165pp; English.  
 PS The present sequence encodes a human desaturase enzyme. The sequence was  
 CC identified based on homology between human cDNA sequences and Mortierella  
 CC alpina desaturase gene sequences. The specification describes methods for  
 CC desaturating a fatty acid and for producing a desaturated fatty acid by  
 CC expressing increased levels of a desaturase. The enzyme can be used for  
 CC desaturating fatty acids. The enzyme can be used to produce  
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,  
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The  
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis  
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma,  
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They  
 CC can also be used to inhibit platelet aggregation, cause vasodilation,  
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth  
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding  
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,  
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic  
 CC encephalomyelitis and chronic fatigue after viral infections, treat  
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and  
 CC inflammatory skin disorders.  
 XX Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;  
 SQ  
 Query Match 57.5%; Score 1830.4; DB 19; Length 1843;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 630 GTCCTCTACTTGGCAATGGCTGGATTCCTACCTCATCAGCGCTTTGTCTCTGCTACC 689  
 |||||TACTTTGGCAATGGCTGGATTCCTACCTCATCAGCGCTTTGTCTCTGCTACC 60  
 |||||GGCCCAAGCTGGATGGCTGCAATGATATTAGCCACCTGTCTGTCTACAGAAA 749  
 |||||GGCCCAAGCTGGATGGCTGCAATGATATTAGCCACCTGTCTGTCTACAGAAA 120  
 |||||AGTGAACCAACCTGTGCACAAATTCGTCATTTGAGGCTTAAAGGGTGCCTCTGCC 809  
 |||||AGTGAACCAACCTGTGCACAAATTCGTCATTTGAGGCTTAAAGGGTGCCTCTGCC 180

810 AACTGTGGAAATCATGCCACTTCCAGCACAGCCCAAGCCTAACATCTTCCACAGGAT 869  
 181 AACTGTGGAAATCATGCCACTTCCAGCACAGCCCAAGCCTAACATCTTCCACAGGAT 240  
 870 CCCGATGTGAACATGCTGCAGCTGTTTGTCTGGGCGAAATGGCAGCCCATCGAGTACGGC 929  
 241 CCCGATGTGAACATGCTGCAGCTGTTTGTCTGGGCGAAATGGCAGCCCATCGAGTACGGC 300  
 930 AAGAAGAGCTGAAATACCTGCGCTCAATCAATCAGCAGCAAGAAATCTTCTCTGATTTGGG 989  
 301 AAGAAGAGCTGAAATACCTGCGCTCAATCAATCAGCAGCAAGAAATCTTCTCTGATTTGGG 360  
 990 CGCGCGTGTCTATCCCATCTGATTTCCAGTACCAGATCATCATGACCATGCTCCAT 1049  
 361 CGCGCGTGTCTATCCCATCTGATTTCCAGTACCAGATCATCATGACCATGCTCCAT 420  
 1050 AAGAAGAGCTGAAATACCTGCGCTCAATCAATCAGCAGCAAGAAATCTTCTCTGATTTGGG 1109  
 421 AAGAAGAGCTGAAATACCTGCGCTCAATCAATCAGCAGCAAGAAATCTTCTCTGATTTGGG 480  
 1110 ATCCCTTTTACGGCATCTGCGGAGCCCTCTTCTCTCACTTCACTGATTTCTGAG 1169  
 481 ATCCCTTTTACGGCATCTGCGGAGCCCTCTTCTCTCACTTCACTGATTTCTGAG 540  
 1170 AGCCACTGTTGTGTGGGTCAACAGATGAATCACATCGTCACTGAGATTCAGCAGG 1229  
 541 AGCCACTGTTGTGTGGGTCAACAGATGAATCACATCGTCACTGAGATTCAGCAGG 600  
 1230 GCTTACCTGTACTGTTGAGTACAGCAGTGCAGCAGCAGTGCAGGAGGAGGAGTCTTC 1289  
 601 GCTTACCTGTACTGTTGAGTACAGCAGTGCAGCAGCAGTGCAGGAGGAGTCTTC 660  
 1290 TTTCAACGACTGTTTCACTGAGCAGCAGTGCAGGAGTGCAGCAGCAGTCTTCTCCAC 1349  
 661 TTTCAACGACTGTTTCACTGAGCAGCAGTGCAGGAGTGCAGCAGCAGTCTTCTCCAC 720  
 1350 ATGCCCGGCAACATTTACAGATTCGCGCGCTGTTGAGTCTTATGTGCAAGCAT 1409  
 721 ATGCCCGGCAACATTTACAGATTCGCGCGCTGTTGAGTCTTATGTGCAAGCAT 780  
 1410 GSCATTGAATACAGAGAGCGCTACTGAGGCGCTGCTGAGCATCATCAGTCTCCCTG 1469  
 781 GSCATTGAATACAGAGAGCGCTACTGAGGCGCTGCTGAGCATCATCAGTCTCCCTG 840  
 1470 AAGAAGTCTGGAAGCTGTGGTGGAGCCTTACCTTCAATGAAGCAGCAGCAGCAG 1529  
 841 AAGAAGTCTGGAAGCTGTGGTGGAGCCTTACCTTCAATGAAGCAGCAGCAGCAG 900  
 1530 GACACGTTGGGAGGAGTGCAGGTTGGTGTGATGCCAGAGGAATGATGGGCTTTTGTTC 1589  
 901 GACACGTTGGGAGGAGTGCAGGTTGGTGTGATGCCAGAGGAATGATGGGCTTTTGTTC 960  
 1590 TGAGGGGTCTCCGAGAGGCTGTGTATGCTATGCTCAAGGAGCAGCAGCAGTGTGATCTTCT 1649  
 961 TGAGGGGTCTCCGAGAGGCTGTGTATGCTATGCTCAAGGAGCAGCAGCAGTGTGATCTTCT 1020  
 1650 CCCTTTCT 1709  
 1021 CCCTTTCT 1080  
 1710 CTGCCCCCT 1769  
 1081 CTGCCCCCT 1140  
 1770 TTCCAAAGGAGCAGAGAGTGGCCACCGGGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 1829  
 1141 TTCCAAAGGAGCAGAGAGTGGCCACCGGGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 1200  
 1830 CTAAAGATGGGAGGAGCAGCAGGCTCCATGGGTCTGGCTGTGGCTGTGGCTGTGGCTGTGG 1889  
 1201 CTAAAGATGGGAGGAGCAGCAGGCTCCATGGGTCTGGCTGTGGCTGTGGCTGTGGCTGTGG 1260

PR 11-APR-1997; 97US-0834033.  
PR 11-APR-1997; 97US-0834655.  
PA (ALBO ) ABBOTT LAB.  
PA (CALB ) CALGENE LLC.  
XX  
XX Chaudhary S, Huang Y, Knutzen D, Leonard AE, Mukerji P;  
PI Thurmond J;  
XX  
XX WP1; 1999-080739/07.  
DR P-FSDB; AAWS5513.  
DR  
XX  
XX Nucleic acid construct able to express fatty acid desaturase in  
PT plants - useful in human or animal nutrition, as cosmetics and  
PT therapeutically, e.g. for restenosis, cancer and diabetes  
PT  
XX  
XX Claim 48; Page 160-161; 210pp; English.  
XX  
XX The invention relates to a nucleic acid construct that contains at least  
CC one of the nucleotide sequences (AAW00889 to AAW00891) encoding  
CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AAW95504 to  
CC AAW95506) respectively coupled to an expression control sequence  
CC functional in plants. Recombinant plant cells containing at least one DNA  
CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the  
CC production of polyunsaturated fatty acid (PUFA). These recombinant cells  
CC or plants containing them are used to produce oils such as linoleic  
CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic  
CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils  
CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or  
CC dietary supplements or substitutes, for use in humans or animals; (iii)  
CC for treating disorders associated with inadequate consumption or  
CC production of PUFA (or their metabolites such as prostaglandins), e.g.  
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,  
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,  
CC and (v) as animal feeds. Fragments of the DNA are used as probes to  
CC isolate related coding sequences. Recombinant plants can produce high  
CC yields of PUFA, since new pathways can be created and unwanted ones  
CC suppressed. Plants can be engineered to express oils of particular PUFA  
CC composition, e.g. one similar to that in human milk, and product recovery  
CC is simpler than with e.g. fish. Sequences AAW00904-910 represent DNA  
CC sequences of various contigs of human desaturase genes which are similar  
CC to the M. alpina desaturase sequences.  
XX  
XX Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

AAX00909  
ID AAX00909 standard; DNA; 1843 BP.

Query Match 57 58. Score 1830 4. DB 20. Length 1843.

Best Local Similarity 99.9%; Pred: No. 0;  
Matches 1842: Conservative 0: Mismatches 1: Indels 1: Gaps 1

07 639 539

| Accession | Sequence  | Length |
|-----------|---|--------|
| Dδ        | 1 GTCTTTTACTTTGGCAATGGCTGGATTCTTACCTCATCACGCCCTTGTCTTGTGTACG 60     | 60     |
| Qγ        | 690 TCTAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAAA 749 | 749    |
| Dδ        | 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAAA 120 | 120    |

750 CCCAAGTGGAAACCACTTGTCCACAAATTCGTCAATTGCCCACTTAAAGGGTGCCCTCTGCC 809  
QY  
QY

121 CCCAAGTGGAAACCACCTTGTCTCCACAATTCGTCA<sup>1</sup>TGGCCACTTAAGGGTGCCTCTGCC 180

QY 810 AACTGGTGAATCATCGCCACTTCCAGCACCGCCACGCTAACATCTTCCACAAGGAT 869

100

DB 181 AACGCTGGAAATCATCGCCACTTCCAGCACCCAGCCTAACATCTTCCACAAGGAT 240

[illegible]

QY 870 CCCGATGTAACATGCTGCACGGTGTTCGATCTCGGCGAATGGCAGCCCATCGAGTACGGC 523

241 CCCGATGTGAACATGCTGCACGTGTTTGTCTCGGGGAATGGCAGCCCATCGAGTACGGC 300 Db

930 AAGAAGAGCTGAATACCTGCCCTACAATCACCAGCACGAATACTTCTTCCTGATTGGG 989

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities related to the project. It emphasizes the need for transparency and accountability in financial management.

2. The second part outlines the various methods used to collect and analyze data, ensuring that the information gathered is reliable and valid. This includes both qualitative and quantitative approaches.

3. The third section details the results of the research, highlighting key findings and trends observed during the study period. It provides a comprehensive overview of the data collected.

4. Finally, the fourth part presents conclusions drawn from the analysis, along with recommendations for future research and practical applications based on the findings.

301 AAGAAGAAGCTGAAAATACCTGCCCCTACAAATCACCGACGGAATACTTCTTCTGATGGG 360



CC desaturated fatty acid by expressing increased levels of a desaturase.  
 CC The enzyme can be used for desaturating fatty acids. The enzyme can be  
 CC used to produce polyunsaturated fatty acids, which can be used for  
 CC treating malnutrition, in pharmaceutical compositions, in cosmetics or  
 CC in animal feed. The polyunsaturated fatty acids can be used for treating  
 CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,  
 CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.  
 CC They can also be used to inhibit platelet aggregation, cause  
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel  
 CC wall smooth muscle and fibrous tissue, reduce or prevent  
 CC gastro-intestinal bleeding and other side effects caused by non-steroidal  
 CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual  
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after  
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory  
 CC syndrome, hypertension and inflammatory skin disorders.  
 XX  
 SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Query Match 57.5%; Score 1830.4; DB 20; Length 1843;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 630 GTCTTCTACTTTGGGAATGGCTGGATTCCTACCTCTATCAGGCGTTTGTCTGTAC 689  
 DB 1 GTCTTTTACTTTGGGAATGGCTGGATTCCTACCTCTATCAGGCGTTTGTCTGTAC 60

QY 690 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 749  
 DB 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAA 120

QY 750 CCCAGTGGAAACACCTTTGTCTCAAAATCTGTATTTGGCCACTTAAAGGTGTCTGTCC 809  
 DB 121 CCCAAGTGAACACCTTTGTCTCAAAATCTGTATTTGGCCACTTAAAGGTGTCTGTCC 180

QY 810 AACTGTGGAATCATCGCCACTTCAGACACCAAGCCCTCAATCTTCCACAGGAT 869  
 DB 181 AACTGTGGAATCATCGCCACTTCAGACACCAAGCCCTCAATCTTCCACAGGAT 240

QY 870 CCGATGTGAACATCGCTGCACTGTCTTTGTTCTGGGCGAATGGAGCCCATCGATAGCGC 929  
 DB 241 CCGATGTGAACATCGCTGCACTGTCTTTGTTCTGGGCGAATGGAGCCCATCGATAGCGC 300

QY 930 AAGAAGACTGAATACCTGCGCTTACAAATCACAGACCAAGAACTTCTTCTGATTGGG 989  
 DB 301 AAGAAGACTGAATACCTGCGCTTACAAATCACAGACCAAGAACTTCTTCTGATTGGG 360

QY 990 CCGCGCTGCTCATCCCATGATTTTCCAGTACAGATCATCATGACATGATGCTCCAT 1049  
 DB 361 CCGCGCTGCTCATCCCATGATTTTCCAGTACAGATCATCATGACATGATGCTCCAT 420

QY 1050 AAGAAGCTGGGTGGAACCTGGCGCTGGCGCTCAGCTACTACATCCGGTTCTTATCACCTAC 1109  
 DB 421 AAGAAGCTGGGTGGAACCTGGCGCTGGCGCTCAGCTACTACATCCGGTTCTTATCACCTAC 480

QY 1110 ATCCCTTTCTAGGGATCCTGGAGCCCTCTTTTCTCACTTCATCAGTTCTCTGGAG 1169  
 DB 481 ATCCCTTTCTAGGGATCCTGGAGCCCTCTTTTCTCACTTCATCAGTTCTCTGGAG 540

QY 1170 AGCACTGTTTGTGTGGGTACACAGATGAATCACATCGTCAATGGAGATTGACCAAGAG 1229  
 DB 541 AGCACTGTTTGTGTGGGTACACAGATGAATCACATCGTCAATGGAGATTGACCAAGAG 600

QY 1230 GCTACCGTGTACTGTTTGTAGTACAGCTGACAGCCACCTGCACTGAGGAGTCTCTTC 1289  
 DB 601 GCTACCGTGTACTGTTTGTAGTACAGCTGACAGCCACCTGCACTGAGGAGTCTCTTC 660

QY 1290 TTCAAGCTGTTTCACTGTGACACCTTAACTTCCAGATTGAGACCACTCTTCCCAACC 1349  
 DB 661 TTCAAGCTGTTTCACTGTGACACCTTAACTTCCAGATTGAGACCACTCTTCCCAACC 720

QY 1350 ATGCCCGGACAACTTACACAGATCGCCCGCTGTGTGATCTCTATGTGCAAGCAT 1409  
 DB 721 ATGCCCGGACAACTTACACAGATCGCCCGCTGTGTGATCTCTATGTGCAAGCAT 780

QY 1410 GGCAATTGAATACAGAGGAGCGGCTACTAGGGCCCTGCTGGACATCATCAGGTCCCTG 1469  
 DB 781 GGCAATTGAATACAGAGGAGCGGCTACTAGGGCCCTGCTGGACATCATCAGGTCCCTG 840

QY 1470 AAGAAGTCTCGGAAGCTGTGGCTGAGCGCTACCTTCAAAATGAAGGACACAGCCCGG 1529  
 DB 841 AAGAAGTCTCGGAAGCTGTGGCTGAGCGCTACCTTCAAAATGAAGGACACAGCCCGG 900

QY 1530 GACACCGTGGGAGGAGGCTGAGGTGGGTGATGGCCAGAGGAATGATGGGCTTTTGTTC 1589  
 DB 901 GACACCGTGGGAGGAGGCTGAGGTGGGTGATGGCCAGAGGAATGATGGGCTTTTGTTC 960

QY 1590 TGAGGGGTGTCAGAGAGGCTGTGTATGACCTGTACAGGACCCCATGTGTGATCTTCT 1649  
 DB 961 TGAGGGGTGTCAGAGAGGCTGTGTATGACCTGTACAGGACCCCATGTGTGATCTTCT 1020

QY 1650 CCTTTCT 1709  
 DB 1021 CCTTTCT 1080

QY 1710 CTGCGCT 1769  
 DB 1081 CTGCGCT 1140

QY 1770 TTCAAAGGAGCAGAGAGGTGGCCACCGGGGGTGGCTCTCTCTCTCTCTCTCTCTCT 1829  
 DB 1141 TTCAAAGGAGCAGAGAGGTGGCCACCGGGGGTGGCTCTCTCTCTCTCTCTCTCTCTCT 1200

QY 1830 CTTAAAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1889  
 DB 1201 CTTAAAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260

QY 1890 TGGTCACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1949  
 DB 1261 TGGTCACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320

QY 1950 GGTCTCTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2009  
 DB 1321 GGTCTCTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380

QY 2010 CCATTGCTTCAACCTTTTCTATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2069  
 DB 1381 CCATTGCTTCAACCTTTTCTATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440

QY 2070 GCAGCTCGGTTAAGTACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2129  
 DB 1441 GCAGCTCGGTTAAGTACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500

QY 2130 ACAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2189  
 DB 1501 ACAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560

QY 2190 ACCCTGGGCTTTCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2249  
 DB 1561 ACCCTGGGCTTTCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620

QY 2250 ACCAAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2309  
 DB 1621 ACCAAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

QY 2310 GGGGCGGCTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2369  
 DB 1681 GGGGCGGCTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740

QY 2370 TCCAAAGATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2429  
 DB 1741 TCCAAAGATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800

QY 2430 CAGCCAAATTCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2473  
 DB 1801 CAGCCAAATTCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1843



|  |  |  |  |  |  |
|--|--|--|--|--|--|
| <p>RESULT 22<br/>ID AAA49938 standard; cDNA; 1843 BP.</p>  |  |  |  |  |  |
| <p>AC AAA49938;<br/>DT 10-OCT-2000 (first entry)<br/>XX Human delta-5-desaturase-related contig 2535.<br/>DE Delta-5-desaturase; human; polyunsaturated fatty acid;<br/>KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;<br/>KW docosahexaenoic acid; nutrition; feedstuff; ss.<br/>OS Homo sapiens.<br/>XX Key Location/Qualifiers<br/>FH 1..885<br/>FT CDS /tag= a<br/>XX</p>  |  |  |  |  |  |
| <p>XX WO200040705-A2.<br/>XX 13-JUL-2000.<br/>XX 29-DEC-1999; 99WO-US31163.<br/>XX 08-JAN-1999; 99US-0227613.<br/>XX (ABBO ) ABBOTT LAB.<br/>XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;<br/>PI WFI; 2000-465975/40.<br/>DR P-PSDB; AA95448.<br/>XX New polypeptide useful for preparation of nutritional supplements based<br/>PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids<br/>PT at carbon 5 -<br/>XX Example 1; Fig 7; 127pp; English.</p>   |  |  |  |  |  |
| <p>CC The present sequence is that of contig 2535, a contig produced<br/>CC from overlapping contigs 2511785 (see AAA49937) and 3506132 (see<br/>CC AAA49935), which were isolated from the Incyte Lifeseq database on<br/>CC the basis of homology to Mortierella alpina delta-5-desaturase and<br/>CC delta-6-desaturase cDNA sequences. The contig includes a partial<br/>CC open reading frame. It overlaps with another isolated contig,<br/>CC 3554933 (see AAA49936), creating a final contig, 253338a (see<br/>CC AAA49939), that contains a partial open reading frame which aligns<br/>CC with M. alpina delta-5 and delta-6-desaturase sequences. The<br/>CC contig was utilised in the isolation of cDNA (see AAA49932) encoding<br/>CC human delta-5-desaturase (see AA95445). Delta-5-desaturase<br/>CC catalyzes the conversion of dihomogamma-linolenic acid to<br/>CC arachidonic acid and of 20:4n-3 to eicosapentaenoic acid.<br/>CC Reconstituted enzyme, expressed in prokaryotic or eukaryotic hosts<br/>CC using the isolated human delta-5-desaturase cDNA, can be used in<br/>CC the production of polyunsaturated fatty acids that may be added to<br/>CC nutritional, veterinary and pharmaceutical compositions.</p> |  |  |  |  |  |
| <p>XX Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;<br/>SQ Query Match 57.5%; Score 1830.4; DB 21; Length 1843;<br/>Best Local Similarity 99.9%; Pred. No. 0;<br/>Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;</p>   |  |  |  |  |  |
| <p>QY 630 GTCCTTACTTTGGCAATGCGTGGAATCCTACCCTCATCAGGCCTTGCTGTCTTACC 689<br/>Db 1 GCTTTTACTTTGGCAATGCGTGGAATCCTACCCTCATCAGGCCTTTGCTGTCTTACC 60</p>   |  |  |  |  |  |
| <p>QY 690 TTCAGGCCAAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 749<br/>Db 61 TTCTCAGGCCAAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120</p>  |  |  |  |  |  |







PS Example 9; Page 147-148; 161pp; English.

XX AAA14588-94 represent contigs of a human desaturase. The specification

CC describes a Mortierella alpina delta5-desaturase. The protein is

CC involved in the biosynthesis of poly-unsaturated long chain fatty

CC acids (PUFAs). The polynucleotide is to produce PUFAs, especially

CC arachidonic acid. The oils produced by the invention are used in

CC pharmaceutical compositions, infant formulas, dietary supplements,

CC dietary substitutes, and cosmetics. The nutritional compositions can be

CC used to treat normal individuals temporality exposed to stress, or

CC individuals having specialized needs due to chronic or acute diseases

CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or

CC malabsorption, and other disorders such as restenosis after angioplasty,

CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,

CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated

CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,

CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,

CC acute respiratory syndrome, hypertension, inflammatory skin disorders,

CC as well as reduce blood score, inhibit platelet aggregation, cause

CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and

CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for

CC geriatric treatments).

XX SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;

Query Match 57.5%; Score 1830.4; DB 21; Length 1843;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 630 GTCTTCTACTTTGGCAATGGCTGGATTCCTACCTCATCAGCGCCCTTGTCTTGTCTAC 689

DB 1 GTCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCAGCGCCCTTGTCTTGTCTAC 60

QY 690 TCTCAGGCCCAAGCTGGATGGCTGGCAATGATATGGCCACTGTCTGTCTACAGAAA 749

DB 61 TCTCAGGCCCAAGCTGGATGGCTGGCAATGATATGGCCACTGTCTGTCTACAGAAA 120

QY 750 CCCAAGTGGAAACCACTTGTCCCAAAATTCGTATTGGCCACTTAAAGGGTGGCTTGGCC 809

DB 121 CCCAAGTGGAAACCACTTGTCCCAAAATTCGTATTGGCCACTTAAAGGGTGGCTTGGCC 180

QY 810 AACTGTGGGAATCATGCCCACTTCCAGCAACCAAGCCCAAGCTTAACTTCCCAAGGAT 869

DB 181 AACTGTGGGAATCATGCCCACTTCCAGCAACCAAGCCCAAGCTTAACTTCCCAAGGAT 240

QY 870 CCGGATGTGAATCATGCCCACTTCCAGCAACCAAGCCCAAGCTTAACTTCCCAAGGAT 929

DB 241 CCGGATGTGAATCATGCCCACTTCCAGCAACCAAGCCCAAGCTTAACTTCCCAAGGAT 300

QY 930 AAGAAGAGCTGAAATACCTTCCAGCAACCAAGCCCAAGCTTAACTTCCCAAGGAT 989

DB 301 AAGAAGAGCTGAAATACCTTCCAGCAACCAAGCCCAAGCTTAACTTCCCAAGGAT 360

QY 990 CCGCGCTGTCTATCCCAATGATTTCCAGTACCAATCATATGATGATGATGATGATGAT 1049

DB 361 CCGCGCTGTCTATCCCAATGATTTCCAGTACCAATCATATGATGATGATGATGATGAT 420

QY 1050 AAGAAGCTGGGTGGACCTTGGCGGTGAGTACTTACATCCGGTTCCTTCACTACCTAC 1109

DB 421 AAGAAGCTGGGTGGACCTTGGCGGTGAGTACTTACATCCGGTTCCTTCACTACCTAC 480

QY 1110 ATCCCTTTTACGGCATCTGGAGCCCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1169

DB 481 ATCCCTTTTACGGCATCTGGAGCCCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540

QY 1170 AGCCACTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1229

DB 541 AGCCACTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600

QY 1230 GCCTTACCGTGTACTGGTGTACTGATCCAGTGTACAGCCACCTTGGAGTGGAGTCTTTC 1289

DB 601 GCCTTACCGTGTACTGGTGTACTGATCCAGTGTACAGCCACCTTGGAGTGGAGTCTTTC 660

QY 1290 TTCAACGAGCTGGTTTCACTGAGACACCTTAACTTCCAGATTGAGCACCACCTTCTTCCCCACC 1349

DB 661 TTCAACGAGCTGGTTTCACTGAGACACCTTAACTTCCAGATTGAGCACCACCTTCTTCCCCACC 720

QY 1350 ATGCCCGGCGACAACTTACACAGATCGCCCGCTGGTGAAGTCTTATGTGCCAGCAT 1409

DB 721 ATGCCCGGCGACAACTTACACAGATCGCCCGCTGGTGAAGTCTTATGTGCCAGCAT 780

QY 1410 GGCATTGAATACACAGAGAGAGCGCTTACTGAGGGCCCTCTGTCGACATCATCAGGTCCCTG 1469

DB 781 GGCATTGAATACACAGAGAGAGCGCTTACTGAGGGCCCTCTGTCGACATCATCAGGTCCCTG 840

QY 1470 AAGAAGTCTGGGAAGCTGTGGCTGAGACCTTCAAAATGAGCCACAGCCCGCCG 1529

DB 841 AAGAAGTCTGGGAAGCTGTGGCTGAGACCTTCAAAATGAGCCACAGCCCGCCG 900

QY 1530 GACACCTGTGGGAAGGGGTGACAGTGGGGTGTATGGCCAGAGGAATGATGGGTCTTGTTC 1589

DB 901 GACACCTGTGGGAAGGGGTGACAGTGGGGTGTATGGCCAGAGGAATGATGGGTCTTGTTC 960

QY 1590 TGAGGGGTGTCCAGAGAGGTGTGTATGACATCTCAGGACCCCATGTGATCTTCT 1649

DB 961 TGAGGGGTGTCCAGAGAGGTGTGTATGACATCTCAGGACCCCATGTGATCTTCT 1020

QY 1650 CCCTTCT 1709

DB 1021 CCCTTCT 1080

QY 1710 CTGCCCCCTCTCAGCCGTGAGCCATCAGCCATGGCCCTCCAGTGTCTCTAGCCCTTTC 1769

DB 1081 CTGCCCCCTCTCAGCCGTGAGCCATCAGCCATGGCCCTCCAGTGTCTCTAGCCCTTTC 1140

QY 1770 TTCCAGAGGACAGAGAGGTGGCCACCGGGGTGGCTGTGCTTACCTTCCACTCTCTGCCC 1829

DB 1141 TTCCAGAGGACAGAGAGGTGGCCACCGGGGTGGCTGTGCTTACCTTCCACTCTCTGCCC 1200

QY 1830 CTAAAGATGGAGAGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTTCAGCC 1889

DB 1201 CTAAAGATGGAGAGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTTCAGCC 1260

QY 1890 TGGTCACTAGGCATCACCCCGCTTTTGGTCTTTCAGATGCTCTTGGGTTCATAGGGCA 1949

DB 1261 TGGTCACTAGGCATCACCCCGCTTTTGGTCTTTCAGATGCTCTTGGGTTCATAGGGCA 1320

QY 1950 GGTCTTGTCTGGGCGAGGGCCCTTGAACCTTCCGGCTGTGCTTCACTCTCCCTGACGGCTG 2009

DB 1321 GGTCTTGTCTGGGCGAGGGCCCTTGAACCTTCCGGCTGTGCTTCACTCTCCCTGACGGCTG 1380

QY 2010 CCATTGGTCCACCCCTTTTCATAGAGAGGCTGTGTTGTTTACAAAGCTCGGCTCTCCCTCT 2069

DB 1381 CCATTGGTCCACCCCTTTTCATAGAGAGGCTGTGTTGTTTACAAAGCTCGGCTCTCCCTCT 1440

QY 2070 GCAGCTGGTTPAAGTACCCGAGGCTCTCTTAAAGATCTCAGGGCCCGAGCCCGCGGGC 2129

DB 1441 GCAGCTGGTTPAAGTACCCGAGGCTCTCTTAAAGATCTCAGGGCCCGAGCCCGCGGGC 1500

QY 2130 ACAGCCAGCCAAACCTTGGCCCTTGGAGAGTCTTCCACCCCATCTACTAGAGTCTG 2189

DB 1501 ACAGCCAGCCAAACCTTGGCCCTTGGAGAGTCTTCCACCCCATCTACTAGAGTCTG 1560

QY 2190 ACCCTGGGCTTTACGGGGCCCTTTCACCGCCCTTCCCAACTTGAAGCTGTGACCTTGGG 2249

DB 1561 ACCCTGGGCTTTACGGGGCCCTTTCACCGCCCTTCCCAACTTGAAGCTGTGACCTTGGG 1620

QY 2250 ACCAAAGGGGAGTCTCTGCTCTTGTGACTCAGCAGAGGAGTGGCCAGTTCAGGGA 2309

DB 1621 ACCAAAGGGGAGTCTCTGCTCTTGTGACTCAGCAGAGGAGTGGCCAGTTCAGGGA 1680

QY 2310 GGGGCGGCTGGCTGGAGGCTCAGCCCATCTCCAGCTTTTCTCAGGGTGTCTCTGAGG 2369

DB 1681 GGGGCGGCTGGCTGGAGGCTCAGCCCATCTCCAGCTTTTCTCAGGGTGTCTCTGAGG 1740

QY 2370 TCCAAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTTATCAGCTGGGCGAGTGC 2429

|   |                                  |  |      |
|---|----------------------------------|--|------|
| Db  | 1741                             | TCCAGAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGGCTCTGTATACAGCTGGGCAGTGC   | 1800 |
| Qy  | 2430                             | CAGGCAATCCCTGGCCATTGGCCCCCAGGGGACGTGGGCCCTG  | 2473 |
| Db  | 1801                             | CAGCCCAATCCCTGGCCATTGGCCCCA-GGGGACGTGGGCCCTG   | 1843 |
| RESULT 25   |                                  |  |      |
| ABS71825  |                                  |  |      |
| ID  | ABS71825 standard; DNA; 1843 BP. |  |      |
| XX  | AC                               | ABS71825;  |      |
| XX  | DT                               | 02-DEC-2002 (first entry)  |      |
| XX  | DE                               | Human deltas-desaturase gene #7.   |      |
| XX  | KW                               | Human; deltas-desaturase; polyunsaturated fatty acid; DGLA;  |      |
| KW  | KW                               | dihomo-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;  |      |
| KW  | KW                               | eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;  |      |
| XX  | OS                               | gene; ds.  |      |
| XX  | OS                               | Homo sapiens.  |      |
| XX  | PN                               | US6432684-B1.  |      |
| XX  | PD                               | 13-AUG-2002.   |      |
| XX  | PF                               | 08-JAN-1999; 99US-0227613.   |      |
| XX  | PR                               | 11-APR-1997; 97US-0833610.   |      |
| PR  | PR                               | 10-APR-1998; 98WO-US07422.   |      |
| XX  | PA                               | (ABBO ) ABBOTT LAB.  |      |
| XX  | PI                               | Mukerji P, Leonard AE, Huang Y, Das T;   |      |
| XX  | DR                               | WPI; 2002-689761/74.   |      |
| XX  | PT                               | Nucleic acids encoding human DELTA5-desaturase, useful for catalysing the conversion of dihomogamma-linolenic acid to arachidonic acid and in the conversion of 20:4n-3 to eicosapentaenoic acid -   |      |
| XX  | PS                               | Example 1; Figure 7; 88pp; English.  |      |
| XX  | CC                               | The invention relates to an isolated human deltas-desaturase nucleotide sequence (I) which desaturates polyunsaturated fatty acids at carbon 5. The nucleotide sequence (I) may be used in the recombinant production of vectors and host cells for the production of deltas-desaturase. Deltas-desaturase may be utilised in the conversion of dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or polyunsaturated fatty acids produced from it may be added to pharmaceutical compositions, nutritional compositions, animal feeds, as well as other products such as cosmetics. ABS71819-ABS71854 |      |
| CC  | CC                               | represent human deltas-desaturase coding sequences and PCR primers of the invention.   |      |
| XX  | SQ                               | Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;   |      |
| Query Match 57.5%; Score 1830.4; DB 24; Length 1843;          |                                  |  |      |
| Best Local Similarity 99.9%; Pred. No. 0;                     |                                  |  |      |
| Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1; |                                  |  |      |
| Qy  | 630                              | GTCTTCTACTTTGGCAATGGCTGGATTCCTACCTCATCAGGCGCTTGTCTGTCTAC   | 689  |
| Db  | 1                                | GTCTTCTACTTTGGCAATGGCTGGATTCCTACCTCATCAGGCGCTTGTCTGTCTAC   | 60   |
| Qy  | 690                              | TCTCAGGCCCAAGTGGTGGCTGCACATGATTATGGCCACCTGTCTGTCTACAGAAA   | 749  |
| Db  | 61                               | TCTCAGGCCCAAGTGGTGGCTGCACATGATTATGGCCACCTGTCTGTCTACAGAAA   | 120  |

|    |      |   |      |
|----|------|---|------|
| Qy | 750  | CCCAAGTGGAAACCACTTGTTCACAAATTCGTTCNTTGGCCACTTAAAGGGTCTCTGGCC  | 809  |
| Db | 121  | CCCAAGTGGAAACCACTTGTTCACAAATTCGTTCNTTGGCCACTTAAAGGGTCTCTGGCC  | 180  |
| Qy | 810  | AACCTGTGGAATCATCGCCACTTCCAGCACCCAGCCCAAGCCTAACATCTTCCAAAGGAT  | 869  |
| Db | 181  | AACCTGTGGAATCATCGCCACTTCCAGCACCCAGCCCAAGCCTAACATCTTCCAAAGGAT  | 240  |
| Qy | 870  | CCCGATGTGAACATGCTGCACGTGTTTGTCTCTGGGGAATGGCAGCCCATCGAGTACGGC  | 929  |
| Db | 241  | CCCGATGTGAACATGCTGCACGTGTTTGTCTCTGGGGAATGGCAGCCCATCGAGTACGGC  | 300  |
| Qy | 930  | AAGAAGAGCTGAAATACCTTGCCTCAATCAATCAACAGCAGGAATCTTCTTCTGATTGGG  | 989  |
| Db | 301  | AAGAAGAGCTGAAATACCTTGCCTCAATCAATCAACAGCAGGAATCTTCTTCTGATTGGG  | 360  |
| Qy | 990  | CCGCCGTCTCATCCCATGTAATTTCCAGTACAGATCATCATGACCATGATGCTCCAT     | 1049 |
| Db | 361  | CCGCCGTCTCATCCCATGTAATTTCCAGTACAGATCATCATGACCATGATGCTCCAT     | 420  |
| Qy | 1050 | AAGAACTGGGTGGACCTGGGCGCTGAGCTACTACATCCGGTTCCTTATCATCACTAC     | 1109 |
| Db | 421  | AAGAACTGGGTGGACCTGGGCGCTGAGCTACTACATCCGGTTCCTTATCATCACTAC     | 480  |
| Qy | 1110 | ATCCCTTTCTACGGCATTCCTGGAGCCCTCTTCTTCTCACTTCATCAGGTTCTCTGAG    | 1169 |
| Db | 481  | ATCCCTTTCTACGGCATTCCTGGAGCCCTCTTCTTCTCACTTCATCAGGTTCTCTGAG    | 540  |
| Qy | 1170 | AGCCACTGGTTGTGTGGGTACACAGATGAATACATCGTCATGGAGATTGACCCAGGAG    | 1229 |
| Db | 541  | AGCCACTGGTTGTGTGGGTACACAGATGAATACATCGTCATGGAGATTGACCCAGGAG    | 600  |
| Qy | 1230 | GCCTACCTGTGATCGTTTCACTAGCCAGCTGACAGCCACTGTCGAACTGGAGAGTCTTC   | 1289 |
| Db | 601  | GCCTACCTGTGATCGTTTCACTAGCCAGCTGACAGCCACTGTCGAACTGGAGAGTCTTC   | 660  |
| Qy | 1290 | TTCAACGACTGGTTTCACTAGCCAGCTTAACTTCCAGATTGAGCACCACCTCTTCCCCACC | 1349 |
| Db | 661  | TTCAACGACTGGTTTCACTAGCCAGCTTAACTTCCAGATTGAGCACCACCTCTTCCCCACC | 720  |
| Qy | 1350 | ATGCCCCGGGCAAACTTACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT    | 1409 |
| Db | 721  | ATGCCCCGGGCAAACTTACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCAT    | 780  |
| Qy | 1410 | GGCATTGATACCAAGAGAGCCCTACTGAGGGCCCTGCTGGACATCATCAGTCTCCTG     | 1469 |
| Db | 781  | GGCATTGATACCAAGAGAGCCCTACTGAGGGCCCTGCTGGACATCATCAGTCTCCTG     | 840  |
| Qy | 1470 | AAGAAGTCTGGAAAGCTGTGGCTGGAGCCCTTACCTTCAAAATGAAGCCACAGCCCGCG   | 1529 |
| Db | 841  | AAGAAGTCTGGAAAGCTGTGGCTGGAGCCCTTACCTTCAAAATGAAGCCACAGCCCGCG   | 900  |
| Qy | 1530 | GACACCGTGGGAAAGGGGTGAGTGGGTGATGGCCAGAGGAATGATGGGCTTTTGTTC     | 1589 |
| Db | 901  | GACACCGTGGGAAAGGGGTGAGTGGGTGATGGCCAGAGGAATGATGGGCTTTTGTTC     | 960  |
| Qy | 1590 | TGAGGGGTGTCGAGAGGCTGGTGTATGCACTGTCTACGGACCCCATGTTGGATCTTCT    | 1649 |
| Db | 961  | TGAGGGGTGTCGAGAGGCTGGTGTATGCACTGTCTACGGACCCCATGTTGGATCTTCT    | 1020 |
| Qy | 1650 | CCCTTTCT    | 1709 |
| Db | 1021 | CCCTTTCT    | 1080 |
| Qy | 1710 | CTGCCCCCT   | 1769 |
| Db | 1081 | CTGCCCCCT   | 1140 |
| Qy | 1770 | TTCCAAAGGAGCAGAGAGTGGCCACCGGGGGTGGCTCTGTCTCTCTCTCTCTCTCTCTCT  | 1829 |
| Db | 1141 | TTCCAAAGGAGCAGAGAGTGGCCACCGGGGGTGGCTCTGTCTCTCTCTCTCTCTCTCTCT  | 1200 |
| Qy | 1830 | CTAAAGATGGGAGGAGACGAGGGTCCATGGGTCTGGGCTGTGAGTCTCTCTCTCTCTCTCT | 1889 |

Db 1201 CTAAGATGGAGGACACAGGGTCCATGGCTGCTGGCTGTGAGTCTCCCTTGCAGCC 1260  
 QY 1890 TGTCTACTAGGATACACCCCGCTTGTGCTTTCAGATGCTTGGGTTTCATAGGGGCA 1949  
 Db 1261 TGTCTACTAGGATACACCCCGCTTGTGCTTTCAGATGCTTGGGTTTCATAGGGGCA 1320  
 QY 1950 GFTCTAGTGGGAGGCGCTTGCCTTCCCGCTGCTGCTTCACTTCCCTGACGGCTG 2009  
 Db 1321 GFTCTAGTGGGAGGCGCTTGCCTTCCCGCTGCTGCTTCACTTCCCTGACGGCTG 1380  
 QY 2010 CATTGGTCCACCTTTCATAGAGGCTGCTTGTTCACAAAGTGGGTTCCCTTCT 2069  
 Db 1381 CATTGGTCCACCTTTCATAGAGGCTGCTTGTTCACAAAGTGGGTTCCCTTCT 1440  
 QY 2070 GCAGCTCGGTAAAGTACCGAGGCTTCTTAAAGATGTCAGGGGCCCGCGCGGGC 2129  
 Db 1441 GCAGCTCGGTAAAGTACCGAGGCTTCTTAAAGATGTCAGGGGCCCGCGCGGGC 1500  
 QY 2130 ACAGCCAGCCCAACCTTGGGCTTGGAGAGTCTTCCACCCATCATAGAGTCTCTG 2189  
 Db 1501 ACAGCCAGCCCAACCTTGGGCTTGGAGAGTCTTCCACCCATCATAGAGTCTCTG 1560  
 QY 2190 ACCCTGGCTTTCACGGGCGCCATTCCACCGCTTCCCAACTTGAGCTGTGACCTTGGG 2249  
 Db 1561 ACCCTGGCTTTCACGGGCGCCATTCCACCGCTTCCCAACTTGAGCTGTGACCTTGGG 1620  
 QY 2250 ACCAAGGGGGAGTCCCTGCTCTTGTGACTCACAGAGCAGTGGCCAGTTCAGGGA 2309  
 Db 1621 ACCAAGGGGGAGTCCCTGCTCTTGTGACTCACAGAGCAGTGGCCAGTTCAGGGA 1680  
 QY 2310 GGGGCGGCTGCTGGAGGCTCAGCCCACTTCCAGCTTTTCTCAGGGTGTCTCTGAGG 2369  
 Db 1681 GGGGCGGCTGCTGGAGGCTCAGCCCACTTCCAGCTTTTCTCAGGGTGTCTCTGAGG 1740  
 QY 2370 TCCAGATCTGAGCAATCTCAGCTTCTTCCAAAGGCTCTGTTATCAGTGGGAGTGC 2429  
 Db 1741 TCCAGATCTGAGCAATCTCAGCTTCTTCCAAAGGCTCTGTTATCAGTGGGAGTGC 1800  
 QY 2430 CAGCCAACTCGGCGCATTTGGCCCGGAGGAGCTGGGCGCTG 2473  
 Db 1801 CAGCCAACTCGGCGCATTTGGCCCGGAGGAGCTGGGCGCTG 1843

RESULT 26

ABS76712  
 ID ABS76712 standard; cDNA; 1843 BP.  
 AC ABS76712;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Human desaturase cDNA contig 2535.  
 XX  
 KW Human; ss; delta5 desaturase; polyunsaturated fatty acid;  
 KW PUFAs; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;  
 KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;  
 KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;  
 KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;  
 KW vasodilation; cholesterol; proliferation of fibrous tissue;  
 KW endometriosis; myalgic encephalomyelitis; human breast milk;  
 KW dietary supplement; chromosome 11q12.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6428990-B1.  
 XX  
 PD 06-AUG-2002.  
 XX  
 PF 12-NOV-1999; 99US-0439261.  
 XX  
 PR 11-APR-1997; 97US-0833610.  
 PR 10-APR-1998; 98WO-0507422.

PR 08-JAN-1999; 99US-0227613.  
 XX (ABBO) ABBOTT LAB.  
 PA Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;  
 PI WPI; 2002-730518/79.  
 XX  
 DR Producing a polyunsaturated fatty acid (PUFA), useful in dietary  
 XX supplements and in treating diseases e.g., cancer, comprises expressing  
 XX human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA  
 XX to convert to product PUFA -  
 XX Example 1; Fig 7; 104pp; English.  
 XX  
 CC The invention relates to producing (M1) a polyunsaturated fatty acid  
 CC (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase  
 CC gene sequence (I); (ii) constructing a vector comprising (I);  
 CC (iii) introducing the vector into a host cell for expression of the  
 CC human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a  
 CC substrate PUFA (III) such that it is converted to a product PUFA (IV).  
 CC The method is useful for producing a polyunsaturated fatty acid  
 CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic  
 CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or  
 CC docosahexaenoic (DHA) acid. The PUFAs produced by the method, such  
 CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or  
 CC docosahexaenoic (DHA) acid, are useful for replicating the PUFA content  
 CC in human breast milk or to alter the presence of PUFAs normally found  
 CC in a non-human mammal's milk. PUFAs produced by (M1) may be added to a  
 CC dietary substitute or supplement, particularly an infant formula, for  
 CC patients undergoing intravenous feeding or for preventing or treating  
 CC malnutrition or other conditions or disease states. The PUFAs are  
 CC useful for producing nutritional compositions e.g., any food or  
 CC preparation for human consumption including for enteral or parenteral  
 CC consumption, which when taken into the body serve to nourish or build  
 CC up tissues or supply energy and/or maintain, restore or support  
 CC adequate nutritional status or metabolic function. The PUFAs are also  
 CC useful in animal feed supplements to alter an animal tissue or milk  
 CC fatty acid composition to one or more desirable for human or animal  
 CC consumption, in animal feed substitutes, animal vitamins or in animal  
 CC topical ointments. The PUFAs produced by this method are useful in  
 CC producing pharmaceutical compositions for treating rough or aging skin,  
 CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
 CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,  
 CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
 CC platelet aggregation, inducing vasodilation, reducing cholesterol  
 CC levels, inhibiting proliferation of fibrous tissue, treating  
 CC endometriosis, and myalgic encephalomyelitis. The gene for delta5  
 CC desaturase is located on chromosome 11q12. The present sequence  
 CC is a partial cDNA for a human delta5 desaturase.  
 XX  
 SQ Sequence 1843 BP; 356 A; 598 C; 466 G; 423 T; 0 other;  
 Query Match 57.5%; Score 1830.4; DB 24; Length 1843;  
 Best Local Similarity 99.9%; Pred.No. 0;  
 Matches 1842; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 630 GTCTTCTACTTGGCAATGGCTGATTCCTTACCTCATCACGCGCTTGTCTGTGCTACC 689  
 Db 1 GTCTTCTACTTGGCAATGGCTGATTCCTTACCTCATCACGCGCTTGTCTGTGCTACC 60  
 QY 690 TCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGGCCACTGTCTGTCTACAGAAA 749  
 Db 61 TCTCAGGCCCAAGCTGGATGCTGCAACATGATTATGGCCACTGTCTGTCTACAGAAA 120  
 QY 750 CCCAAGTGGCAACCACTTGTCCACAAATTCGTTCATTTGGCCACTTAAAGGGTGTCTGTCC 809  
 Db 121 CCCAAGTGGCAACCACTTGTCCACAAATTCGTTCATTTGGCCACTTAAAGGGTGTCTGTCC 180  
 QY 810 AACTGGTGGAAATCATCGCCACTTCCAGACACACGCGCAAGCTTAACATCTTCCACAGGAT 869  
 Db 181 AACTGGTGGAAATCATCGCCACTTCCAGACACACGCGCAAGCTTAACATCTTCCACAGGAT 240

QY 870 CCGATGTGAACATGCTGACAGTGTGTTGTTCTGGGGGAATGACGCCATCGAGTACGGC 929  
Db 241 CCGATGTGAACATGCTGACAGTGTGTTGTTCTGGGGGAATGACGCCATCGAGTACGGC 300  
QY 930 AAGAAGAGCTGAATACCTGCGCTTCAATACACAGACAGAAATCTTCTCTGATGGG 989  
Db 301 AAGAAGAGCTGAATACCTGCGCTTCAATACACAGACAGAAATCTTCTCTGATGGG 360  
QY 990 CCGCGCTGCTCATCCCATGATTTTCCAGTACCCAGATCATCATGACCATGATCTCCAT 1049  
Db 361 CCGCGCTGCTCATCCCATGATTTTCCAGTACCCAGATCATCATGACCATGATCTCCAT 420  
QY 1050 AAGAAGCTGGGTGAGCTGCGCTGCGCTGAGTACTACATCCGCTTCTTCACTACCTAC 1109  
Db 421 AAGAAGCTGGGTGAGCTGCGCTGCGCTGAGTACTACATCCGCTTCTTCACTACCTAC 480  
QY 1110 ATCCCTTTCTACGGCATCTCGGAGCCCTCTTCTTCACTACATGAGTCTCTGGAG 1169  
Db 481 ATCCCTTTCTACGGCATCTCGGAGCCCTCTTCTTCACTACATGAGTCTCTGGAG 540  
QY 1170 AGCCACTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1229  
Db 541 AGCCACTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600  
QY 1230 GCCTACGCTGACTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1289  
Db 601 GCCTACGCTGACTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 660  
QY 1290 TTCAAGACTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1349  
Db 661 TTCAAGACTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 720  
QY 1350 ATGCCCGGCAACATTTACAGATGTGCGCCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1409  
Db 721 ATGCCCGGCAACATTTACAGATGTGCGCCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 780  
QY 1410 GGCAATTGAATACAGAGAGAGCGCTACTGAGGCGCTGCTGAGCATCATCAGTGTCCCTG 1469  
Db 781 GGCAATTGAATACAGAGAGAGCGCTACTGAGGCGCTGCTGAGCATCATCAGTGTCCCTG 840  
QY 1470 AAGAAGTCTGGAGTGTGGCTGAGAGCGCTACTTCAAAATGAAGAGCCAGAGCCCGCG 1529  
Db 841 AAGAAGTCTGGAGTGTGGCTGAGAGCGCTACTTCAAAATGAAGAGCCAGAGCCCGCG 900  
QY 1530 GACACGCTGGGAGAGGCTGAGTGGGTGATGGCCAGAGGAATGATGGCTTTTGTTC 1589  
Db 901 GACACGCTGGGAGAGGCTGAGTGGGTGATGGCCAGAGGAATGATGGCTTTTGTTC 960  
QY 1590 TGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGCTCAAGAGCCCGCTGTTGATCTTTCT 1649  
Db 961 TGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGCTCAAGAGCCCGCTGTTGATCTTTCT 1020  
QY 1650 CCCTTTCT 1709  
Db 1021 CCCTTTCT 1080  
QY 1710 CTGCGCT 1769  
Db 1081 CTGCGCT 1140  
QY 1770 TTCCAGAGAGAGAGAGTGGCCACCGGGGTGGCTGTGCTTCACTCCTCTCTCTCTCTCTCT 1829  
Db 1141 TTCCAGAGAGAGAGAGTGGCCACCGGGGTGGCTGTGCTTCACTCCTCTCTCTCTCTCTCT 1200  
QY 1830 CTAAGATGGAG 1889  
Db 1201 CTAAGATGGAG 1260  
QY 1890 TGGTCACTAGGAGTCAACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTTCATAGGGGCA 1949  
Db 1261 TGGTCACTAGGAGTCAACCCCGCTTTGGTCTTTCAGATGCTCTTGGGTTTCATAGGGGCA 1320

QY 1950 GGTCTAGTGGGAGGCGCCCTGACCTTCCGGCTGGCTTCACTCTCTCTCTCTCTCTCTCT 2009  
Db 1321 GGTCTAGTGGGAGGCGCCCTGACCTTCCGGCTGGCTTCACTCTCTCTCTCTCTCTCTCT 1380  
QY 2010 CCATTGGTCCACCTTTTCATAGAGAGCTGCTTTGTTACAAAGCTCGGCTCTCTCTCTCT 2069  
Db 1381 CCATTGGTCCACCTTTTCATAGAGAGCTGCTTTGTTACAAAGCTCGGCTCTCTCTCTCT 1440  
QY 2070 GCAGCTCGGTAAAGTACCCGAGGCTCTCTTTAAGATGTCCAGGGCCCCAGGCCCGGGG 2129  
Db 1441 GCAGCTCGGTAAAGTACCCGAGGCTCTCTTTAAGATGTCCAGGGCCCCAGGCCCGGGG 1500  
QY 2130 ACAGCAGGCGCAACCTTTGGGCGCTGGAAGAGTCTCCACCCCATCACTAGAGTCTCTG 2189  
Db 1501 ACAGCAGGCGCAACCTTTGGGCGCTGGAAGAGTCTCCACCCCATCACTAGAGTCTCTG 1560  
QY 2190 ACCCTGGGCTTTTCAAGGCGCCCATTTCCACGCTTCCCAACTTTGAGCCTGTGACCTTGGG 2249  
Db 1561 ACCCTGGGCTTTTCAAGGCGCCCATTTCCACGCTTCCCAACTTTGAGCCTGTGACCTTGGG 1620  
QY 2250 ACAGGAGGCGGAGTCT 2309  
Db 1621 ACAGGAGGCGGAGTCT 1680  
QY 2310 GGGGCGGCTGGCTGGAGGCTCAGCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2369  
Db 1681 GGGGCGGCTGGCTGGAGGCTCAGCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
QY 2370 TCCAGAGTCTGGAGCAATCTGAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2429  
Db 1741 TCCAGAGTCTGGAGCAATCTGAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800  
QY 2430 CAGCAATCT 2473  
Db 1801 CAGCAATCT 1843  
RESULT 27  
AAS32517  
ID AAS32517 standard; DNA; 29521 BP.  
XX AAS32517;  
AC AAS32517;  
DT 17-DEC-2001 (first entry)  
XX Human genomic DNA for novel endocrine antigen, SEQ ID No 471.  
DE Human; endocrine antigen; ds; cytostatic; antiinfertility; antidiabetic;  
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;  
KW antiseuse-therap; antibody; endocrine disorder; hormone imbalance;  
KW reproductive disorder; endocrine cancer; pancreatic disorder;  
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;  
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.  
XX Homo sapiens.  
OS  
XX  
PN WO20015319-A2.  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01335.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.









DE Human genomic DNA for novel endocrine antigen, SEQ ID No 470.  
XX  
KW Human; endocrine antigen; ds; cytostatic; antiinfertility; antidiabetic;  
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;  
KW antihypertensive; antibody; endocrine disorder; hormone imbalance;  
KW reproductive disorder; endocrine cancer; pancreatic disorder;  
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;  
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.  
OS  
XX Homo sapiens.  
XX  
XX WO20015319-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01335.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 17-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
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PR 20-OCT-2000; 2000US-0241785.  
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PR 20-OCT-2000; 2000US-0241809.  
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PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
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PR 17-NOV-2000; 2000US-0249216.  
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 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI WPI; 2001-457726/49.  
 DR  
 XX Isolated polypeptide for treating, preventing and prognosing disorders  
 PT related to the endocrine system including endocrine disorders,  
 PT reproductive disorders, and gastrointestinal disorders and also for  
 PT testing and detection e.g. diagnosis -  
 XX  
 PS Disclosure; SEQ ID No 470; 558pp; English.  
 XX  
 CC The invention relates to cDNAs encoding novel human endocrine  
 CC antigens or a fragment having biological activity, a domain, an epitope,  
 CC full length protein, variant, allelic variant or a species homologue of  
 CC the cDNA/antigen. The DNAs and polypeptides are useful for preventing,  
 CC treating or ameliorating a medical condition when administered  
 CC (e.g. by gene therapy or antisense-therapy). Identifying mutations in  
 CC the genes coding for the antigens is useful for diagnosing a pathological  
 CC condition or a susceptibility to a pathological condition. The DNAs,  
 CC antigens and antibodies raised against the antigens useful for treating,  
 CC preventing and/or prognosing disorders related to the endocrine system  
 CC or hormone imbalance or reproductive disorders, cancers of endocrine  
 CC tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal  
 CC glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the  
 CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples  
 CC of diseases and disorders are given in the specification. The present  
 CC sequence is genomic DNA fragment form a gene encoding an endocrine  
 CC antigen of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 29543 BP; 6367 A; 8023 C; 7634 G; 7519 T; 0 other;  
 Query Match 53.5%; Score 1703.4; DB 22; Length 29543;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1721; Conservative 0; Mismatches 11; Indels 1; Gaps 1;  
 QY 1442 GGCCCTGTGTGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGACGCTA 1501  
 DB 27806 GTTCCATCCCCAACITTCAGGTCCCTGAAGAGTCTGGGAAGCTGTGGCTGGACGCTA 27865  
 QY 1502 CTTTCAAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGTGCAGGTGGGTGA 1561  
 DB 27866 CTTTCAAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGTGCAGGTGGGTGA 27925  
 QY 1562 TGGCCAGAGGAATGATGGCTTTTCTCTGAGGGGTGTCCAGAGGCTGTGTATGCACT 1621  
 DB 27926 TGGCCAGAGGAATGATGGCTTTTCTCTGAGGGGTGTCCAGAGGCTGTGTATGCACT 27985  
 QY 1622 GTCACGACCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1681  
 DB 27986 GCTACGACCCCATGTTGGATCTTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 28045  
 QY 1682 CCCCCTATGACCCCTGATGGAGCTGCTCCCTCCCTCAGCCGTGACCCATCAGCCAT 1741  
 DB 28046 CCCCCTATGACCCCTGATGGAGCTGCTCCCTCCCTCAGCCGTGACCCATCAGCCAT 28105  
 QY 1742 GGCCTTCCAGTGCCTCTAGCCCTTCTTCCAGGAGCAGAGAGGTGGCCACCCGGGGT 1801  
 DB 28106 GGCCTTCCAGTGCCTCTAGCCCTTCTTCCAGGAGCAGAGAGGTGGCCACCCGGGGT 28165

QY 1802 GGCTCTGTCTACCTCCACTCTCTGCCCCCTAAGATGGGAGGAGACACGCGTTCATGGG 1861  
 DB 28166 GGCTCTGTCTACCTCCACTCTCTGCCCCCTAAGATGGGAGGAGACACGCGTTCATGGG 28225  
 QY 1862 TCTGGCCTGTGAGTCTCCCTTTGACGCTGGTGCATGAGCATCACCCCGCTTTGGTTCT 1921  
 DB 28226 TCTGGCCTGTGAGTCTCCCTTTGACGCTGGTGCATGAGCATCACCCCGCTTTGGTTCT 28285  
 QY 1922 TCAGATGCTCTTTGGGTTTCATAGGGGCGAGTCTAGTCGGGCGAGGCGCTCAGCCTCC 1981  
 DB 28286 TCAGATGCTCTTTGGGTTTCATAGGGGCGAGTCTAGTCGGGCGAGGCGCTCAGCCTCC 28345  
 QY 1982 GGCTCTGGCTTCACTCTCCCTGACGCTGCATTTGGTCCACCTTTTCATAGAGAGGCTGC 2041  
 DB 28346 GGCTCTGGCTTCACTCTCCCTGACGCTGCATTTGGTCCACCTTTTCATAGAGAGGCTGC 28405  
 QY 2042 TTTGTTACAAAGCTCGGCTCTCCCTCTGACGCTGGTTAAGTACCGAGGCTCTCTTTA 2101  
 DB 28406 TTTGTTACAAAGCTCGGCTCTCCCTCTGACGCTGGTTAAGTACCGAGGCTCTCTTTA 28465  
 QY 2102 AGATGTCCAGGGCCCCCAGGCCCCGCGGACACAGCCAGCCCAAAACCTTTGGGCCCTTGAAGAG 2161  
 DB 28466 AGATGTCCAGGGCCCCCAGGCCCCGCGGACACAGCCAGCCCAAAACCTTTGGGCCCTTGAAGAG 28525  
 QY 2162 TCCCTCACCCCATCACTAGAGTGTCTGACCTTGGCTTTTACGGGCCCCCATTCACCGC 2221  
 DB 28526 TCCCTCACCCCATCACTAGAGTGTCTGACCTTGGCTTTTACGGGCCCCCATTCACCGC 28585  
 QY 2222 CTCCCAACTTGAAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGTCTTTGTGACT 2281  
 DB 28586 CTCCCAACTTGAAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGTCTTTGTGACT 28645  
 QY 2282 CAGCAGAGGAGTGGCCACGTTTCAAGGAGGGGCGCGCTGGCTTGAGGCTCAGCCACCC 2341  
 DB 28646 CAGCAGAGGAGTGGCCACGTTTCAAGGAGGGGCGCGCTGGCTTGAGGCTCAGCCACCC 28705  
 QY 2342 TCCAGCTTTTCTCAGGGTGTCTGAGGTGCCAAGATTTCTGAGCAATCTGACCTTCTCC 2401  
 DB 28706 TCCAGCTTTTCTCAGGGTGTCTGAGGTGCCAAGATTTCTGAGCAATCTGACCTTCTCC 28765  
 QY 2402 AAAGGCTCTGTATCAGCTGGGAGTGCAGCAATCCCTTGCCCAATTTGGCCCCAGGGGG 2461  
 DB 28766 AAAGGCTCTGTATCAGCTGGGAGTGCAGCAATCCCTTGCCCAATTTGGCCCCA -GGGG 28824  
 QY 2462 ACCTGGGCGCTGACGCTCAGAGGGGACCTGGAGCTGGAGGTCTCGTCCAGCCCTCC 2521  
 DB 28825 ACCTGGGCGCTGACGCTCAGAGGGGACCTGGAGCTGGAGGTCTCGTCCAGCCCTCC 28884  
 QY 2522 CCACTCTCGGGGCTGTCTGTGACGCGCTGCTCAGGCACCTCTCTGTCTGAACTGTCC 2581  
 DB 28885 CCACTCTCGGGGCTGTCTGTGACGCGCTGCTCAGGCACCTCTCTGTCTGAACTGTCC 28944  
 QY 2582 CTTACTGTGTTAACTGTGCTCCAGGATGATTTCTGATAGAGGGGCGGCGGCTG 2641  
 DB 28945 CTTACTGTGTTAACTGTGCTCCAGGATGATTTCTGATAGAGGGGCGGCGGCTG 29004  
 QY 2642 GGCTTTGTGACAACTGTGCTTTTCCACCAATGCGCTTGCCTCGGTGGCCCTGACTGTGAG 2701  
 DB 29005 GGCTTTGTGACAACTGTGCTTTTCCACCAATGCGCTTGCCTCGGTGGCCCTGACTGTGAG 29064  
 QY 2702 GAGGGCCAGGGAGGACAGCGGAGTCTCAGAGAGGCTGCTCAGAGGCTGAGGCTGAGG 2761  
 DB 29065 GAGGGCCAGGGAGGACAGCGGAGTCTCAGAGAGGCTGCTCAGAGGCTGAGGCTGAGG 29124  
 QY 2762 GAGGGGCTACCTCATGAGGACCAAGGGTGGAGCTGAGAGAGGAGTGGGGGCTGGAG 2821  
 DB 29125 GAGGGGCTACCTCATGAGGACCAAGGGTGGAGCTGAGAGAGGAGTGGGGGCTGGAG 29184  
 QY 2822 GTGCTGCTAGCTAGGGGACGGGCAAGTGAAGGGAGGAGGAGTCTCTGGAGGATC 2881  
 DB 29185 GTGCTGCTAGCTAGGGGACGGGCAAGTGAAGGGAGGAGGAGTCTCTGGAGGATC 29244  
 QY 2882 CTGAGCTGTGTTGACGTCTAACCCACTAATCAGTTCTTTAGATTTCAGGGGAGGCGCAGC 2941

Db 29245 CTGAGCTGCTGTTGCAGTCTAACCCACTAATCACTTCTAGATTTCAGGGGAGGCGCAGGC 29304  
 Qy 2942 ACCAACACTCAGAAATGGGGGCTTTGGGGAGGCGCCTAGTCCCTCCAGCTCTAAGCAG 3001  
 Db 29305 ACCAACACTCAGAAATGGGGGCTTTGGGGAGGCGCCTAGTCCCTCCAGCTCTAAGCAG 29364  
 Qy 3002 CCAGGAGGAGCTGCACTAAGCATCTGGGTTGCCATGGCAATGGCATGCCCCCAAGCTA 3061  
 Db 29365 CCAGGAGGAGCTGCACTAAGCATCTGGGTTGCCATGGCAATGGCATGCCCCCAAGCTA 29424  
 Qy 3062 CTGTATGCCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 3121  
 Db 29425 CTGTATGCCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 29484  
 Qy 3122 TATCATGTTACTTCCCCACCCCTACATTTTTCGAAATAAATAAAGAAATTTTA 3174  
 Db 29485 TATCATGTTACTTCCCCACCCCTACATTTTTCGAAATAAATAAAGAAATTTTA 29537

## RESULT 29

ABT10147/c

ID ABT10147 standard; cDNA; 185035 BP.

XX AC ABT10147;

XX DT 04-DEC-2002 (first entry)

XX DE Human breast cancer associated coding sequence SEQ ID NO: 281.

XX KW Human; breast specific gene; breast cancer; differential expression;

XX KW Cytostatic; gene therapy; gene; ss.

XX OS Homo sapiens.

XX PN WO200259271-A2.

XX PD 01-AUG-2002.

XX PF 25-JAN-2002; 2002WO-US021176.

XX PR 25-JAN-2001; 2001US-263757P.

XX PR 25-APR-2001; 2001US-286090P.

XX PR 23-MAY-2001; 2001US-292517P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Orr MS, Nation M, Diggans JC, Zeng W;

XX DR WPI; 2002-674803/72.

XX PT Diagnosing breast cancer in a patient comprises detecting the level of

XX PT gene expression in cell or tissue samples, where a differential gene

XX PT expression is indicative of breast cancer.

XX PS Claim 1; SEQ ID NO 281; 260pp + Sequence Listing; English.

XX CC The present invention relates to methods of diagnosing breast cancer in a

XX CC patient, which comprise detecting the level of expression in a tissue

XX CC sample of two or more genes selected from those shown in ABR09867.

XX CC ABR1112, where a differential expression of the genes indicates breast

XX CC cancer. The methods are useful in diagnosing, treating, detecting the

XX CC progression, and in monitoring treatment of breast cancer in patients.

XX CC The methods are also useful as a screening tool for agents that modulate

XX CC the onset or progression of breast cancer. The breast cancer genes may be

XX CC used as diagnostic markers for the prediction or identification of the

XX CC malignant state of breast tissue, for confirming the type and progression

XX CC of cancer, and for drug screening and assays. The present sequence is a

XX CC coding sequence of the invention.

XX CC Note: The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub.published\_pct\_sequences.

SQ Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 other;  
 Query Match 53.5%; Score 1703.4; DB 24; Length 185035;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1721; Conservative 0; Mismatches 11; Indels 1; Gaps 1;  
 Qy 1442 GGCCTCTCTGACATCATAGGTCCCTGAAGAAGTCTGGAAAGCTGTGGTGAACGCTTA 1501  
 Db 14738 GGTCCATCCCACTTTGCAGAGTCCCTGAAGAAGTCTGGAAAGCTGTGGTGAACGCTTA 14679  
 Qy 1502 CTTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAAAGGGTGCAGGTGGGGTGA 1561  
 Db 14678 CTTTCAAAATGAAGCCACAGCCCCCGGACACCGTGGGAAAGGGTGCAGGTGGGGTGA 14619  
 Qy 1562 TGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGTGTATGCACT 1621  
 Db 14618 TGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGTGTATGCACT 14559  
 Qy 1622 GCTCAGGAGCCCATGTTGGATCTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1681  
 Db 14558 GCTCAGGAGCCCATGTTGGATCTTCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 14499  
 Qy 1682 CCCCATAGCACCCCTGCCCTCATGGGACCTGCCCTCCTCAGCCGTGAGCCATCAGCCAT 1741  
 Db 14498 CCCCATAGCACCCCTGCCCTCATGGGACCTGCCCTCCTCAGCCGTGAGCCATCAGCCAT 14439  
 Qy 1742 GGCCTCTCCAGTCTCTAGTCCCTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGT 1801  
 Db 14438 GGCCTCTCCAGTCTCTAGTCCCTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGT 14379  
 Qy 1802 GGCTCTGTCTTACCTCCACTCTCTGCCCTTAAAGATGGGAGGAGACAGCGTCCATGGG 1861  
 Db 14378 GGCTCTGTCTTACCTCCACTCTCTGCCCTTAAAGATGGGAGGAGACAGCGTCCATGGG 14319  
 Qy 1862 TCTGGCTCTGAGTCTCCCTTTCAGGCTGTGTCTAGGAGTCAACCCCTCTTGTCTCT 1921  
 Db 14318 TCTGGCTCTGAGTCTCCCTTTCAGGCTGTGTCTAGGAGTCAACCCCTCTTGTCTCT 14259  
 Qy 1922 TCAGATGCTCTGGGTTTCATAGGGCAGGTCTCTAGTTCGGGCGAGGGCCCTTGACCCCTCCC 1981  
 Db 14258 TCAGATGCTCTGGGTTTCATAGGGCAGGTCTCTAGTTCGGGCGAGGGCCCTTGACCCCTCCC 14199  
 Qy 1982 GGCCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTTCACCCCTTTCATAGAGAGCCCTGC 2041  
 Db 14198 GGCCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTTCACCCCTTTCATAGAGAGCCCTGC 14139  
 Qy 2042 TTTGTTACAAAGCTCGGGTCTCCCTCTGACAGTCTGGTTAAGTACCCGAGGCTCTCTTA 2101  
 Db 14138 TTTGTTACAAAGCTCGGGTCTCCCTCTGACAGTCTGGTTAAGTACCCGAGGCTCTCTTA 14079  
 Qy 2102 AGATGTCAGGGCCCCAGGCCCGGGGACAGCCAGCCCCCAAAACCTTGGGCGCTTGGAAAG 2161  
 Db 14078 AGATGTCAGGGCCCCAGGCCCGGGGACAGCCAGCCCCCAAAACCTTGGGCGCTTGGAAAG 14019  
 Qy 2162 TCCTCCACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCAGCGGGCCCAATTCACCGC 2221  
 Db 14018 TCCTCCACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCAGCGGGCCCAATTCACCGC 13959  
 Qy 2222 TCCTCCAACTTTGAGCTGTGACCTTGGGACCAAAAGGGGAGTCCCTCTCTTGTGACT 2281  
 Db 13958 TCCTCCAACTTTGAGCTGTGACCTTGGGACCAAAAGGGGAGTCCCTCTCTTGTGACT 13899  
 Qy 2282 CAGGAGGAGCTGGCCACGTTTCAGGGAGGGGCGGCTGGCTGAGGCTCAGGCCACCC 2341  
 Db 13898 CAGGAGGAGCTGGCCACGTTTCAGGGAGGGGCGGCTGGCTGAGGCTCAGGCCACCC 13839  
 Qy 2342 TCACGCTTTTCTCAGGGTGTCTGAGGTCCAAGATCTTGAGCAATCTGACCCCTTCTCC 2401  
 Db 13838 TCACGCTTTTCTCAGGGTGTCTGAGGTCCAAGATCTTGAGCAATCTGACCCCTTCTCC 13779  
 Qy 2402 AAAGGCTCTGTATCAGCTGGGAGTGCACCAATCTCTGGCCATTTGGCCCGGAGGG 2461  
 Db 13778 AAAGGCTCTGTATCAGCTGGGAGTGCACCAATCTCTGGCCATTTGGCCCGGAGGG 13720







or plants containing them are used to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid, stearidonic acid, and eicosapentaenoic acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in infant feeding formulas; or dietary supplements or substitutes, for use in humans or animals; (iii) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler than with e.g. fish. Sequences AAX00904-910 represent DNA sequences of various contigs of human desaturase genes which are similar to the M. alpina desaturase sequences.

XX  
SQ Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

Query Match 52.6%; Score 1675; DB 20; Length 1686;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 787 GCCACTTAAGGGTGGCTTCGCAACTGGTGAATCATCGCCACTTCCAGCACCCAGCCA 846  
DB 1 GCCACTTAAGGGTGGCTTCGCAACTGGTGAATCATCGCCACTTCCAGCACCCAGCCA 60  
QY 847 AGCCTAACATTTCCCAAGGATCCCGATGTGAACATGTGACAGTGTGTTCTGGGG 906  
DB 61 AGCCTAACATTTCCCAAGGATCCCGATGTGAACATGTGACAGTGTGTTCTGGGG 120  
QY 907 AATGGCAGCCCATCGAGTACGCAAGAGAGCTGAATACCTGCCCTACATCCAGC 966  
DB 121 AATGGCAGCCCATCGAGTACGCAAGAGAGCTGAATACCTGCCCTACATCCAGC 180  
QY 967 ACGAATACCTTCTCCTGATTTGGGCCCGCTGTCTATCCCTCATGTATTTCCAGTACCAGA 1026  
DB 181 ACGAATACCTTCTCCTGATTTGGGCCCGCTGTCTATCCCTCATGTATTTCCAGTACCAGA 240  
QY 1027 TCATCATGACCATGATGCTCCATAAGAACTGGGTGACCTGGCTGGGCGCTCAGCTACT 1086  
DB 241 TCATCATGACCATGATGCTCCATAAGAACTGGGTGACCTGGCTGGGCGCTCAGCTACT 300  
QY 1087 ACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCC 1146  
DB 301 ACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCC 360  
QY 1147 TCAACTTCATCAGGTTCTCGGAGAGCCACTGGTTTGTGGGTTCACAGATGAATACCA 1206  
DB 361 TCAACTTCATCAGGTTCTCGGAGAGCCACTGGTTTGTGGGTTCACAGATGAATACCA 420  
QY 1207 TCGTCATGGAGATTGACAGGAGCCCTACCTGACCTGTTAGTAGCCAGCTGACAGCCA 1266  
DB 421 TCGTCATGGAGATTGACAGGAGCCCTACCTGACCTGTTAGTAGCCAGCTGACAGCCA 480  
QY 1267 CTTGCAACCGTGGAGAGTCTTCTTCAACGACTGGTTCAGTGGACCACTTAATCCAGA 1326  
DB 481 CTTGCAACCGTGGAGAGTCTTCTTCAACGACTGGTTCAGTGGACCACTTAATCCAGA 540  
QY 1327 TTGAGCACCACTTTCCTCCCATCCATCCCGGCACAACTTACAGAGATCGCCCGCTGG 1386  
DB 541 TTGAGCACCACTTTCCTCCCATCCATCCCGGCACAACTTACAGAGATCGCCCGCTGG 600  
QY 1387 TGAAGTCTCTATGTGCAAGCATGGCAATTTGAATACCAAGAGAGCGCTTACTGAGGGGCC 1446  
DB 601 TGAAGTCTCTATGTGCAAGCATGGCAATTTGAATACCAAGAGAGCGCTTACTGAGGGGCC 660  
QY 1447 TGGTGCATCATCATCGTCCCTGAAAGTCTGGGAGCTGTGGTGGAGCGCTACCTTC 1506  
DB 661 TGGTGCATCATCATCGTCCCTGAAAGTCTGGGAGCTGTGGTGGAGCGCTACCTTC 720  
QY 1507 ACAATGAAGCCACAGCCCGCCGAGCACCGTGGGGAAGGGGTGCAGGTGGGGTGTATGCC 1566

DB 721 ACAAATGAAGCCACAGCCCGGAGACACCGTGGGAGGGGTGCAGGTGGGTGATGGCC 780  
QY 1567 AGAGGAATGATGGCTTTTCTTCTGAGGGGTGTCGAGAGGCTGGTGTATGCACTGCTCA 1626  
DB 781 AGAGGAATGATGGCTTTTCTTCTGAGGGGTGTCGAGAGGCTGGTGTATGCACTGCTCA 840  
QY 1627 CGGACCCCATGTTGGATCTTTCTCCCTTTCTCCTCTCTCTTTCTCTTCACTATCCCCC 1686  
DB 841 CGGACCCCATGTTGGATCTTTCTCCCTTTCTCCTCTCTCTTTCTCTTCACTATCCCCC 900  
QY 1687 ATAGCACCTTGCCTCATGGGACCTGCCCTTCTCCTCAGCCGTACGCCATCAGCATGGCCC 1746  
DB 901 ATAGCACCTTGCCTCATGGGACCTGCCCTTCTCCTCAGCCGTACGCCATCAGCATGGCCC 960  
QY 1747 TCCCAAGTGCCTCCTTAGGCCCTTCTTCCAAAGGACAGAGAGTGGCCACCGGGGGTGGCTC 1806  
DB 961 TCCCAAGTGCCTCCTTAGGCCCTTCTTCCAAAGGACAGAGAGTGGCCACCGGGGGTGGCTC 1020  
QY 1807 TGTCTTACCTCCACTCTCTGCCCTTAAAGATGGGAGGAGACACGCGGTTCATGGGTCTGG 1866  
DB 1021 TGTCTTACCTCCACTCTCTGCCCTTAAAGATGGGAGGAGACACGCGGTTCATGGGTCTGG 1080  
QY 1867 CCTGTAGTCTCCCTTTCAGCCTGGTCACTAGCATCACCCCGCTTTGGTTCTTTCAGA 1926  
DB 1081 CCTGTAGTCTCCCTTTCAGCCTGGTCACTAGCATCACCCCGCTTTGGTTCTTTCAGA 1140  
QY 1927 TGTCTTGGGGTTCATAGGGGAGGTCCTAGTGGGAGGGGCCCCCTGACCCCTCCCGGCT 1986  
DB 1141 TGTCTTGGGGTTCATAGGGGAGGTCCTAGTGGGAGGGGCCCCCTGACCCCTCCCGGCT 1200  
QY 1987 GGCTTCACTCTCCCTGAGCGCTGCCATTTGGTGCACCCCTTTCATAGAGAGGCTCTTGT 2046  
DB 1201 GGCTTCACTCTCCCTGAGCGCTGCCATTTGGTGCACCCCTTTCATAGAGAGGCTCTTGT 1260  
QY 2047 TACAAAGCTCGGGTCTCCCTCTCGAGCTCGGTTAAGTACCCGAGGCTCTCTTAAAGATG 2106  
DB 1261 TACAAAGCTCGGGTCTCCCTCTCGAGCTCGGTTAAGTACCCGAGGCTCTCTTAAAGATG 1320  
QY 2107 TCCAGGGCCCCAGCCCGCGGGGACAGCCAGCCCAACCTTGGGCCCCCTGGAAGGTCCTC 2166  
DB 1321 TCCAGGGCCCCAGCCCGCGGGGACAGCCAGCCCAACCTTGGGCCCCCTGGAAGGTCCTC 1380  
QY 2167 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCAAGGGCCCCCATTCACCGCTCCC 2226  
DB 1381 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCAAGGGCCCCCATTCACCGCTCCC 1440  
QY 2227 CAATTCAGCCTGTGACCTTGGGACCAAGAGGGGAGTCCCTCTCTCTTGTGACTGACGA 2286  
DB 1441 CAATTCAGCCTGTGACCTTGGGACCAAGAGGGGAGTCCCTCTCTCTTGTGACTGACGA 1500  
QY 2287 GAGGAGTGGCCACCTTTCAGGGAGGGGCGGCTGGGCTGGAGGCTCAGCCCACTCCAG 2346  
DB 1501 GAGGAGTGGCCACCTTTCAGGGAGGGGCGGCTGGGCTGGAGGCTCAGCCCACTCCAG 1560  
QY 2347 CTTTTCCTCAGGGTGTCTGAGGTCCAAAGATTCCTGAGCAATCTGACCTTCTCCAAAGG 2406  
DB 1561 CTTTTCCTCAGGGTGTCTGAGGTCCAAAGATTCCTGAGCAATCTGACCTTCTCCAAAGG 1620  
QY 2407 CTCTGTTTATCAGCTGGGAGTGCAGCAATCCTTGSCCAATTTGGCCCCAGGGGAGCTG 2466  
DB 1621 CTCTGTTTATCAGCTGGGAGTGCAGCAATCCTTGSCCAATTTGGCCCCAGGGGAGCTG 1679  
QY 2467 GGCCCTG 2473  
DB 1680 GGCCCTG 1686

RESULT 32  
AAV82640  
ID AAV82640 standard; DNA; 1686 BP.  
XX  
AC AAV82640;



|    |   |               |
|----|---|---------------|
| XX | 11-FEB-1999   | (first entry) |
| DT | Contig 2511785 encoding a desaturase enzyme.                              |               |
| DE | Fatty acid; desaturase; polyunsaturated fatty acid;                       |               |
| XX | malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;      |               |
| KW | cancer; diabetes; eczema; platelet aggregation; vasodilation;             |               |
| KW | cholesterol level; endometriosis; premenstrual syndrome;                  |               |
| KW | myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;     |               |
| KW | acute respiratory syndrome; hypertension; inflammatory skin disorder; ss. |               |
| XX | Homo sapiens.   |               |
| OS | WO9846765-A1.   |               |
| PN | 22-OCT-1998.  |               |
| XX | 10-APR-1998; 98WO-US07422.  |               |
| PD | 11-APR-1997; 97US-0833610.  |               |
| PF | (ABBO ) ABBOTT LAB.   |               |
| PR | (CALJ ) CALGENE LLC.  |               |
| XX | Chaudhary S., Huang Y., Knutzon D., Leonard AE., Mukerji P.;              |               |
| PI | Thurmond J;   |               |
| FI | WPI; 1999-009334/01.  |               |
| DR | P-PSDB; AAWS5133.   |               |
| XX | New nucleic acid encoding deltas and other desaturase enzymes -           |               |
| PT | useful in production of oils of increased arachidonic acid content,       |               |
| PT | used, e.g. for treating cancer, as foods, animal feeds and cosmetics      |               |
| XX | Claim 86; Pages 109-110; 153pp; English.                                  |               |
| XX | The present sequence encodes a human desaturase enzyme. The enzyme        |               |
| CC | sequence is used in the methods of the invention. The specification       |               |
| CC | describes methods for desaturating a fatty acid and for producing a       |               |
| CC | desaturated fatty acid by expressing increased levels of a desaturase.    |               |
| CC | The enzyme can be used for desaturating fatty acids. The enzyme can be    |               |
| CC | used to produce polyunsaturated fatty acids, which can be used for        |               |
| CC | treating malnutrition, in pharmaceutical compositions, in cosmetics or    |               |
| CC | in animal feed. The polyunsaturated fatty acids can be used for treating  |               |
| CC | e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,    |               |
| CC | asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.   |               |
| CC | They can also be used to inhibit platelet aggregation, cause              |               |
| CC | vasodilation, lower cholesterol levels, inhibit proliferation of vessel   |               |
| CC | wall smooth muscle and fibrous tissue, reduce or prevent                  |               |
| CC | gastro-intestinal bleeding and other side effects caused by non-steroidal |               |
| CC | anti-inflammatory drugs, prevent or treat endometriosis and premenstrual  |               |
| CC | syndrome, treat myalgic encephalomyelitis and chronic fatigue after       |               |
| CC | viral infections, treat AIDS, multiple sclerosis, acute respiratory       |               |
| CC | syndrome, hypertension and inflammatory skin disorders.                   |               |
| XX | Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;                    |               |
| SQ | Query Match 52.6%; Score 1675; DB 20; Length 1686;                        |               |
|    | Best Local Similarity 99.9%; Pred. No. 0;                                 |               |
|    | Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;             |               |
| QY | 787 GCCACTTAAAGGGTGCTCTGCCAATCTGPGGAATCATCGCACTTCACAGCACACGCCA 846        |               |
| DB | 1 GCCACTTAAAGGGTGCTCTGCCAATCTGPGGAATCATCGCACTTCACAGCACACGCCA 60           |               |
| QY | 847 AGCCTTAACATCTTCCACAAGGATCCCCATCTGAACATGTGCACGTTTGTCTGGGCG 906         |               |
| DB | 61 AGCCTTAACATCTTCCAAGAATCCCAGATGTGAACATGTGCACGTTTGTCTGGGCG 120           |               |
| QY | 907 AATGCGACCCCATCGAGTAGCGGAAGAACGCTGAATACTCTGCCCTCAACATCACAGC 966        |               |
| DB | 121 AATGCGACCCCATCGAGTAGCGGAAGAACGCTGAATACTCTGCCCTCAACATCACAGC 180        |               |





QY 847 AGCCTAATCTTCCCAAGGATCCCGATGCGTGAACATGCTGCACTGTTTCTTGGGCG 906  
Db 61 AGCCTAAATCTTCCCAAGGATCCCGATGCGTGAACATGCTGCACTGTTTCTTGGGCG 120  
QY 907 AATGSCAGCCCATCGAGTACGCAAGAGAGCTCAATATACCTGCGCTACCAATACCAAGC 966  
Db 121 AATGGAGCCCATCGAGTACGCAAGAGAGCTCAATATACCTGCGCTACCAATACCAAGC 180  
QY 967 ACGAATACCTTCTCTGATTTGGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAAG 1026  
Db 181 ACGAATACCTTCTCTGATTTGGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAAG 240  
QY 1027 TCATCATGACCATGATCGTCCATAGAACTGGTGGAGCTGCGCTGGGCGCTGCTACT 1086  
Db 241 TCATCATGACCATGATCGTCCATAGAACTGGTGGAGCTGCGCTGGGCGCTGCTACT 300  
QY 1087 ACATCCGGTCTTCTCATCACTACCTATCCCTTTCTAGCGCATCTGGAGCCCTCTTTTCC 1146  
Db 301 ACATCCGGTCTTCTCATCACTACCTATCCCTTTCTAGCGCATCTGGAGCCCTCTTTTCC 360  
QY 1147 TCNACTTCATCAGTTCCTGGAGAGCCACTGTTTGTGGGTGCACAGATGATACCA 1206  
Db 361 TCAACTTCATCAGTTCCTGGAGAGCCACTGTTTGTGGGTGCACAGATGATACCA 420  
QY 1207 TCGTCATGAGATGACCAAGAGGCTACCGTGACTGTTCACTAGCCAGCTGACAGCA 1266  
Db 421 TCGTCATGAGATGACCAAGAGGCTACCGTGACTGTTCACTAGCCAGCTGACAGCA 480  
QY 1267 CCGTCAAGCTGGAGAGCTGCTTCTCAAGACTGTTTCACTGGAGACCTTACTTCCAGA 1326  
Db 481 CCGTCAAGCTGGAGAGCTGCTTCTCAAGACTGTTTCACTGGAGACCTTACTTCCAGA 540  
QY 1327 TTGAGCACCACTCTTCCCAACCATGCGCGGACAACTTACAGAGATGCGCGCGCTGG 1386  
Db 541 TTGAGCACCACTCTTCCCAACCATGCGCGGACAACTTACAGAGATGCGCGCGCTGG 600  
QY 1387 TGAAGTCTCATGTGCAAGATGCGATTAATACAGGAGAGCGCTACTAGAGGCC 1446  
Db 601 TGAAGTCTCATGTGCAAGATGCGATTAATACAGGAGAGCGCTACTAGAGGCC 660  
QY 1447 TGTGAGACATCATCAGTTCCTGAGAGTCTGGGAGCTGTTGGTGGAGCTGCTACCTTC 1506  
Db 661 TGTGAGACATCATCAGTTCCTGAGAGTCTGGGAGCTGTTGGTGGAGCTGCTACCTTC 720  
QY 1507 ACAAAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGTGCAGGTGGGTGATGGCC 1566  
Db 721 ACAAAATGAAGCCACAGCCCCCGGACACCGTGGGAGAGGGTGCAGGTGGGTGATGGCC 780  
QY 1567 AGAGGATGATGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGNGTATGCACTGCTCA 1626  
Db 781 AGAGGATGATGGCTTTTGTCTGAGGGGTGTCGAGAGGCTGNGTATGCACTGCTCA 840  
QY 1627 CGGACCCCATGTTGGATCTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686  
Db 841 CGGACCCCATGTTGGATCTTCTCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
QY 1687 ATAGCACCTCCCTCATGAGAGCTGCTCCCTCTGAGGCTGAGGCTGAGGCTGAGGCT 1746  
Db 901 ATAGCACCTCCCTCATGAGAGCTGCTCCCTCTGAGGCTGAGGCTGAGGCTGAGGCT 960  
QY 1747 TCCAGTGCCTCTCTAGCCCTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1806  
Db 961 TCCAGTGCCTCTCTAGCCCTTCTTCCAGGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1020  
QY 1807 TGTCTTACCTCCACTCTCTGCGCTTAAAGATGGAGGAGACCAAGCGTCCATGGTCTGG 1866  
Db 1021 TGTCTTACCTCCACTCTCTGCGCTTAAAGATGGAGGAGACCAAGCGTCCATGGTCTGG 1080  
QY 1867 CCTGTGAGTCTCCCTTTCAGGCTGCTGCTAGGATCACCTCCCGCTTTGGTCTTCCAGA 1926  
Db 1081 CCTGTGAGTCTCCCTTTCAGGCTGCTGCTAGGATCACCTCCCGCTTTGGTCTTCCAGA 1140  
QY 1927 TGCTCTTGGGGTTCATAGGGGAGGTCCTAGTGGGCGAGGGGCCCTGACCCCTCCGGCT 1986

Db 1141 TGCTCTTGGGGTTCATAGGGGAGGTCCTAGTGGGCGAGGCCCTGACCCCTCCGGCT 1200  
QY 1987 GGCTTCACTCTCCCTGACCGGCTGCCATTGGTCCACCCCTTTCATAGAGAGCGCTGCTTGT 2046  
Db 1201 GGCTTCACTCTCCCTGACCGGCTGCCATTGGTCCACCCCTTTCATAGAGAGCGCTGCTTGT 1260  
QY 2047 TACAAGAGCTGGGTCTCCCTGCTGAGCTCGGTAACTAGTACCCGAGGCTCTCTTAAGATG 2106  
Db 1261 TACAAGAGCTGGGTCTCCCTGCTGAGCTCGGTAACTAGTACCCGAGGCTCTCTTAAGATG 1320  
QY 2107 TCCAGGGCCCCAGGCGCGCGGCGACAGCCAGCCCAAACTTGGGCCCTGGAAGAGTCCCT 2166  
Db 1321 TCCAGGGCCCCAGGCGCGCGGCGACAGCCAGCCCAAACTTGGGCCCTGGAAGAGTCCCT 1380  
QY 2167 CACCCCATCACTAGAGTCTCTGACCTGGGCTTTCAGGGGCCCATTCACCGCTCC 2226  
Db 1381 CACCCCATCACTAGAGTCTCTGACCTGGGCTTTCAGGGGCCCATTCACCGCTCC 1440  
QY 2227 CAACCTTGAAGCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCA 2286  
Db 1441 CAACCTTGAAGCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCA 1500  
QY 2287 GAGCAGTGGCCAGTTCAGGAGGGCGCGCTGGCTGGAGCTCAGCCAGCGCTCCAG 2346  
Db 1501 GAGCAGTGGCCAGTTCAGGAGGGCGCGCTGGCTGGAGCTCAGCCAGCGCTCCAG 1560  
QY 2347 CTCTTCTCAGGGTGTCTGAGGTCCAAAGATTCTGGAGCAATCTGACCTTCTCCAAAG 2406  
Db 1561 CTCTTCTCAGGGTGTCTGAGGTCCAAAGATTCTGGAGCAATCTGACCTTCTCCAAAG 1620  
QY 2407 CTCTGTTATCAGCTGGGCACTGCCAGCAATCTCTGGCCATTTGGGCCCGAGGAGCTG 2466  
Db 1621 CTCTGTTATCAGCTGGGCACTGCCAGCAATCTCTGGCCATTTGGGCCCGAGGAGCTG 1679  
QY 2467 GGCCCTG 2473  
Db 1680 GGCCCTG 1686

RESULT 35  
AAAA14592  
ID AAA14592 standard; DNA; 1686 BP.  
XX  
AC AAA14592;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Nucleotide sequence of a contig of a human desaturase enzyme.  
XX  
KW Delta5-desaturase; poly-unsaturated long chain fatty acid; PUPA;  
KW arachidonic acid; infant formula; dietary supplement; dietary substitute;  
KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;  
KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;  
KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;  
KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;  
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
KW acute respiratory syndrome; hypertension; inflammatory skin disorder;  
KW blood score; platelet aggregation; vasodilation;  
KW gastro-intestinal bleeding; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200020603-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 29-SEP-1999; 99WO-US22692.  
XX  
PR 05-OCT-1998; 98US-0103109.  
XX  
PA (ABSO ) ABBOTT LAB.  
XX

PI Mukerji P, Huang Y, Parker-Barnes JH, Das T;  
 XX WPI; 2000-364599/31.  
 DR P-PSDB; AAY84701.  
 XX  
 PT Novel transgenic insect cell with modified delta-5-desaturase  
 PT production, useful for altering fatty acid biosynthesis -  
 XX  
 XX Example 9; Page 146-147; 161pp; English.  
 XX  
 CC AAA14588-94 represent contigs of a human desaturase. The specification  
 CC describes a Mortierella alpina delta5-desaturase. The protein is  
 CC involved in the biosynthesis of poly-unsaturated long chain fatty  
 CC acids (PUFAs). The polynucleotide is to produce PUFAs, especially  
 CC arachidonic acid. The oils produced by the invention are used in  
 CC pharmaceutical compositions, infant formulas, dietary supplements,  
 CC dietary substitutes, and cosmetics. The nutritional compositions can be  
 CC used to treat normal individuals temporally exposed to stress, or  
 CC individuals having specialized needs due to chronic or acute diseases  
 CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or  
 CC malabsorption, and other disorders such as restenosis after angioplasty,  
 CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,  
 CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated  
 CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,  
 CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,  
 CC acute respiratory syndrome, hypertension, inflammatory skin disorders,  
 CC as well as reduce blood score, inhibit platelet aggregation, cause  
 CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and  
 CC fibrous tissue, prevent or reduce gastro-intestinal bleeding, and for  
 CC geriatric treatments).  
 XX  
 XX Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

Query Match 52.6%; Score 1675; DB 21; Length 1686;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1327 TTGAGCACCACTCTTCCCCACCATGCCCCGCGACAACTTACACAGATGCCCCCGCTGG 1386  
 DB 541 TTGAGCACCACTCTTCCCCACCATGCCCCGCGACAACTTACACAGATGCCCCCGCTGG 600  
 QY 1387 TGAAGTCTCTATGTGCCAAGCATGGCAATGAATACAGGAGAGCCGCTACTAGGGGCC 1446  
 DB 601 TGAAGTCTCTATGTGCCAAGCATGGCAATGAATACAGGAGAGCCGCTACTAGGGGCC 660  
 QY 1447 TGCTGGACATCATCAGGTCCCTGAAGAACTCTGGGAAGCTGTGGCTGGAGCCCTACCTTC 1506  
 DB 561 TGCTGGACATCATCAGGTCCCTGAAGAACTCTGGGAAGCTGTGGCTGGAGCCCTACCTTC 720  
 QY 1507 ACAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGGTGACGTGGGGTATGGCC 1566  
 DB 721 ACAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGGTGACGTGGGGTATGGCC 780  
 QY 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGAGCTGGTGTATGCACTGTCTCA 1626  
 DB 781 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGAGCTGGTGTATGCACTGTCTCA 840  
 QY 1627 CGGACCCCATGTTGGATCTTTCTCCCTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686  
 DB 841 CGGACCCCATGTTGGATCTTTCTCCCTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
 QY 1687 ATAGCACCTGCCCTCATGGGACCTGCCCTCCCTCAGCGGTACGCCATCAGCCATGAGCC 1746  
 DB 901 ATAGCACCTGCCCTCATGGGACCTGCCCTCCCTCAGCGGTACGCCATCAGCCATGAGCC 960  
 QY 1747 TCCAGTGCCTCTCAGGCCCTTCTTCAAGAGAGAGAGGTGGCCACCGGGGGTGGCTC 1806  
 DB 961 TCCAGTGCCTCTCAGGCCCTTCTTCAAGAGAGAGAGGTGGCCACCGGGGGTGGCTC 1020  
 QY 1807 TGTCTACTCCACTCTGCCCCCTAAAGATGGGAGAGACAGCGGTCCATGGGTCTGG 1866  
 DB 1021 TGTCTACTCCACTCTGCCCCCTAAAGATGGGAGAGAGACAGCGGTCCATGGGTCTGG 1080  
 QY 1867 CCGTGTAGTCTCCCTTGCAGCCTGGTCACTAGGATCAACCCCGCTTGTGTTCTTCTCAGA 1926  
 DB 1081 CCGTGTAGTCTCCCTTGCAGCCTGGTCACTAGGATCAACCCCGCTTGTGTTCTTCTCAGA 1140  
 QY 1927 TGCTTTGGGGTTCATAGGGGAGGTCTAGTGGGAGGGCCCTGACCCCTCCCGGCT 1986  
 DB 1141 TGCTTTGGGGTTCATAGGGGAGGTCTAGTGGGAGGGCCCTGACCCCTCCCGGCT 1200  
 QY 1987 GCGTTCACTCTCCCTGACGGGTGCCATTTGTCACCTTTTTCATAGAGAGGCTCTTTGT 2046  
 DB 1201 GCGTTCACTCTCCCTGACGGGTGCCATTTGTCACCTTTTTCATAGAGAGGCTCTTTGT 1260  
 QY 2047 TACAAGCTCGGCTCTCTCTGAGTCTGGTTAAGTACCGGAGGCTCTCTTAAGATG 2106  
 DB 1261 TACAAGCTCGGCTCTCTCTGAGTCTGGTTAAGTACCGGAGGCTCTCTTAAGATG 1320  
 QY 2107 TCCAGGGCCCCAGGGCCCGGGGACAGCCAGCCAAACCTTTGGGCTCTGGAAGAGTCTCTC 2166  
 DB 1321 TCCAGGGCCCCAGGGCCCGGGGACAGCCAGCCAAACCTTTGGGCTCTGGAAGAGTCTCTC 1380  
 QY 2167 CACCCCATCCTAGAGTGTCTGACCTTGGGTTTTCAGGGCCCCATTTCCACCGCTCC 2226  
 DB 1381 CACCCCATCCTAGAGTGTCTGACCTTGGGTTTTCAGGGCCCCATTTCCACCGCTCC 1440  
 QY 2227 CAACCTTGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCTCTTTGTGACTCAGCA 2286  
 DB 1441 CAACCTTGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCTCTTTGTGACTCAGCA 1500  
 QY 2287 GAGGAGTGGCCACGTTTCAGGAGGGGGCGGCTGGCCCTGGAGGCTCAGCCACCCCTCCAG 2346  
 DB 1501 GAGGAGTGGCCACGTTTCAGGAGGGGGCGGCTGGCCCTGGAGGCTCAGCCACCCCTCCAG 1560  
 QY 2347 CTTTCTCAGAGTGTCTCTGAGTCCAAGATTTCTGGAGCAATCTCACCTTTCTCCAAAGG 2406  
 DB 1561 CTTTCTCAGAGTGTCTCTGAGTCCAAGATTTCTGGAGCAATCTCACCTTTCTCCAAAGG 1620  
 QY 2407 CTTCTTATCAGTGGGAGTGCACAGCAATCCCTTGGGCAATTTGGCCCCAGGGGACGTG 2466

Db 1621 CTCCTGATACAGTGGGAGTCCGAGCAATCCCTGGCCATTTGGCCCA-GGGACGTG 1679

QY 2467 GGCCCTG 2473

Db 1680 GGCCCTG 1686

RESULT 36

ABS71824

ID ABS71824 standard; DNA; 1686 BP.

XX AC

XX ABS71824;

DT 02-DSC-2002 (first entry)

XX DE Human delta5-desaturase gene #6.

XX KW Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

KW dihomogamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;

KW eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;

XX KW gene; ds.

OS Homo sapiens.

XX US6432684-B1.

XX 13-AUG-2002.

XX 08-JAN-1999; 99US-0227613.

XX 11-APR-1997; 97US-0833610.

XX 10-APR-1998; 98WO-US07422.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Das T;

XX WFI; 2002-689761/74.

XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing

PT the conversion of dihomogamma-linolenic acid to arachidonic acid and

PT in the conversion of 20:4n-3 to eicosapentaenoic acid -

XX Example 1; Figure 6; 88pp; English.

XX The invention relates to an isolated human delta5-desaturase nucleotide

CC sequence (I) which desaturates polyunsaturated fatty acids at

CC carbon 5. The nucleotide sequence (I) may be used in the recombinant

CC production of vectors and host cells for the production of delta5-

CC desaturase. Delta5-desaturase may be utilised in the conversion of

CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the

CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or

CC polyunsaturated fatty acids produced from it may be added to

CC pharmaceutical compositions, nutritional compositions, animal feeds, as

CC well as other products such as cosmetics. ABS71819-ABS71854

CC represent human delta5-desaturase coding sequences and PCR primers of

CC the invention.

XX Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

QY Query Match 52.6%; Score 1675; DB 24; Length 1686;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 787 GCACCTAAAGGGTGCCCTGCGCAACTGGTGGGAATCATGCCACTTCCAGCACCGCCA 846

Db 1 GCACCTAAAGGGTGCCCTGCGCAACTGGTGGGAATCATGCCACTTCCAGCACCGCCA 60

QY 847 AGCCTAACATCTTCCCAAGGATCCCGATGTGAACATGTGACCGTGTGTTTCTGGCG 906

Db 61 AGCCTAACATCTTCCCAAGGATCCCGATGTGAACATGTGACCGTGTGTTTCTGGCG 120

QY 907 AATGGAGCCCATCGAGTACGCGCAAGAAAGCTGAATACCTGCGCCTACAATCACCAGC 966

Db 121 AATGGAGCCCATCGAGTACGCGCAAGAAAGCTGAATACCTGCGCCTACAATCACCAGC 180

QY 967 ACGAATACCTTCTTCGTATGGCCCGCGCTGCTATCCCATGATTTCCAGTACGAGA 1026

Db 181 ACGAATACCTTCTTCGTATGGCCCGCGCTGCTATCCCATGATTTCCAGTACGAGA 240

QY 1027 TCATCATGACCATGATCGTCCATAAGAACTGGGTGACCTGGCCCTGGGCGCTCAGTACT 1086

Db 241 TCATCATGACCATGATCGTCCATAAGAACTGGGTGACCTGGCCCTGGGCGCTCAGTACT 300

QY 1087 ACATCCGGTTCTTCATCACACTCATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 1146

Db 301 ACATCCGGTTCTTCATCACACTCATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 360

QY 1147 TCAACTTTCATCAGTTCCTCGAGAGCCACTGGTTTGTGGGTCAACAGATGAATCACA 1206

Db 361 TCAACTTTCATCAGTTCCTCGAGAGCCACTGGTTTGTGGGTCAACAGATGAATCACA 420

QY 1207 TCGTCAATGAGATGACCAAGAGCGCTACCGTGACTGGTTCACTAGCGAGCTGACAGCCA 1266

Db 421 TCGTCAATGAGATGACCAAGAGCGCTACCGTGACTGGTTCACTAGCGAGCTGACAGCCA 480

QY 1267 CTTGCAACGTGGAGAGTCTCTTCAACGACTGTTTCAGTGACACCTTTAACTTCAGGA 1326

Db 481 CTTGCAACGTGGAGAGTCTCTTCAACGACTGTTTCAGTGACACCTTTAACTTCAGGA 540

QY 1327 TTGAGCAACCACTTCTTCCCAACCATGCCCGCACACTTTACACAAGATCGCCCGCTGG 1386

Db 541 TTGAGCAACCACTTCTTCCCAACCATGCCCGCACACTTTACACAAGATCGCCCGCTGG 600

QY 1387 TGAAGTCTCTATGTCGAAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1446

Db 601 TGAAGTCTCTATGTCGAAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 660

QY 1447 TGCTGACATCATCAGTCCCTGGAAGAGTCTGGAGAGTGTGGTGGAGCGCTACCTTC 1506

Db 661 TGCTGACATCATCAGTCCCTGGAAGAGTCTGGAGAGTGTGGTGGAGCGCTACCTTC 720

QY 1507 ACAATGAAGCCACAGCCCGGGACACCGTGGGAGAGGGTGCAGTGGGGTGGTGGCC 1566

Db 721 ACAATGAAGCCACAGCCCGGGACACCGTGGGAGAGGGTGCAGTGGGGTGGTGGCC 780

QY 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGTCTCA 1626

Db 781 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGTCTCA 840

QY 1627 CGGACCCCATGTTGGATCTTTCTCCCTTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686

Db 841 CGGACCCCATGTTGGATCTTTCTCCCTTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900

QY 1687 ATAGCACCCCTGCTCATGGACCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1746

Db 901 ATAGCACCCCTGCTCATGGACCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960

QY 1747 TCCAGTGCCTCTTAGCGCCCTCTTTCACAGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1806

Db 961 TCCAGTGCCTCTTAGCGCCCTCTTTCACAGAGCAGAGAGTGGCCACCGGGGGTGGCTC 1020

QY 1807 TGTCTACTCTCCACTCTCTGCCCCCTAAAGATGGGAGAGACACCGGCTCATGGGTCTGG 1866

Db 1021 TGTCTACTCTCCACTCTCTGCCCCCTAAAGATGGGAGAGACACCGGCTCATGGGTCTGG 1080

QY 1867 CTTGTGAGTCTCCCTTTGAGCGCTGGTCACTPAGGCATCAACCCCGCTTTGGTCTTCAGA 1926

Db 1081 CTTGTGAGTCTCCCTTTGAGCGCTGGTCACTPAGGCATCAACCCCGCTTTGGTCTTCAGA 1140

QY 1927 TGCTCTTGGGGTTCATAGGGGACGTCTCTAGTGGGAGGGCCCTCTACCTCCCGGCT 1986

Db 1141 TGCTCTTGGGGTTCATAGGGGACGTCTCTAGTGGGAGGGCCCTCTACCTCCCGGCT 1200

QY 1987 GGCTTACTCTCCCTGACGGCTGCCATTTGGTCCACCTTTTCATAGAGAGGGCTCTTGT 2046



Db 1201 GGTTCACCTCCCTGACGGTGCATGCTGTCACCCCTTCATAGAGGCGCTGCTTTGT 1260  
 QY 2047 TACAAAGCTCGGGTCTCCCTCTCTGACAGCTCGGTTAAGTACCGAGGCGCTCTCTTAAGATG 2106  
 Db 1261 TACAAAGCTCGGGTCTCCCTCTCTGACAGCTCGGTTAAGTACCGAGGCGCTCTCTTAAGATG 1320  
 QY 2107 TCCAGGGCCCGAGGCGCGGGGACAGCCAGGCGCAACCTTGGGCGCTGGAAGTCTCTC 2166  
 Db 1321 TCCAGGGCCCGAGGCGCGGGGACAGCCAGGCGCAACCTTGGGCGCTGGAAGTCTCTC 1380  
 QY 2167 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCACTGGGCGCCCATTCACCGCTCTCC 2226  
 Db 1381 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCACTGGGCGCCCATTCACCGCTCTCC 1440  
 QY 2227 CAACCTGAGCTGTGACCTTGGGACCAAGAGGGGAGTCCCTGCTCTGTGACTCAGCA 2286  
 Db 1441 CAACCTGAGCTGTGACCTTGGGACCAAGAGGGGAGTCCCTGCTCTGTGACTCAGCA 1500  
 QY 2287 GAGGCACTGCCACGTTTCAAGGAGGGGCGGGCTGAGGCTCAGCCACCTCCAG 2346  
 Db 1501 GAGGCACTGCCACGTTTCAAGGAGGGGCGGGCTGAGGCTCAGCCACCTCCAG 1560  
 QY 2347 CTTTCTCAGGCTGCTGAGTCCCAAGATTCTGAGCAATCTGACCTTCTCCAAAGG 2406  
 Db 1561 CTTTCTCAGGCTGCTGAGTCCCAAGATTCTGAGCAATCTGACCTTCTCCAAAGG 1620  
 QY 2407 CTCTGTATCAGTGGGAGTGCAGCCCAATCCCTGGCCATTGGGCGCCAGGGGACGCTG 2466  
 Db 1621 CTCTGTATCAGTGGGAGTGCAGCCCAATCCCTGGCCATTGGGCGCCCA-GGGGACGCTG 1679  
 QY 2467 GGCCCTG 2473  
 Db 1680 GGCCCTG 1686

## RESULT 37

ABS76711  
 ID ABS76711 standard; cDNA; 1686 BP.

AC ABS76711;

DT 12-DEC-2002 (first entry)

DE Human desaturase cDNA edited contig 2511785.

XX Human; ss; delta5 desaturase; polyunsaturated fatty acid;  
 KW PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;  
 KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;  
 KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;  
 KW AIDS; multiple sclerosis; blood pressure; platelet aggregation;  
 KW vasodilation; cholesterol; proliferation of fibrous tissue;  
 KW endometriosis; myalgic encephalomyelitis; human breast milk;  
 KW dietary supplement; chromosome 11q12.

XX Homo sapiens.

OS US6428990-B1.

PN 06-AUG-2002.

PF 12-NOV-1999; 99US-0439261.

PR 11-APR-1997; 97US-0833610.

PR 10-APR-1998; 98WO-US07422.

PR 08-JAN-1999; 99US-0227613.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

PI WPI; 2002-730518/79.

DR

PT Producing a polyunsaturated fatty acid (PUFA), useful in dietary  
 PT supplements and in treating diseases e.g., cancer, comprises expressing  
 PT human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA  
 PT to convert to product PUFA -  
 XX  
 PS  
 XX Example 1; Fig 6; 104pp; English.

CC The invention relates to producing (M1) a polyunsaturated fatty acid  
 CC (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase  
 CC gene sequence (I); (ii) constructing a vector comprising (I);  
 CC (iii) introducing the vector into a host cell for expression of the  
 CC human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a  
 CC substrate PUFA (III) such that it is converted to a product PUFA (IV).  
 CC The method is useful for producing a polyunsaturated fatty acid  
 CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic  
 CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or  
 CC as arachaeonic (DHA) acid. The PUFAs produced by the method, such  
 CC as arachaeonic (DHA) acid, are useful for replicating the PUFA content  
 CC of human breast milk or to alter the presence of PUFAs normally found  
 CC in a non-human mammal's milk. PUFAs produced by (M1) may be added to a  
 CC dietary substitute or supplement, particularly an infant formula, for  
 CC patients undergoing intravenous feeding or for preventing or treating  
 CC malnutrition or other conditions or disease states. The PUFAs are  
 CC useful for producing nutritional compositions e.g., any food or  
 CC preparation for human consumption including for enteral or parenteral  
 CC consumption, which when taken into the body serve to nourish or build  
 CC up tissues or supply energy and/or maintain, restore or support  
 CC adequate nutritional status or metabolic function. The PUFAs are also  
 CC useful in animal feed supplements to alter an animal tissue or milk  
 CC fatty acid composition to one or more desirable for human or animal  
 CC consumption, in animal feed substitutes, animal vitamins or in animal  
 CC topical ointments. The PUFAs produced by this method are useful in  
 CC producing pharmaceutical compositions for treating rough or aging skin,  
 CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
 CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,  
 CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
 CC platelet aggregation, inducing vasodilation, reducing cholesterol  
 CC levels, inhibiting proliferation of fibrous tissue, treating  
 CC endometriosis, and myalgic encephalomyelitis. The gene for delta5  
 CC desaturase is located on chromosome 11q12. The present sequence  
 CC is a partial cDNA for a human delta5 desaturase.

XX Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

SQ Query Match 52.6%; Score 1675; DB 24; Length 1686;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 787 GCCACTTAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCACTTCCAGCACACGCCCA 846  
 Db 1 GCCACTTAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCACTTCCAGCACACGCCCA 60  
 QY 847 AGCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCAGCTGTTTCTGGGCG 906  
 Db 61 AGCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCAGCTGTTTCTGGGCG 120  
 QY 907 AATGGCAGCCCATCGAGTACGGCAAGAGAGAGCTGAATACCTGCCCTACAATCACCAGC 966  
 Db 121 AATGGCAGCCCATCGAGTACGGCAAGAGAGAGCTGAATACCTGCCCTACAATCACCAGC 180  
 QY 967 ACGAATACCTTCTCTGATTGGGCGCGCTGCTCATCCCGCATGATTTTCAGTACCAGA 1026  
 Db 181 ACGAATACCTTCTCTGATTGGGCGCGCTGCTCATCCCGCATGATTTTCAGTACCAGA 240  
 QY 1027 TCATCATGACCATGATGTCCTCATTAAGACTGGGTGGACCTGGCTGGGCGCTGAGTACT 1086  
 Db 241 TCATCATGACCATGATGTCCTCATTAAGACTGGGTGGACCTGGCTGGGCGCTGAGTACT 300  
 QY 1087 ACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 1146  
 Db 301 ACATCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTCGGAGCGCTCTTTTC 360







PT detection, prevention, and treatment of various disorders such as  
 XX cancer and immune system disorders -  
 PS Claim 1; Page 351-352; 442pp; English.  
 XX  
 CC The polynucleotide sequences given in AAC60025-C60071 encode the human  
 CC secreted proteins represented in AAB34854-B34900. Sequences  
 CC AAB34901-B34976 are fragments of proteins encoded by the genes, and also  
 CC proteins with which they share sequence homology. The proteins have  
 CC activities based on the tissues in which their encoding genes are  
 CC expressed. Examples of the proteins activities include: neuroprotective;  
 CC cytosolic; cardioactive; immunomodulatory; general muscular activity;  
 CC vulniferous; general gastrointestinal activity; nephrotropic;  
 CC antineoplastic; gynaecological; and antibacterial. The human secreted  
 CC proteins, polynucleotides, antagonists and/or agonists of the invention  
 CC may be useful in treating, preventing and/or diagnosing various  
 CC diseases, disorders and conditions such as neural, immune, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal and  
 CC proliferative disorders and cancer. They may also be used in the  
 CC treatment of wounds, and infectious diseases. The polypeptides may be  
 CC used as a food additive or preservative to increase storage capabilities.  
 CC Sequences AAC60016-C60024 and AAB34853 are used in the course of the  
 CC invention during the identification and characterisation of the protein  
 CC and nucleotide sequences.  
 XX  
 SQ Sequence 1536 BP; 306 A; 464 C; 456 G; 310 T; 0 other;

Query Match 44.2%; Score 1408.4; DB 21; Length 1536;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1494; Conservative 0; Mismatches 11; Indels 9; Gaps 7;

QY 1671 TCTTACATCTCCCATAGACACCTGCTCCCTCATGAGGACCTGCTCCCTCAGCCGTCAG 1730  
 DB 8 TCCGACATCTCCCATAGACACCTGCTCCCTCATGAGGACCTGCTCCCTCAGCCGTCAG 67

QY 1731 CCATCAGCAGTGGCCCTCCAGTGCCTCCTAGCCCTCTTCCAAAGGACGAGAGTGG 1790  
 DB 68 CCATCAGCAGTGGCCCTCCAGTGCCTCCTAGCCCTCTTCCAAAGGACGAGAGTGG 127

QY 1791 CCACCGGGGGTGGTCTGCTGCTACCTCCACCTCTGCGCCCTCAAGATGGGAGGACGAG 1850  
 DB 128 CCACCGGGGGTGGTCTGCTGCTACCTCCACCTCTGCGCCCTCAAGATGGGAGGACGAG 186

QY 1851 CGGTCCATGGGCTGGCTGTGAGTCTCCCTTGACGCTGGTCACTAGGATCACCCCTC 1910  
 DB 187 CGGTCCATGGGCTGGCTGTGAGTCTCCCTTGACGCTGGTCACTAGGATCACCCCTC 246

QY 1911 GCTTTGGTCTTCAGATGCTCTTGGGTTTCATAGGGCAGGTCCTAGTCCGGGAGGGCCC 1970  
 DB 247 GCTTTGGTCTTCAGATGCTCTTGGGTTTCATAGGGCAGGTCCTAGTCCGGGAGGGCCC 306

QY 1971 CTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATGGTCCACCTTTTCATA 2030  
 DB 307 CTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATGGTCCACCTTTTCATA 366

QY 2031 GAGAGGCTGCTTTGTTTCAAGCTCGGGTCTCCCTCTCGAGCTGGTTAAGTACCCGA 2090  
 DB 367 GAGAGGCTGCTTTGTTTCAAGCTCGGGTCTCCCTCTCGAGCTGGTTAAGTACCCGA 426

QY 2091 GCGCTCTCTTAAGATGTCCAGGGCCCGAGGGCCCGGGCCAGCCAGCCCAAACTTTGGG 2150  
 DB 427 GCGCTCTCTTAAGATGTCCAGGGCCCGAGGGCCCGGGCCAGCCAGCCCAAACTTTGGG 486

QY 2151 CCCTGGAGAGTCTCCACCCCATCACTAGAGTGTCTTGACCTGGGCTTTTCAGGGCCC 2210  
 DB 487 CCCTGGAGAGTCTCCACCCCATCACTAGAGTGTCTTGACCTGGGCTTTTCAGGGCCC 545

QY 2211 CATTCACCGCTCCCGAACTTGGCTGTGACCTTGGGACCAAGGGGAGTCCCTCGT 2270  
 DB 546 CATTCACCGCTCCCGAACTTGGCTGTGACCTTGGGACCAAGGGGAGTCTCTCGT 604

QY 2271 CTCCTGTGACTCAGCAGGAGTGGCCACCTTCAGGAGGGGGCGGCTGCCCTGGAGGC 2330

DB 605 CTCTTGTGACTCAGCAGAGGAGTGGCCACGTTTCAGG--AGGGGCGGTGGCTGGAGGC 662  
 QY 2331 TCAGCCCAACCTCCAGCTTTTCTCAGGGTGTCTCAGAGTCCAGAGTCTGAGCAATCT 2390  
 DB 663 TCAGCCCAACCTCCAGCTTTTCTCAGGGTGTCTCAGAGTCCAGAGTCTGAGCAATCT 722  
 QY 2391 GACCTTCTCCAAAGGCTCTGTATTATCAGTGGGAGTGCAGCCAACTCCCTGGCCATTG 2450  
 DB 723 GACCTTCTCCAAAGGCTCTGTATTATCAGTGGGAGTGCAGCCAACTCCCTGGCCATTG 781  
 QY 2451 GCCCAGGGGAGCTGGGCTGCTGAGGCTGCAGAGGGGAGTGCAGTGGAGGTTCTGT 2510  
 DB 782 GCCCAGGGG--ACGTGGGCTGCAGGCTGCAGAGGGGAGTGCAGTGGAGTTCGT 839  
 QY 2511 CCAGAGCTCCCTCATCTCGGGGCTGTGTGTGACGCGGCTGCTCAGGCACTCTCCTGT 2570  
 DB 840 CCAGAGCTCCCTCATCTCGGGGCTGTGTGTGAGCGGCTGCTCAGGCACTCTCCTGT 899  
 QY 2571 CTGAACCTGCTTACTGTGTGTAACTGTGCTCAGGATGATCTCTATAGGAGGGG 2630  
 DB 900 CTGAACCTGCTTACTGTGTGTAACTGTGCTCAGGATGATCTCTATAGGAGGGG 959  
 QY 2631 CGCAGGGCTGGGCTGTGACAACTCTGCTTTCACCATGCGCTTGCCTCGGTGGCCC 2690  
 DB 960 CGCAGGGCTGGGCTGTGACAACTCTGCTTTCACCATGCG-CTTGCTCGGTGGCCC 1018  
 QY 2691 TGACTGTGAGGAGGGGCTGAGGAGGAGGAGGAGTCTCAGGAGGAGTGCCT 2750  
 DB 1019 TGACTGTGAGGAGGGGCTGAGGAGGAGGAGGAGTCTCAGGAGGAGTGCCT 1078  
 QY 2751 GAGGGCTGGGAGGGGCTGCTCATGAGGACGAGGCTGAGTGAAGAGGAGGAGT 2810  
 DB 1079 GAGGGCTGGGAGGGGCTGCTCATGAGGACGAGGCTGAGTGAAGAGGAGGAGT 1138  
 QY 2811 GGGGCTGAGGCTGTGCTGAGTGGGACGAGGCTGAGGAGGAGGAGGAGT 2870  
 DB 1139 GGGGCTGAGGCTGTGCTGAGTGGGACGAGGCTGAGGAGGAGGAGGAGT 1198  
 QY 2871 CTGGGAGGATCTGAGTCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 2930  
 DB 1199 CTGGGAGGATCTGAGTCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1258  
 QY 2931 GAAGGAGGACCAACAACTCAGATGGGCTTTTGGGGAGGGGCTAGTCCGCCA 2990  
 DB 1259 GAAGGAGGACCAACAACTCAGATGGGCTTTTGGGGAGGGGCTAGTCCGCCA 1318  
 QY 2991 GCTTAAGCAGCAGGAGGAGTCTGATGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3050  
 DB 1319 GCTTAAGCAGCAGGAGGAGTCTGATGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1378  
 QY 3051 CCCCCAGCTACTGTATGCCCGGAGGAGGAGTGAACCCATAGGAGGCTG 3110  
 DB 1379 CCCCCAGCTACTGTATGCCCGGAGGAGGAGTGAACCCATAGGAGGCTG 1438  
 QY 3111 ATCGTAATGTTTATGTTTACTTCCCGAGGAGGAGTGAACCCATAGGAGGCTG 3170  
 DB 1439 ATCGTAATGTTTATGTTTACTTCCCGAGGAGGAGTGAACCCATAGGAGGCTG 1498  
 QY 3171 TTTAAAAA 3184  
 DB 1499 TTTAAAAA 1512

RESULT 40  
 AB273361  
 ID AB273361 standard; cDNA; 1536 BP.  
 XX  
 AC AB273361;  
 XX  
 DT 12-MAY-2003 (first entry)  
 XX  
 DE Secreted protein-encoding gene 81 cDNA clone HDPCW16, SEQ ID NO:91.  
 XX

KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;  
 KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;  
 KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;  
 KW drug screening; chromosome identification; chromosome mapping;  
 KW cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;  
 KW antianaemic; vulnary; chromosome 11q12-13.1; gene; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200277013-A2.  
 XX  
 XX 03-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US09370.  
 XX  
 XX 12-MAR-2001; 2001US-278650P.  
 XX  
 XX 12-SEP-2001; 2001US-095082.  
 XX  
 XX 12-SEP-2001; 2001US-095083.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 XX  
 XX WPI; 2003-040578/03.  
 XX  
 XX P-FSDB; ABR01027.  
 XX  
 XX New human secreted proteins and nucleic acids, useful for detecting or  
 PT treating cancer or other hyperproliferative disorders, autoimmune  
 PT disorders, inflammatory disorders, HIV disease, hepatitis or anemia -  
 XX  
 XX Claim 21; Page 1206; 247app; English.  
 XX  
 XX ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted  
 CC protein genes, and ABP00947-ABP01363 represent the proteins they encode.  
 CC ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The  
 CC invention also encompasses antibodies specific for the secreted proteins,  
 CC the use of the secreted proteins in drug screening and recombinant  
 CC vectors and host cells comprising a nucleic acid of the invention. The  
 CC secreted proteins are thought to be involved in biological activities  
 CC associated with cellular signalling, cellular differentiation, cell  
 CC migration, prohormone activation and neurotransmitter activity. The  
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
 CC fragments specific for the secreted proteins, and modulators of protein  
 CC activity are useful for diagnosing or treating cancers or other  
 CC hyperproliferative disorders. Additionally, the secreted proteins and  
 CC their nucleic acids may also be used in the treatment of autoimmune  
 CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS  
 CC (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote  
 CC wound healing. Nucleic acids of the invention may be used for chromosome  
 CC identification, chromosome mapping, in gene therapy, for identifying  
 CC individuals from minute biological samples, as hybridisation probes, and  
 CC as molecular weight markers. The present sequence represents a human  
 CC secreted protein-encoding cDNA clone of the invention.  
 XX  
 XX Sequence 1536 BP; 306 A; 464 C; 456 G; 310 T; 0 other;  
 SQ  
 Query Match 44.2%; Score 1408.4; DB 25; Length 1536;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1494; Conservative 0; Mismatches 11; Indels 9; Gaps 7;  
 QY 1671 TCTTCACATCTCCGCAATAGACACCTGCTCCCTATGGAGCTGCTCCCTCAGCCGTCAG 1730  
 DB 8 TCCGCAATCTCCCCATAGACACCTGCTCCCTATGGAGCTGCTCCCTCAGCCGTCAG 67  
 QY 1731 CCATCAGCCATGGCCCTCCAGTGCCTCTCTAGCCCTTCTTCCAGGAGCAGAGAGTGG 1790  
 DB 68 CCATCAGCCATGGCCCTCCAGTGCCTCTCTAGCCCTTCTTCCAGGAGCAGAGAGTGG 127  
 QY 1791 CCACCGGGGTGGCTCTGTCTACTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1850  
 DB 128 CCACCGGGGTGGCTCTGTCTACTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 186  
 QY 1851 CGGTCCATGGGTCTGGGCTGTGAGTCTCCCTTGCAGCCTGGTCACTAGGCATCACCCCC 1910

DB 187 CGGTCCATGGGTCTGGCCTGTGAGTCTCCCTTTGAGCCCTGGTCACTAGGCATCACCCCC 246  
 QY 1911 GCTTTGGTCTTTCAGATGCTCTTTGGGGTTCATAGGGGAGGCTCTAGTCTGGGAGAGGGCC 1970  
 DB 247 GCTTTGGTCTTTCAGATGCTCTTTGGGGTTCATAGGGGAGGCTCTAGTCTGGGAGAGGGCC 306  
 QY 1971 CTGACCCCTCCGGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCCCTTTTATA 2030  
 DB 307 CTGACCCCTCCGGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCCCTTTTATA 366  
 QY 2031 GAGAGGCTGCTTTGTTTAAAGCTCGGGTCTCCCTCTCTGACGCTCGTCTAGTACCCGA 2090  
 DB 367 GAGAGGCTGCTTTGTTTAAAGCTCGGGTCTCCCTCTCTGACGCTCGTCTAGTACCCGA 426  
 QY 2091 GGCCTCTCTTAAAGATGTCAGAGGCCGCCAGGCCCGGGGACACAGCCAGCCCAACCTTTGGG 2150  
 DB 427 GGCCTCTCTTAAAGATGTCAGAGGCCGCCAGGCCCGGGGACACAGCCAGCCCAACCTTTGGG 486  
 QY 2151 CCCTGGAAGAGTCTCCACCCCTACATAGAGTGTCTGACCTCGGCTTTTCAAGGGCCC 2210  
 DB 487 CCCTGGAAGA-TCCCTCACCCCTACATAGAGTGTCTGACCTCGGCTTTTCAAGGGCCC 545  
 QY 2211 CATTCCACCCGCTCCCACTTGGAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGT 2270  
 DB 546 CATTCCACCCGCTCCCACTTGGAGCTGTGACCTTTGGGACCAAGGGGAGTCCCTCGT 604  
 QY 2271 CTCTTTGATCTAGCAGAGCAGTGGCCAGTTTCAAGGAGGGGCGGCTGGCTGAGGCG 2330  
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 QY 2331 TCAGCCACCCCTCCAGCTTTTCTCAGGGTGTCTCAGGGTCCCAAGATCTTGGAGCAATCT 2390  
 DB 663 TCAGCCACCCCTCCAGCTTTTCTCAGGGTGTCTCAGGGTCCCAAGATCTTGGAGCAATCT 722  
 QY 2391 GACCCCTTCTCAAAGGCTCTGTTATCAGCTGGGAGTGGCCAGCAATCTTGGCCCAATTG 2450  
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 QY 2451 GCGGAGGGGAGCTGGGCGCTCCAGCTCAGAGGGGCACTGAGCTGGGAGGCTCTCGT 2510  
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 QY 2511 CCCAGCCCTCCCATCTCGGGGCTGTGTGTGACGCGCTGCTCAGGCACTCTCTCTGT 2570  
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 QY 2631 CGGAGGGCTGGGCGCTTGTGACCAATCTGCGCTTTCCACCATGCGCTTGGTGGGCC 2690  
 DB 960 CGGAGGGCTGGGCGCTTGTGACCAATCTGCGCTTTCCACCATGCGCTTGGTGGGCC 1018  
 QY 2691 TGACTGTGAGGAGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2750  
 DB 1019 TGACTGTGAGGAGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1078  
 QY 2751 GAGGGCTGGGGAGGGGTACCTCATGAGGACAGGGGTGAGGCTGAGAGGAGGAGGAGG 2810  
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 DB 1139 GGGGGCTGGAGGTCTGTGTAGCTGAGGGAGCGGGCAAGTGAAGGGAGGAGGAGGAGGAGG 1198  
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 DB 1199 CTGGAGGATCTCAGCTGTCTGTGTAGCTGTAAACCCACTAATCAGTCTTCTAGATTCAGGG 1258  
 QY 2931 GAAGGGGAGGACCAACCACTCAGATGGGGGCTTTCGGGAGGAGGAGGAGGAGGAGGAGGAGG 2990

Db 1259 GAAGGGCAGGCACCAACTCAGAAATGGGGGCTTTCGGGGAGGGCCCTAGTCCCCCCA 1318  
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Db 1319 GCTCTAAGCAGCCAGGAGGACCTGCATCTAAGCATCTGGGTTGCCATGGCAATGGCATG 1378  
Qy 3051 CCCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGGCAGAAATGAACCCATAGGAGCTG 3110  
Db 1379 CCCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGGCAGAAATGAACCCATAGGAGCTG 1438  
Qy 3111 ATCGTAATGTTTATCATGTTTACTTCCCCACCCCTACATTTTGGAAATAAAATAAGGAAT 3170  
Db 1439 ATCGTAATGTTTATCATGTTTACTTCCCCACCCCTACATTTTGGAAATAAAATAAGGAAT 1498  
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Db 1499 TTTAAAAA 1512

Search completed: December 10, 2003, 13:03:55  
Job time : 574 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: December 9, 2003, 10:07:15 ; Search time 46 Seconds

(without alignments)  
1532.056 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

Sequence: 1 MCKGNGQGGAAAEVSVPT.....DIIRSLKSGKLWLDAYLHK 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                 |
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| 1          | 2438  | 100.0       | 444    | 21 | AAV59182 Human oxidoreducta |
| 2          | 2425  | 99.5        | 444    | 21 | AA441810 Human CRFX ORF1574 |
| 3          | 2425  | 99.5        | 444    | 21 | AAV97539 Human fatty acid d |
| 4          | 2425  | 99.5        | 444    | 22 | AAE11083 Human delta-6-desa |
| 5          | 2425  | 99.5        | 444    | 22 | AAV93425 Human polypeptide, |
| 6          | 2425  | 99.5        | 473    | 22 | AAE11084 C-terminal tagged  |
| 7          | 2190  | 89.8        | 444    | 22 | AAV51801 Rat fatty acid des |
| 8          | 2190  | 89.8        | 444    | 22 | AAE11081 Rat delta-6-desatu |
| 9          | 2186  | 89.7        | 473    | 22 | AAE11082 C-terminal tagged  |

|    |        |      |     |    |                             |
|----|--------|------|-----|----|-----------------------------|
| 10 | 1940.5 | 79.6 | 432 | 23 | ABG94691 Human delta5-desat |
| 11 | 1940.5 | 79.6 | 432 | 23 | ABG96508 Human partial desa |
| 12 | 1940.5 | 79.6 | 465 | 23 | ABG94704 Human delta5-desat |
| 13 | 1940.5 | 79.6 | 465 | 23 | ABG96523 Human partial desa |
| 14 | 1935   | 79.4 | 432 | 21 | AAV95446 Human delta-5-desa |
| 15 | 1935   | 79.4 | 746 | 19 | AAW84156 Human desaturase e |
| 16 | 1935   | 79.4 | 746 | 20 | AAW85135 A desaturase enzym |
| 17 | 1935   | 79.4 | 752 | 21 | AAV92618 Human desaturase h |
| 18 | 1935   | 79.4 | 753 | 20 | AAW95514 Amino acid sequenc |
| 19 | 1935   | 79.4 | 753 | 21 | AAV84703 Amino acid sequenc |
| 20 | 1790   | 73.4 | 322 | 22 | AAV93456 Human polypeptide, |
| 21 | 1646   | 67.5 | 294 | 21 | AAV95448 Human delta-5-desa |
| 22 | 1646   | 67.5 | 608 | 19 | AAW84155 Human desaturase e |
| 23 | 1646   | 67.5 | 608 | 20 | AAW85134 A desaturase enzym |
| 24 | 1646   | 67.5 | 614 | 21 | AAV92617 Human desaturase h |
| 25 | 1646   | 67.5 | 615 | 20 | AAW95513 Amino acid sequenc |
| 26 | 1646   | 67.5 | 615 | 21 | AAV84702 Amino acid sequenc |
| 27 | 1628.5 | 66.8 | 356 | 23 | ABG94699 Human delta5-desat |
| 28 | 1628.5 | 66.8 | 356 | 23 | ABG96517 Human partial desa |
| 29 | 1594   | 65.4 | 286 | 21 | AAV88942 Breast and ovarian |
| 30 | 1560.5 | 64.0 | 445 | 21 | AAV97540 Human fatty acid d |
| 31 | 1560.5 | 64.0 | 445 | 21 | AAV83229 CYB5RP fatty acid  |
| 32 | 1560.5 | 64.0 | 445 | 24 | ABU08788 Human delta 6 desa |
| 33 | 1560.5 | 64.0 | 490 | 22 | AAW25786 Human protein sequ |
| 34 | 1527   | 62.6 | 446 | 22 | ABG10281 Novel human diagno |
| 35 | 1516   | 62.2 | 444 | 21 | AAV97538 Human fatty acid d |
| 36 | 1516   | 62.2 | 473 | 23 | AAE14740 C-terminal tagged  |
| 37 | 1515   | 62.1 | 444 | 24 | ABU08789 Human delta 6 desa |
| 38 | 1515   | 62.1 | 501 | 22 | AAV93314 Human polypeptide, |
| 39 | 1512   | 62.0 | 444 | 22 | AAV94041 Human protein sequ |
| 40 | 1508   | 61.9 | 444 | 21 | AAV95445 Human delta-5-desa |
| 41 | 1508   | 61.9 | 444 | 22 | AAV31686 Amino acid sequenc |
| 42 | 1508   | 61.9 | 444 | 23 | ABG94694 Human delta5-desat |
| 43 | 1508   | 61.9 | 444 | 23 | ABG96510 Human delta5 desat |
| 44 | 1508   | 61.9 | 445 | 23 | ABG96522 Human delta5 desat |
| 45 | 1508   | 61.9 | 445 | 23 | ABG96528 Human delta5 desat |

ALIGNMENTS

RESULT 1

AAV59182  
ID AAV59182 standard; Protein; 444 AA.

XX AC AAV59182;

XX DT 28-MAR-2000 (first entry)

XX DE Human oxidoreductase protein (HORP)-5 (clone 008879).

XX KW Human oxidoreductase protein; HORP; neurological; autoimmune; cancer;  
XX KW reproduction; cell proliferation; vesicle trafficking; endocrine.

XX OS Homo sapiens.

XX PN WO200000622-A2.

XX PD 06-JAN-2000.

XX PF 29-JUN-1999; 99WO-US14711.

XX PR 30-JUN-1998; 98US-0091177.

XX PR 16-JUL-1998; 98US-0155241.

XX (INCY-) INCYTE PHARM INC.

XX PA Bardman O, Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ;

XX PI Gorgone GA, Baughn MR;

XX PI C-terminal tagged

XX DR WPI; 2000-117171/10.

XX DR N-PSDB; AAZ48247.

XX





QY 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180  
DB 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180  
QY 181 DYGHLSVYRKPKWNHVKFVIGHLKGSANWNNHRRHFQHHAKPNIPHKDPDNNMLHVFV 240  
DB 181 DYGHLSVYRKPKWNHVKFVIGHLKGSANWNNHRRHFQHHAKPNIPHKDPDNNMLHVFV 240  
QY 241 LGWQPIEYGGKKLKYLPYNHCHYEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
DB 241 LGWQPIEYGGKKLKYLPYNHCHYEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
QY 301 SYIRPFITYIPFYGILGALLFLNFIPLSHWFWVVTOMNHIWETDQAYRDWFSQ 360  
DB 301 SYIRPFITYIPFYGILGALLFLNFIPLSHWFWVVTOMNHIWETDQAYRDWFSQ 360  
QY 361 TATCNVEQSFNDWFSGHLNFOIEHLLPPTMPRNLHKKIAPLVKSLCAKGIYOEKPLL 420  
DB 361 TATCNVEQSFNDWFSGHLNFOIEHLLPPTMPRNLHKKIAPLVKSLCAKGIYOEKPLL 420  
QY 421 RALLDIIRSLKXSGKMLDAYLHK 444  
DB 421 RALLDIIRSLKXSGKMLDAYLHK 444

RESULT 3

AA97539  
ID AA97539 standard; Protein; 444 AA.  
AC AA97539;  
DT 15-JAN-2001 (first entry)  
DE Human fatty acid desaturase 2 protein sequence.  
XX Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;  
KW liver disease; coronary artery disease; cancer.  
XX Homo sapiens.  
XX EP1035207-A1.  
XX 13-SEP-2000.  
XX 09-MAR-1999; 99EP-0104664.  
XX 09-MAR-1999; 99EP-0104664.  
XX (MULT-) MULTIGENE BIOTECH GMBH.  
XX Weber BHF, Marquardt A;  
XX WPI: 2000-559875/52.  
XX N-PSDB; AAA90953.  
XX Novel cDNA molecules encoding three human fatty acid desaturases,  
PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,  
PT coronary artery disease and cancer -  
XX Claim 1; Page 41-43; 72pp; English.

CC This sequence is the human fatty acid desaturase, FADS2, of the  
CC invention. An antibody directed against the 3 FADS molecule of the  
CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or  
CC therapeutic purposes. The FADS coding sequences are useful in gene  
CC therapy. The polypeptide and antibodies are useful in screening for  
CC modulating drugs. The polypeptides are also useful for treating liver  
CC disease, coronary artery disease and cancer.  
CC Note: Two copies of the sequence listing are present within this  
CC patent, which contain different sequence listings. AAA90952 and AAA90955 are  
CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are  
CC stated as being SEQ ID's 7-22.

XX SQ Sequence 444 AA;  
Query Match 99.5%; Score 2425; DB 21; Length 444;  
Best Local Similarity 99.5%; Pred. No. 1.1e-256;  
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGKGNQGEAGAAREVSVPTFSWEEIQHNLRTDGLVIDRKVYNTKWSIQHPGGQRVI 60  
DB 1 MGKGNQGEAGAAREVSVPTFSWEEIQHNLRTDGLVIDRKVYNTKWSIQHPGGQRVI 60  
QY 61 GHYAGEDATDAFRAPHPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKA 120  
DB 61 GHYAGEDATDAFRAPHPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKA 120  
QY 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180  
DB 121 EDMNLFKTNHVFLLAHIALESIAWFTVYFGNGWIPTLITAFVLATSOAQAGWLOH 180  
QY 181 DYGHLSVYRKPKWNHVKFVIGHLKGSANWNNHRRHFQHHAKPNIPHKDPDNNMLHVFV 240  
DB 181 DYGHLSVYRKPKWNHVKFVIGHLKGSANWNNHRRHFQHHAKPNIPHKDPDNNMLHVFV 240  
QY 241 LGWQPIEYGGKKLKYLPYNHCHYEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
DB 241 LGWQPIEYGGKKLKYLPYNHCHYEYFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
QY 301 SYIRPFITYIPFYGILGALLFLNFIPLSHWFWVVTOMNHIWETDQAYRDWFSQ 360  
DB 301 SYIRPFITYIPFYGILGALLFLNFIPLSHWFWVVTOMNHIWETDQAYRDWFSQ 360  
QY 361 TATCNVEQSFNDWFSGHLNFOIEHLLPPTMPRNLHKKIAPLVKSLCAKGIYOEKPLL 420  
DB 361 TATCNVEQSFNDWFSGHLNFOIEHLLPPTMPRNLHKKIAPLVKSLCAKGIYOEKPLL 420  
QY 421 RALLDIIRSLKXSGKMLDAYLHK 444  
DB 421 RALLDIIRSLKXSGKMLDAYLHK 444

RESULT 4

AAE11083  
ID AAE11083 standard; Protein; 444 AA.  
XX AAE11083;  
DT 18-DEC-2001 (first entry)  
XX Human delta-6-desaturase (hD6D-1).  
XX Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;  
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;  
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;  
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;  
KW cardiovascular disease; Crohn's disease; congenital liver disease;  
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;  
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;  
KW autoimmune disorder; hypercholesterolemia; atopic disorder; hD6D-1;  
KW gene therapy; human.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT Domain 53..76 /note= "Cytochrome b5 motif"  
FT Region 180..184 /note= "His II box"  
FT Region 217..221 /note= "His II box"  
FT Region 382..386 /note= "His III box"  
XX WO200170993-A2.

[illegible]

Dd 421 RALLDIIRSLKSGKLWLDLAYLHK 444

RESULT 5  
AAM93425  
AAM93425 standard; Protein; 444 AA.

XX XX  
AC AC  
XX XX  
DT 06-NOV-2001 (first entry)  
XX XX  
DE Human polypeptide, SEQ ID NO: 3050.  
XX XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
OS Homo sapiens.  
XX XX  
EP EPI130094-A2.  
XX XX  
PD 05-SEP-2001.  
XX XX  
PF 07-JUL-2000; 2000EF-0114089.  
XX XX  
PR 08-JUL-1999; 99JP-0194486.  
PR 11-JAN-2000; 2000JP-0118774.  
PR 02-MAY-2000; 2000JP-0183765.  
XX XX  
FA (HELI-) HELIX RES INST.  
XX XX  
FI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
DR WPI; 2001-524255/58.  
DR N-PSDB; AAK94346.  
XX XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their  
PT use in genetic manipulation -  
XX XX  
PS Claim 8; SEQ ID NO 3050; 1380pp + sequence listing; English.  
CC The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
CC molecules have been determined. Primers for synthesising the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesised by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily  
CC without any special methods. The present sequence is a polypeptide  
CC encoded by a full length human cDNA of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.  
XX XX  
SQ Sequence 444 AA;

Query Match 99.5%; Score 2425; DB 22; Length 444;  
Best Local Similarity 99.5%; Pred. No. 1.1e-256; Gaps 0;  
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGNGCGGAAREVSVPFTSWEIEIQKHNLRTDGLVIDEKVYNITKWSIQHPGGORVI 60  
Db 1 MGKGNGCGGAAREVSVPFTSWEIEIQKHNLRTDRLWLIDRKVYNITKWSIQHPGGORVI 60

QY 61 GHYAGEDATDAFRAPHDPLEFVGKFLKELLIGELAPEPSODHGKNSKITDEFALRKT 120  
Db 61 GHYAGEDATDAFRAPHDPLEFVGKFLKELLIGELAPEPSODHGKNSKITDEFALRKT 120

QY 121 EDNMLFKTNHVFLLLAHHIALESIAFWTFYFGNGWIPTLTAFVLATSQAQAGWLQH 180  
Db 121 EDNMLFKTNHVFLLLAHHIALESIAFWTFYFGNGWIPTLTAFVLATSQAQAGWLQH 180

QY 181 DYGHLSVTYKPKWNHLVKHFVIGHLKGSANWWHRHFQHHAKPNI PHKD PDVNNMLHV 240

Db 181 DYGLSVYRKPKWNLVHKFVIGHLKGASANNWNRHFQHHAKPNIFHDKPDVNNMLHVFV 240  
 QY 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOYQIIMTMIHVKWVYDLAWAV 300  
 Db 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOYQIIMTMIHVKWVYDLAWAV 300  
 QY 301 SYIRFFTYIPFYGILGALLFLNPIRFLESHWFWVTQMNHIVWEIDQAYRDWFSQ 360  
 Db 301 SYIRFFTYIPFYGILGALLFLNPIRFLESHWFWVTQMNHIVWEIDQAYRDWFSQ 360  
 QY 361 TATCNVEQSFNDWFSGHLNFQIEHLLPPTVPRNLHKLAPLVKSLCAKGIYEQKPLL 420  
 Db 361 TATCNVEQSFNDWFSGHLNFQIEHLLPPTVPRNLHKLAPLVKSLCAKGIYEQKPLL 420  
 QY 421 RALLDIIRSLKSGKMLDAYLHK 444  
 Db 421 RALLDIIRSLKSGKMLDAYLHK 444

## RESULT 6

AAE11084  
 ID AAE11084 standard; Protein; 473 AA.

AC AAE11084;

DT 18-DEC-2001 (first entry)

DE C-terminal tagged human delta-6-desaturase (hδ6D-1).

KW Delta-6-desaturase gene; δ6D; lipid metabolism disorder; atopic eczema;  
 mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;  
 Gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;  
 endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;  
 cardiovascular disease; Crohn's disease; congenital liver disease;  
 schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;  
 arterial hypertension; atherosclerosis; chronic inflammatory disorder;  
 autoimmune disorder; hypercholesterolaemia; atopic disorder; hδ6D-1;  
 gene therapy; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 451..464

FT /note= "V5 tag"

FT Region 468..473

FT /note= "6xHis tag"

XX WO200170993-A2.

XX 27-SEP-2001.

XX 26-MAR-2001; 2001WO-CA00398.

XX 24-MAR-2000; 2000CA-2301158.

XX (SCOT-) SCOTIA HOLDINGS PLC.

XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;

XX WPI; 2001-611507/70.

XX Nucleic acid encoding delta-6-desaturase gene useful for treating  
 atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,  
 gastrointestinal disorders, viral infections and post viral fatigue -

XX Example 4; Fig 5; 164pp; English.

XX The invention relates to polynucleotides that control delta-6  
 desaturase genes (δ6D) and methods useful for identifying compounds  
 which inhibit or promote the activity of mammalian δ6D. Compounds  
 which modulate δ6D gene segments are useful for treating lipid  
 metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid  
 arthritis, Sjogren's syndrome, gastrointestinal disorders, viral

CC infections and post viral fatigue, pre-menstrual syndrome,  
 endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,  
 cardiovascular disease, Crohn's disease, cancer, congenital liver  
 disease, schizophrenia, diabetes and diabetic complications including  
 diabetic neuropathy, nephropathy and retinopathy. Compounds of the  
 invention are also useful for inhibiting progressive and acute  
 disorders such as arterial hypertension, atherosclerosis, chronic  
 inflammatory and autoimmune disorders, hypercholesterolaemia and  
 other atopic disorders. δ6D genes are useful in gene therapy. The  
 present sequence is C-terminal tagged human delta-6-desaturase  
 (hδ6D-1) enzyme.

XX Sequence 473 AA;

Query Match 99.5%; Score 2425; DB 22; Length 473;

Best Local Similarity 99.5%; Pred. No. 1.3e-256;

Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKGGNQGEAAREVSVPTFSWEIQKHNLTDSGLVIDRKVYNIITKWSICHPGQQRVI 60

Db 1 MGKGGNQGEAAREVSVPTFSWEIQKHNLTDRWLVIDRKVYNIITKWSICHPGQQRVI 60

QY 61 GHYAGEDATDAFAPHDLEFVGKFLKPLLIIGELAPESPQDHGKSKITEDFRALRKTA 120

Db 61 GHYAGEDATDAFAPHDLEFVGKFLKPLLIIGELAPESPQDHGKSKITEDFRALRKTA 120

QY 121 EDNLEKTNHVFLLLAHIIALESTAMFTVFYFGNGWIPTLITAFVLATSOAQAGWLOH 180

Db 121 EDNLEKTNHVFLLLAHIIALESTAMFTVFYFGNGWIPTLITAFVLATSOAQAGWLOH 180

QY 181 DYGLHSVYRKPKWNLVHKFVIGHLKGASANNWNRHFQHHAKPNIFHDKPDVNNMLHVFV 240

Db 181 DYGLHSVYRKPKWNLVHKFVIGHLKGASANNWNRHFQHHAKPNIFHDKPDVNNMLHVFV 240

QY 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOYQIIMTMIHVKWVYDLAWAV 300

Db 241 LGEWQPIEYGGKKLKYLPYNHOFHEFFLIGPPLIPMYFOYQIIMTMIHVKWVYDLAWAV 300

QY 301 SYIRFFTYIPFYGILGALLFLNPIRFLESHWFWVTQMNHIVWEIDQAYRDWFSQ 360

Db 301 SYIRFFTYIPFYGILGALLFLNPIRFLESHWFWVTQMNHIVWEIDQAYRDWFSQ 360

QY 361 TATCNVEQSFNDWFSGHLNFQIEHLLPPTVPRNLHKLAPLVKSLCAKGIYEQKPLL 420

Db 361 TATCNVEQSFNDWFSGHLNFQIEHLLPPTVPRNLHKLAPLVKSLCAKGIYEQKPLL 420

QY 421 RALLDIIRSLKSGKMLDAYLHK 444

Db 421 RALLDIIRSLKSGKMLDAYLHK 444

## RESULT 7

AA51801

ID AA51801 standard; Protein; 444 AA.

AC AA51801;

XX 29-JAN-2002 (first entry)

XX Rat fatty acid desaturase.

XX Rat; fatty acid desaturase; unsaturated long-chain fatty acid production;  
 fermentation.

XX Rattus norvegicus.

XX WO200175069-A1.

XX 11-OCT-2001.

XX 31-MAR-2000; 2000WO-JP02129.

XX 31-MAR-2000; 2000WO-JP02129.

XX (IDM ) IDEMITSU PETROCHEM CO LTD.  
 XX Suzuki O, Ono K, Aki T, Shimauchi T, Nakajima T, Kondo A;  
 XX WPI; 2001-648552/74.  
 XX N-PSDB; AAI66599.  
 XX New microorganism for the efficient expression of long-chain  
 PT unsaturated fatty acids into the medium, comprises Saccharomyces  
 PT transformed by a fatty acid desaturase gene -  
 XX Disclosure; Page 26-27; 29pp; Japanese.  
 XX The present invention relates to a microorganism transformed by a gene  
 CC encoding a fatty acid desaturase and having the ability to secrete lipids  
 CC into the medium. This can be used for the efficient production of  
 CC unsaturated long-chain fatty acids by fermentation. The present sequence  
 CC is the fatty acid desaturase from Rattus norvegicus.  
 XX  
 SQ Sequence 444 AA;  
 Query Match 89.8%; Score 2190; DB 22; Length 444;  
 Best Local Similarity 87.8%; Pred. No. 6.7e-231;  
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;  
 QY 1 MGKGGNQGEGAAREVSVPTFSWEEIQKHLNLTDSGLVIDRKVNITKWSIQHPGGORVI 60  
 Db 1 MGKGGNQGEGSTELQAPMPTFRWEEIQKHLNLTDRWLVIDRKVNITKWSIQHPGGHVI 60  
 QY 61 GHYAGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120  
 Db 61 GHYSGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120  
 QY 121 EDMNLFKTNHVPFLLLAHIIALESIAWFTVYFGNGMIPTLITAFVLATSQAQAGWLQ 180  
 Db 121 EDMNLFKTNHVPFLLSHIIVMESIAWFTVYFGNGMIPTVITAFVLATSQAQAGWLQ 180  
 QY 181 DYGHLSVYRKPKWNLVHKFVIGHLKGSANWNNHRRHFOHAKPNIEHKDPDVMMLHVFV 240  
 Db 181 DYGHLSVYKSIWNHIVHKFVIGHLKGSANWNNHRRHFOHAKPNIEHKDPDVKSLHVFV 240  
 QY 241 LGSWQIEYQKKLKYLPYNHQHEYFLLIGPFLIPMYFYQIIMTIVHKWVDLAWAV 300  
 Db 241 LGSWQIEYQKKLKYLPYNHQHEYFLLIGPFLIPMYFYQIIMTIVHRRDWDVLAWAI 300  
 QY 301 SYVIRFFTYIPYIGLALLFNFTIRFLESHWFWVVTQNHIVMEIDOEAYRDWFSOL 360  
 Db 301 SYVARFFTYIPYIGLALVFLNFTIRFLESHWFWVVTQNHIVMEIDLDHYRDWFSOL 360  
 QY 361 TATCNVEQSFNDWFSGLNLFQIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLL 420  
 Db 361 AATCNVEQSFNDWFSGLNLFQIEHLLFPTMPRHNLKIAPLVKSICAKHGIEYQEKPLL 420  
 QY 421 RALLDIIRSLKSGKWLDAYLHK 444  
 Db 421 RALLDIVSSLKSGKWLDAYLHK 444

RESULT 8  
 AAE11081  
 ID AAE11081 standard; Protein; 444 AA.  
 XX  
 AC AAE11081;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Rat delta-6-desaturase (rd6D-1).  
 XX  
 KW Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;  
 KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;  
 KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;  
 KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;

KW cardiovascular disease; Crohn's disease; congenital liver disease;  
 KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;  
 KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;  
 KW autoimmune disorder; hypercholesterolaemia; atopic disorder; rd6D-1;  
 KW gene therapy; rat.  
 XX  
 OS Rattus sp.  
 XX  
 XX Key Location/Qualifiers  
 XX 53..76  
 FT Domain /note= "Cytochrome b5 motif"  
 FT Region 180..184  
 FT /note= "His II box"  
 FT Region 217..221  
 FT /note= "His II box"  
 FT Misc-difference 240  
 FT /note= "Encoded by GCC"  
 FT Region 382..386  
 FT /note= "His III box"  
 XX  
 PN W0200170993-A2.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 26-MAR-2001; 2001WO-CA00398.  
 PF  
 XX 24-MAR-2000; 2000CA-2301158.  
 PR  
 XX (SCOT-) SCOTIA HOLDINGS PLC.  
 FA  
 XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;  
 PI  
 XX WPI; 2001-611507/70.  
 DR  
 XX N-PSDB; AAI19402.  
 DR  
 XX Nucleic acid encoding delta-6-desaturase gene useful for treating  
 PT atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,  
 PT gastrointestinal disorders, viral infections and post viral fatigue -  
 PT  
 XX Example 3; Fig 5; 164pp; English.  
 PS  
 XX The invention relates to polynucleotides that control delta-6  
 CC desaturase genes (D6D) and methods useful for identifying compounds  
 CC which inhibit or promote the activity of mammalian D6D. Compounds  
 CC which modulate D6D gene segments are useful for treating lipid  
 CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid  
 CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral  
 CC infections and post viral fatigue, pre-menstrual syndrome,  
 CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,  
 CC cardiovascular disease, Crohn's disease, cancer, congenital liver  
 CC disease, schizophrenia, diabetes and diabetic complications including  
 CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the  
 CC invention are also useful for inhibiting progressive and acute  
 CC disorders such as arterial hypertension, atherosclerosis, chronic  
 CC inflammatory and autoimmune disorders, hypercholesterolaemia and  
 CC other atopic disorders. D6D genes are useful in gene therapy. The  
 CC present sequence is rat delta-6-desaturase (rd6D-1).  
 XX  
 SQ Sequence 444 AA;  
 Query Match 89.8%; Score 2190; DB 22; Length 444;  
 Best Local Similarity 87.8%; Pred. No. 6.7e-231;  
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;  
 QY 1 MGKGGNQGEGAAREVSVPTFSWEEIQKHLNLTDSGLVIDRKVNITKWSIQHPGGORVI 60  
 Db 1 MGKGGNQGEGSTELQAPMPTFRWEEIQKHLNLTDRWLVIDRKVNITKWSIQHPGGHVI 60  
 QY 61 GHYAGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120  
 Db 61 GHYSGEDATDAFRAHLDLDFVCKFLKPLLIGELAPEPSQDHGKNSKITDFRALRXTA 120  
 QY 121 EDMNLFKTNHVPFLLLAHIIALESIAWFTVYFGNGMIPTLITAFVLATSQAQAGWLQ 180  
 Db 121 EDMNLFKTNHVPFLLSHIIVMESIAWFTVYFGNGMIPTVITAFVLATSQAQAGWLQ 180

121 EDMNLFKTNHLPFPILLSHIIVMESIAWFTLSYFGNGWIPVTITAFVLATSOAQAGWLQH 180  
181 DYGHLSVYRKPNHVLVHKVIGHLKASANWNNHRRHFOHAKPNI FHKDPDVMVHLVVF 240  
181 DYGHLSVYKKSINWHI VHKVIGHLKASANWNNHRRHFOHAKPNI FHKDPDVKSLHVF 240  
241 LGWQPIEYGGKKLKYLPYNHQBHEFFLIPGPPLLIPMYFOYQIIMTMVHKWVDLAWAV 300  
241 LGWQPIEYGGKKLKYLPYNHQBHEFFLIPGPPLLIPMYFOYQIIMTMVHKWVDLAWAI 300  
301 SYIRPFITYIPFYGILGALLFNIRFLESHWFWVTQNMHIVMEIDQAYRDWESSOL 360  
301 SYARPFYTYIPFYGILGALLFNIRFLESHWFWVTQNMHIVMEIDQAYRDWESSOL 360  
361 TATCNVQSFNDWFSGHLNFQIEHLLFPTMPRNLHAKIAPLVKSLCAKHGIEYQEKPLL 420  
361 AATCNVQSFNDWFSGHLNFQIEHLLFPTMPRNLHAKIAPLVKSLCAKHGIEYQEKPLL 420  
421 RALLDIIRSLKSKGKWLMDAYLHK 444  
421 RALLDIVSSLKSKGELMDAYLHK 444

RESULT 9  
ID AAE11082 standard; Protein; 473 AA.  
AC AAE11082;  
XX  
XX  
DT 18-DEC-2001 (first entry)  
DE C-terminal tagged rat delta-6-desaturase (rD6D-1).  
XX  
XX  
KW Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;  
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;  
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;  
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;  
KW cardiovascular disease; Crohn's disease; congenital liver disease;  
KW schizoprenia; diabetic neuropathy; nephropathy; retinopathy; cancer;  
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;  
KW autoimmune disorder; hypercholesterolaemia; atopic disorder; rD6D-1;  
KW gene therapy; rat.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT Region 451..464  
FT /note= "v5 tag"  
FT Region 468..473  
FT /note= "6xHis tag"  
XX  
XX WO200170993-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 26-MAR-2001; 2001WO-CA00398.  
XX  
XX 24-MAR-2000; 2000CA-2301158.  
XX  
XX (SCOT-) SCOTIA HOLDINGS PLC.  
XX  
XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;  
XX WPI; 2001-611507/70.  
XX  
XX Nucleic acid encoding delta-6-desaturase gene useful for treating  
XX atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,  
XX gastrointestinal disorders, viral infections and post viral fatigue -  
XX Example 3; Fig 5; 164pp; English.  
XX  
XX The invention relates to polynucleotides that control delta-6

desaturase genes (D6D) and methods useful for identifying compounds  
CC which inhibit or promote the activity of mammalian D6D. Compounds  
CC which modulate D6D gene segments are useful for treating lipid  
CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid  
CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral  
CC infections and post viral fatigue, pre-menstrual syndrome, endo-  
CC metoriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,  
CC cardiovascular disease, Crohn's disease, cancer, congenital liver  
CC disease, schizoprenia, diabetes and diabetic complications including  
CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the  
CC invention are also useful for inhibiting progressive and acute  
CC disorders such as arterial hypertension, atherosclerosis, chronic  
CC inflammatory and autoimmune disorders, hypercholesterolaemia and  
CC other atopic disorders. D6D genes are useful in gene therapy. The  
CC present sequence is C-terminal tagged rat delta-6-desaturase  
CC (rD6D-1) enzyme.  
XX  
XX  
SQ Sequence 473 AA;  
Query Match 89.7%; Score 2186; DB 22; Length 473;  
Best Local Similarity 87.6%; Fred. No. 2e-230;  
Matches 389; Conservative 26; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MGKGNQGEAGAEVSVPTFSWEIQRHNLRTDGLVIDRKVYNTKWSIQHGGQRV 60  
DB 1 MGKGNQGEAGAEVSVPTFSWEIQRHNLRTDGLVIDRKVYNTKWSIQHGGQRV 60  
QY 61 GHYAGEDATDAFAPHPDLEFVGKPLKPLLIGELAPEPSODHGKNSKITEDFALR 120  
DB 61 GHYAGEDATDAFAPHPDLEFVGKPLKPLLIGELAPEPSODHGKNSKITEDFALR 120  
QY 121 EDMNLFKTNHVPFLLIHLAIIAIESIAWFTVYFGNGWIPVTITAFVLATSOAQAG 180  
DB 121 EDMNLFKTNHVPFLLIHLAIIAIESIAWFTVYFGNGWIPVTITAFVLATSOAQAG 180  
QY 181 DYGHLSVYRKPNHVLVHKVIGHLKASANWNNHRRHFOHAKPNI FHKDPDVMVHLV 240  
DB 181 DYGHLSVYKKSINWHI VHKVIGHLKASANWNNHRRHFOHAKPNI FHKDPDVKSLH 240  
QY 241 LGWQPIEYGGKKLKYLPYNHQBHEFFLIPGPPLLIPMYFOYQIIMTMVHKWVDLAW 300  
DB 241 LGWQPIEYGGKKLKYLPYNHQBHEFFLIPGPPLLIPMYFOYQIIMTMVHKWVDLAW 300  
QY 301 SYIRPFITYIPFYGILGALLFNIRFLESHWFWVTQNMHIVMEIDQAYRDWESSOL 360  
DB 301 SYARPFYTYIPFYGILGALLFNIRFLESHWFWVTQNMHIVMEIDQAYRDWESSOL 360  
QY 361 TATCNVQSFNDWFSGHLNFQIEHLLFPTMPRNLHAKIAPLVKSLCAKHGIEYQEK 420  
DB 361 AATCNVQSFNDWFSGHLNFQIEHLLFPTMPRNLHAKIAPLVKSLCAKHGIEYQEK 420  
QY 421 RALLDIIRSLKSKGKWLMDAYLHK 444  
DB 421 RALLDIVSSLKSKGELMDAYLHK 444

RESULT 10  
ID ABG94691 standard; Protein; 432 AA.  
XX  
XX AC ABG94691;  
XX  
XX DT 02-DEC-2002 (first entry)  
XX  
XX Human delta5-desaturase #1.  
XX  
XX Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;  
XX dihomono-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;  
XX eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;  
XX enzyme.  
XX  
XX Homo sapiens.  
XX

PN US6432684-B1.  
XX 13-AUG-2002.  
XX 08-JAN-1999; 99US-0227613.  
XX 11-APR-1997; 97US-0833610.  
XX 10-APR-1998; 98WO-US07422.  
XX (ABBO ) ABBOTT LAB.  
XX Mukerji P, Leonard AE, Huang Y, Das T;  
XX WPI; 2002-689761/74.  
XX Nucleic acids encoding human DELTAS-desaturase, useful for catalysing  
XX the conversion of dihomogamma-linolenic acid to arachidonic acid and  
XX in the conversion of 20:4n-3 to eicosapentaenoic acid -  
XX  
XX Example 1; Figure 9; 89pp; English.  
XX The invention relates to an isolated human deltas-desaturase nucleotide  
XX sequence (I) which desaturates polyunsaturated fatty acids at  
XX carbon 5. The nucleotide sequence (I) may be used in the recombinant  
XX production of vectors and host cells for the production of deltas-  
XX desaturase. Deltas-desaturase may be utilised in the conversion of  
XX dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the  
XX conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA or  
XX polyunsaturated fatty acids produced from it may be added to  
XX pharmaceutical compositions, nutritional compositions, animal feeds, as  
XX well as other products such as cosmetics. ABG94691-ABG94708 represent  
XX human deltas-desaturase amino acid sequences of the invention.  
XX  
XX Sequence 432 AA;  
Query Match 79.6%; Score 1940.5; DB 23; Length 432;  
Best Local Similarity 81.8%; Pred. No. 1.4e-203;  
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;  
QY 19 PT---FSWEEIQKHNRDTSGLVIDEKYNIKFSIOHPGGQGVTHYAGDADAPAF 75  
DB 3 PTPRYFTNDEVAQSCCEERNLVIDRKVYNISEFTRRHPHGGSRVISHAGQADTPFVAF 62  
QY 76 HPDLEFVGKFLKLLIGELAPESPDSODHGKNSKITEDFALFKTAEDMNLFTNHFVFL 135  
DB 63 HINKGLVKYKMSLLIGELSPQSPFPTKXKELTDFELRATVRMGLMKANHFVFL 122  
QY 136 LLAHIIALSIATFTVYFGNGWIPLTITAFVATSOAQAGLQHDYGHLSVYRKPKNH 195  
DB 123 YLLHILLDGAALTLVWFGTSLPFLLCVLLSAVQAQAGLQHDYGHLSVYRKPKNH 182  
QY 196 LVHKFVIGHLKGSANWNNHRRHPOHAKPNIHKDPDVMNLHVFLGEWQPIEYGGKLLK 255  
DB 183 LVKHFVIGHLKGSANWNNHRRHPOHAKPNIHKDPDVMNLHVFLGEWQPIEYGGKLLK 242  
QY 256 YLPYNHQQEYFFLIGPLLPIMYFQYQIIMTMVHKQWDLAWAVSYIRFTITIPFVG 315  
DB 243 YLPYNHQQEYFFLIGPLLPIMYFQYQIIMTMVHKQWDLAWAVSYIRFTITIPFVG 302  
QY 316 ILGALLFLNFIRESHFWVWVTKMNHVMEIDQEAIRDFWFSQLTATCNVQSFPNDWF 375  
DB 303 ILGALLFLNFIRESHFWVWVTKMNHVMEIDQEAIRDFWFSQLTATCNVQSFPNDWF 362  
QY 376 SGHLNFQIEHLLFPTMFRNHLNHLKIAPLVKSCLKAGHIEYQEKPLRALDLIRSLKSGK 435  
DB 363 SGHLNFQIEHLLFPTMFRNHLNHLKIAPLVKSCLKAGHIEYQEKPLRALDLIRSLKSGK 422  
QY 436 LWLDAYLHK 444  
DB 423 LWLDAYLHK 431

RESULT 11

ABG96508  
ID ABG96508 standard; Protein; 432 AA.  
XX  
AC ABG96508;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human partial desaturase protein from contig 253538a.  
XX  
XX Human; enzyme; deltas desaturase; polyunsaturated fatty acid;  
XX PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;  
XX inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;  
XX kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;  
XX AIDS; multiple sclerosis; blood pressure; platelet aggregation;  
XX vasodilation; cholesterol; proliferation of fibrous tissue;  
XX endometriosis; myalgic encephalomyelitis; human breast milk;  
XX dietary supplement; chromosome 11q12.  
XX  
OS Homo sapiens.  
XX  
XX US6428990-B1.  
XX  
XX 06-AUG-2002.  
XX  
XX 12-NOV-1999; 99US-0439261.  
XX  
XX 11-APR-1997; 97US-0833610.  
XX 10-APR-1998; 98WO-US07422.  
XX 08-JAN-1999; 99US-0227613.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;  
XX  
XX WPI; 2002-730518/79.  
XX N-PSDB; ABS76713.  
XX  
XX Producing a polyunsaturated fatty acid (PUFA), useful in dietary  
XX supplements and in treating diseases e.g., cancer, comprises expressing  
XX human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA  
XX to convert to product PUFA -  
XX  
XX Example 1; Fig 9; 104pp; English.  
XX  
XX The invention relates to producing (M1) a polyunsaturated fatty acid  
XX (PUFA), comprising: (i) isolating a fully defined human Deltas-Desaturase  
XX gene sequence (I); (ii) constructing a vector comprising (I);  
XX (iii) introducing the vector into a host cell for expression of the  
XX human Deltas-desaturase enzyme (II); and (iv) exposing (II) to a  
XX substrate PUFA (III) such that it is converted to a product PUFA (IV).  
XX The method is useful for producing a polyunsaturated fatty acid  
XX such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic  
XX acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or  
XX docosahexaenoic (DHA) acid. The PUFAs produced by the method, such  
XX as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or  
XX docosahexaenoic (DHA) acid, are useful for replicating the PUFA content  
XX of human breast milk or to alter the presence of PUFAs normally found  
XX in a non-human mammal's milk. PUFAs produced by (M1) may be added to a  
XX dietary substitute or supplement, particularly an infant formula, for  
XX patients undergoing intravenous feeding or for preventing or treating  
XX malnutrition or other conditions or disease states. The PUFAs are  
XX useful for producing nutritional compositions e.g., any food or  
XX preparation for human consumption including for enteral or parenteral  
XX consumption, which when taken into the body serve to nourish or build  
XX up tissues or supply energy and/or maintain, restore or support  
XX adequate nutritional status or metabolic function. The PUFAs are also  
XX useful in animal feed supplements to alter an animal tissue or milk  
XX fatty acid composition to one or more desirable for human or animal  
XX consumption, in animal feed substitutes, animal vitamins or in animal  
XX topical ointments. The PUFAs produced by this method are useful in  
XX producing pharmaceutical compositions for treating rough or aging skin,  
XX injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
XX asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,

CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
 CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
 CC platelet aggregation, inducing vasodilation, reducing cholesterol  
 CC levels, inhibiting proliferation of fibrous tissue, treating  
 CC endometriosis, and myalgic encephalomyelitis. The gene for delta5  
 CC desaturase is located on chromosome 11q12. The present sequence  
 XX is a partial human delta5 desaturase protein.  
 SQ Sequence 432 AA;

Query Match 79.6%; Score 1940.5; DB 23; Length 432;  
 Best Local Similarity 81.8%; Pred. No. 1.4e-203;  
 Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

Qy 19 PT---FWEETQKHLRTDGLVDRKVNITKWSIQHGGQVRVIGHYAGEDATDAFRAF 75  
 Db 3 PTPRYFTWDEVAQSGCEERLWIDRVKYNISEFTTRHPGGSRVISHYAGQDATDPFVAF 62

Qy 76 HPDLFVGVKLPKLLIGELAPEEPSQDHGKNSKITEDFRALRKYTAEDMNLKTNHVPFLL 135  
 Db 63 HINKGLVKYNNLSLIGELSPQSFPEPTKNEKLTDEFRELATVERMGLMKANHVPFLL 122

Qy 136 LLAHIIALESATWTFVFGNGWITLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNH 195  
 Db 123 YLLHILLDGAWLTLWFGTSFLLCAVLLSAVQAQAGWLQHDYGHLSVYRKPKWNH 182

Qy 196 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 255  
 Db 183 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 242

Qy 256 YLPYNHGHYEFLLGPPLIPMYQYQIIMTWIHKWVDLAWAVSYIRFFITYIPFYG 315  
 Db 243 YLPYNHGHYEFLLGPPLIPMYQYQIIMTWIHKWVDLAWAVSYIRFFITYIPFYG 302

Qy 316 ILGALLFLNFIREFLSSHFWVVTQNNHIVMEIDQAYRDWFFSSQLTATCNVEQSFNDWF 375  
 Db 303 ILGALLFLNFIREFLSSHFWVVTQNNHIVMEIDQAYRDWFFSSQLTATCNVEQSFNDWF 362

Qy 376 SGHLNFOIEHLLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIIRSLKSGK 435  
 Db 363 SGHLNFOIEHLLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIIRSLKSGK 422

Qy 436 LWLDAYLHK 444  
 Db 423 LWLDAYLHK 431

RESULT 12  
 ABG94704  
 XX ID ABG94704 standard; Protein; 465 AA.  
 XX AC ABG94704;  
 XX DT 02-DEC-2002 (first entry)  
 XX DE Human delta5-desaturase #14.  
 XX Human delta5-desaturase; polyunsaturated fatty acid; DGLA;  
 XX dihydro-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;  
 XX eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;  
 XX enzyme.  
 XX Homo sapiens.  
 XX OS US6432684-B1.  
 XX PN 13-AUG-2002.  
 XX PD 08-JAN-1999; 99US-0227613.  
 XX EF 11-APR-1997; 97US-0833610.  
 XX PR 10-APR-1998; 98WO-US07422.  
 XX XX

PA (ABRO ) ABBOTT LAB.  
 XX Mukerji P, Leonard AE, Huang Y, Das T;  
 XX WPI; 2002-689761/74.  
 XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing  
 PT the conversion of dihydro-gamma-linolenic acid to arachidonic acid and  
 PT in the conversion of 20:4n-3 to eicosapentaenoic acid -  
 XX Example 1; Figure 29; 88pp; English.  
 PS The invention relates to an isolated human delta5-desaturase nucleotide  
 XX sequence (i) which desaturates polyunsaturated fatty acids at  
 CC carbon 5. The nucleotide sequence (i) may be used in the recombinant  
 CC production of vectors and host cells for the production of delta5-  
 CC desaturase. Delta5-desaturase may be utilised in the conversion of  
 CC dihydro-gamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the  
 CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA Or  
 CC polyunsaturated fatty acids produced from it may be added to  
 CC pharmaceutical compositions, nutritional compositions, animal feeds, as  
 CC well as other products such as cosmetics. ABG94691-ABG94708 represent  
 CC human delta5-desaturase amino acid sequences of the invention.  
 XX Sequence 465 AA;  
 SQ Sequence 465 AA;

Query Match 79.6%; Score 1940.5; DB 23; Length 465;  
 Best Local Similarity 81.8%; Pred. No. 1.6e-203;  
 Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

Qy 19 PT---FSWEEIQKHLRTDGLVDRKVNITKWSIQHGGQVRVIGHYAGEDATDAFRAF 75  
 Db 3 PTPRYFTWDEVAQSGCEERLWIDRVKYNISEFTTRHPGGSRVISHYAGQDATDPFVAF 62

Qy 76 HPDLFVGVKLPKLLIGELAPEEPSQDHGKNSKITEDFRALRKYTAEDMNLKTNHVPFLL 135  
 Db 63 HINKGLVKYNNLSLIGELSPQSFPEPTKNEKLTDEFRELATVERMGLMKANHVPFLL 122

Qy 136 LLAHIIALESATWTFVFGNGWITLITAFVLATSOAQAGWLQHDYGHLSVYRKPKWNH 195  
 Db 123 YLLHILLDGAWLTLWFGTSFLLCAVLLSAVQAQAGWLQHDYGHLSVYRKPKWNH 182

Qy 196 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 255  
 Db 183 LVHKEFVIGHLKASANNWNRHFOHAKPNIFHKDPDNNMLHVPVLGEWOPIEYKKKLLK 242

Qy 256 YLPYNHGHYEFLLGPPLIPMYQYQIIMTWIHKWVDLAWAVSYIRFFITYIPFYG 315  
 Db 243 YLPYNHGHYEFLLGPPLIPMYQYQIIMTWIHKWVDLAWAVSYIRFFITYIPFYG 302

Qy 316 ILGALLFLNFIREFLSSHFWVVTQNNHIVMEIDQAYRDWFFSSQLTATCNVEQSFNDWF 375  
 Db 303 ILGALLFLNFIREFLSSHFWVVTQNNHIVMEIDQAYRDWFFSSQLTATCNVEQSFNDWF 362

Qy 376 SGHLNFOIEHLLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIIRSLKSGK 435  
 Db 363 SGHLNFOIEHLLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIIIRSLKSGK 422

Qy 436 LWLDAYLHK 444  
 Db 423 LWLDAYLHK 431

RESULT 13  
 ABG96523  
 XX ID ABG96523 standard; Protein; 465 AA.  
 XX AC ABG96523;  
 XX DT 12-DEC-2002 (first entry)  
 XX DE Human partial desaturase from cDNA contig 253538a.  
 XX XX



Human; enzyme; delta5 desaturase; polyunsaturated fatty acid;  
 PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;  
 inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;  
 kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;  
 AIDS; multiple sclerosis; blood pressure; platelet aggregation;  
 vasodilation; cholesterol; proliferation of fibrous tissue;  
 endometriosis; myalgic encephalomyelitis; human breast milk;  
 dietary supplement; chromosome 11q12.

OS Homo sapiens.

XX US6428990-B1.

PD 06-AUG-2002.

XX 12-NOV-1999; 99US-0439261.

XX 11-APR-1997; 97US-0833610.

PR 10-APR-1998; 98WO-US07422.

PR 08-JAN-1999; 99US-0227613.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

XX WPI; 2002-730518/79.

Producing a polyunsaturated fatty acid (PUFA), useful in dietary  
 supplements and in treating diseases e.g., cancer, comprises expressing  
 human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA  
 to convert to product PUFA.

Example 1; Fig 29; 10app; English.

The invention relates to producing (M) a polyunsaturated fatty acid  
 (PUFA), comprising: (i) isolating a fully defined human delta5-desaturase  
 gene sequence (I); (ii) constructing a vector comprising (I);  
 (iii) introducing the vector into a host cell for expression of the  
 human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a  
 substrate PUFA (III) such that it is converted to a product PUFA (IV).  
 The method is useful for producing a polyunsaturated fatty acid  
 such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic  
 acid, (n-3)-docosapentaenoic acid, (n-6)-docosahexaenoic acid and/or  
 docosahexaenoic (DHA) acid. The PUFAs produced by the method, such  
 as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or  
 docosahexaenoic (DHA) acid, are useful for replicating the PUFA content  
 of human breast milk or to alter the presence of PUFAs normally found  
 in a non-human mammal's milk. PUFAs produced by (M) may be added to a  
 dietary substitute or supplement, particularly an infant formula, for  
 patients undergoing intravenous feeding or for preventing or treating  
 malnutrition or other conditions or disease states. The PUFAs are  
 useful for producing nutritional compositions e.g., any food or  
 preparation for human consumption including for enteral or parenteral  
 consumption, which when taken into the body serve to nourish or build  
 up tissues or supply energy and/or maintain, restore or support  
 adequate nutritional status or metabolic function. The PUFAs are also  
 useful in animal feed supplements to alter an animal tissue or milk  
 fatty acid composition to one or more desirable for human or animal  
 consumption, in animal feed substitutes, animal vitamins or in animal  
 topical ointments. The PUFAs produced by this method are useful in  
 producing pharmaceutical compositions for treating rough or aging skin,  
 injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
 asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,  
 cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
 sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
 platelet aggregation, inducing vasodilation, reducing cholesterol  
 levels, inhibiting proliferation of fibrous tissue, treating  
 endometriosis, and myalgic encephalomyelitis. The gene for delta5  
 desaturase is located on chromosome 11q12. The present sequence  
 is a partial human delta5 desaturase protein.

Sequence 465 AA;

Query Match 79.6%; Score 1940.5; DB 23; Length 465;  
 Best Local Similarity 81.8%; Pred. No. 1.6e-203;  
 Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;  
 QY 19 PT---FSMEEIOKHNLRDLSGLVIDRKVYNTKWSIOHPGQCRVIGHVAGEDATDAFRAF 75  
 Db 3 PTPRVFTWDEVAQRSGCERWLVDRKYNISETRRHPFGGSRVISHYAGDADDPVAF 62  
 QY 76 HPDLFVKGFLKPLIGELAPEEPSQHGKNSKITEDFRALRKTAEDMNLFKTNHVFLL 135  
 Db 63 HINKGLVKYNNLSLIGLSPESFETKNTKELTDFRELRATVERMGLMKANHFLL 122  
 QY 136 LLAHIIALESIAWFTVPVFGNGWIPLTITAFVLTASQAQGLQHDYGHLSVYRKPKNW 195  
 Db 123 YLLHILLDGAALTLVWFGTSFLPFLCAVLLSVAQAQGLQHDYGHLSVYRKPKNW 182  
 QY 196 LVHKFVIGHLKGSANWNNHRRHFQHKAPNIFHKDPDNNMLHVFVLGEWQPIEYKKL 255  
 Db 183 LVHKFVIGHLKGSANWNNHRRHFQHKAPNIFHKDPDNNMLHVFVLGEWQPIEYKKL 242  
 QY 256 YLPYNHQHEYFELIGPPLIPMYFOYQIIMTWIHKWVDLAWAVSYIRFFIYIPFYG 315  
 Db 243 YLPYNHQHEYFELIGPPLIPMYFOYQIIMTWIHKWVDLAWAVSYIRFFIYIPFYG 302  
 QY 316 ILGALLFINFIRFLESHFVWVTVQNHIVMEIDQEAAYRDFESSQITATCNVEQSF 375  
 Db 303 ILGALLFINFIRFLESHFVWVTVQNHIVMEIDQEAAYRDFESSQITATCNVEQSF 362  
 QY 376 SGHLNFQIEHLPFTMPRHNLKIAPLVKSICAKHGIEYQEKPLRLALDIIIRSLKSGK 435  
 Db 363 SGHLNFQIEHLPFTMPRHNLKIAPLVKSICAKHGIEYQEKPLRLALDIIIRSLKSGK 422  
 QY 436 LMLDAVLHK 444  
 Db 423 LMLDAYLHK 431

RESULT 14

AAAY95446

ID AAAY95446 standard; Protein; 432 AA.

AC AAAY95446;

XX 10-OCT-2000 (first entry)

DE Human delta-5-desaturase-related contig 253538a-encoded protein.

XX Delta-5-desaturase; human; polyunsaturated fatty acid;

XX arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;

XX docosahexaenoic acid; nutrition; feedstuff.

OS Homo sapiens.

XX WO200040705-A2.

XX 13-JUL-2000.

XX 29-DEC-1999; 99WO-US31163.

XX 08-JAN-1999; 99US-0227613.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;

XX WPI; 2000-465975/40.

XX N-PSDB; AAA49939.

XX New polypeptide useful for preparation of nutritional supplements based

XX upon human Delta5-desaturase, desaturates polyunsaturated fatty acids

XX at carbon 5 -

XX Example 1; Fig 9; 127pp; English.

```

XX The present sequence is that of the polypeptide encoded by the
CC partial open reading frame of contig 253538a (see A449939). The
CC translated sequence shows homology to Mortierella alpina
CC delta-5-desaturase and delta-6-desaturase sequences, suggesting a
CC human desaturase-like protein. The contig was utilised in the
CC isolation of cDNA (see A449932) encoding human delta-5-desaturase
CC (see A449945). Delta-5-desaturase catalyzes the conversion of
CC dihomogamma-linolenic acid to arachidonic acid and of 20:4n-3 to
CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic
CC or eukaryotic hosts using the isolated human delta-5-desaturase
CC cDNA, can be used in the production of polyunsaturated fatty acids
CC that may be added to nutritional, veterinary and pharmaceutical
CC compositions.
XX SQ Sequence 432 AA;

Query Match 79.4%; Score 1935; DB 21; Length 432;
Best Local Similarity 81.9%; Pred. No. 5.8e-203;
Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;

Qy 19 FT---FSWEEIQKHLRTDGLVIDRKVNITKWSIQHGGQGVIGHYAGEDATDAFRAF 75
Db 3 PTPRYFTWDEVAQRSGCEERLWIDRKVNISBFTRRHGGSRVISHYAGQDATDPFVAF 62
Qy 76 HPDLFVGVKLPKLLIGELAPEPSQDHGKNSKITEDFRALRKTADNMLFKTNHVFLL 135
Db 63 HINKGLVKKNYNSLLIGELSPQSFPTKKNKLTDFEELRATVERMGLMKANHVFFLL 122
Qy 136 LLAHIIALESIAFTVFYFGNGWIPITLITAFVL-ATSOAQAGWLQHDYGHLSYVRKPKWN 194
Db 123 YLLHILLDGAALWLTWVFGTSFLFLCAVLLSAVQQAQAGWLQHDYGHLSYVRKPKWN 182
Qy 195 HLHVKPFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 254
Db 183 HLHVKPFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 242
Qy 255 KYPYNHGHYEYFFLIGPPLIPMFYQYQIIMTVHKNWVDLAWAVSYIRFIYIPFY 314
Db 243 KYPYNHGHYEYFFLIGPPLIPMFYQYQIIMTVHKNWVDLAWAVSYIRFIYIPFY 302
Qy 315 GILGALLFLNPIRFLSHFWVWQMHVMEIDQEAIRYDFWFSQLTATCNVQSFNDW 374
Db 303 GILGALLFLNPIRFLSHFWVWQMHVMEIDQEAIRYDFWFSQLTATCNVQSFNDW 362
Qy 375 FSGHNLFOIEHLLPPTPRHNLKIAPLVKSCLAKHGIEYQEKPLLRALLDIIRSLKSG 434
Db 363 FSGHNLFOIEHLLPPTPRHNLKIAPLVKSCLAKHGIEYQEKPLLRALLDIIRSLKSG 422
Qy 435 KLWLDAYLHK 444
Db 423 KLWLDAYLHK 432

RESULT 15
ID AAW84156 standard; Protein; 746 AA.
AC AAW84156;
AC AAW84156;
DT 15-FEB-1999 (first entry)
XX Human desaturase enzyme encoded by contig 253538a.
DE Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
XX acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
XX

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```

FH Key Location/Qualifiers
FT Misc-difference 746 /note= "not specified"
XX WO9846763-A1.
XX 22-OCT-1998.
XX 10-APR-1998; 98WO-US071126.
XX 11-APR-1997; 97US-0834655.
XX (ABBO ) ABBOTT LAB.
XX (CALJ ) CALGENE LLC.
XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
XX Thurmond J;
XX WPI; 1998-594582/50.
XX N-PSDB; AAV63643.
XX New isolated fatty acid desaturase enzymes - used for the production
XX of polyunsaturated fatty acids for use in, e.g. pharmaceutical
XX compositions, nutritional compositions, cosmetics or animal feed
XX Example 12; Pages 124-126; 165pp; English.
XX The present sequence is a human desaturase enzyme. The cDNA sequence was
XX identified based on homology between human cDNA sequences and Mortierella
XX alpina desaturase gene sequences. The specification describes methods for
XX desaturating a fatty acid and for producing a desaturated fatty acid by
XX expressing increased levels of a desaturase. The enzyme can be used for
XX desaturating fatty acids. The enzyme can be used to produce
XX polyunsaturated fatty acids, which can be used for treating malnutrition,
XX in pharmaceutical compositions, in cosmetics or in animal feed. The
XX polyunsaturated fatty acids can be used for treating e.g. restenosis
XX after angioplasty, inflammation, rheumatoid arthritis, asthma,
XX psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
XX can also be used to inhibit platelet aggregation, cause vasodilation,
XX lower cholesterol levels, inhibit proliferation of vessel wall smooth
XX muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
XX and other side effects caused by non-steroidal anti-inflammatory drugs
XX prevent or treat endometriosis and premenstrual syndrome, treat myalgic
XX encephalomyelitis and chronic fatigue after viral infections, treat
XX AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
XX inflammatory skin disorders.
XX Sequence 746 AA;

Query Match 79.4%; Score 1935; DB 19; Length 746;
Best Local Similarity 81.9%; Pred. No. 1.3e-202;
Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;

Qy 19 FT---FSWEEIQKHLRTDGLVIDRKVNITKWSIQHGGQGVIGHYAGEDATDAFRAF 75
Db 3 PTPRYFTWDEVAQRSGCEERLWIDRKVNISBFTRRHGGSRVISHYAGQDATDPFVAF 62
Qy 76 HPDLFVGVKLPKLLIGELAPEPSQDHGKNSKITEDFRALRKTADNMLFKTNHVFLL 135
Db 63 HINKGLVKKNYNSLLIGELSPQSFPTKKNKLTDFEELRATVERMGLMKANHVFFLL 122
Qy 136 LLAHIIALESIAFTVFYFGNGWIPITLITAFVL-ATSOAQAGWLQHDYGHLSYVRKPKWN 194
Db 123 YLLHILLDGAALWLTWVFGTSFLFLCAVLLSAVQQAQAGWLQHDYGHLSYVRKPKWN 182
Qy 195 HLHVKPFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 254
Db 183 HLHVKPFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDVMNLHVFLGEMQPIEYKCKKL 242
Qy 255 KYPYNHGHYEYFFLIGPPLIPMFYQYQIIMTVHKNWVDLAWAVSYIRFIYIPFY 314
Db 243 KYPYNHGHYEYFFLIGPPLIPMFYQYQIIMTVHKNWVDLAWAVSYIRFIYIPFY 302

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QY 315 GILGALLFLNFRFLESHFVWVQVNHVMEIDQAYRDWFFSSOLTATCNVEQSFNDW 374  
 Db 303 GILGALLFLNFRFLESHFVWVQVNHVMEIDQAYRDWFFSSOLTATCNVEQSFNDW 362  
 QY 375 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSG 434  
 Db 363 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSG 422  
 QY 435 KLWLDAYLHK 444  
 Db 423 KLWLDAYLHK 432

## RESULT 16

AAW85135  
 ID AAW85135 standard; Protein; 746 AA.

XX AC AAW85135;

DT 11-FEB-1999 (first entry)

DE A desaturase enzyme encoded by contig 253538a.

XX Fatty acid; desaturase; polyunsaturated fatty acid;  
 XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Misc-difference 746 /note= "not specified"

FT MO9846765-A1.

PN 22-OCT-1998.

XX 10-APR-1998; 98MO-US07422.

XX 11-APR-1997; 97US-0833610.

XX (ABBO ) ABBOTT LAB.

XX (CALJ ) CALGENE LLC.

XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;

XX Thurmond J;

XX WPI; 1999-009334/01.

XX N-PSDB; AAW82642.

XX New nucleic acid encoding deltas and other desaturase enzymes -

XX useful in production of oils of increased arachidonic acid content,

XX used, e.g. for treating cancer, as foods, animal feeds and cosmetics

XX Claim 87; Pages 119-120; 153pp; English.

XX The present sequence represents a human desaturase enzyme. The enzyme

XX sequence is used in the methods of the invention. The specification

XX describes methods for desaturating a fatty acid and for producing a

XX desaturated fatty acid by expressing increased levels of a desaturase.

XX The enzyme can be used for desaturating fatty acids. The enzyme can be

XX used to produce polyunsaturated fatty acids, which can be used for

XX treating malnutrition. In pharmaceutical compositions, in cosmetics or

XX in animal feed. The polyunsaturated fatty acids can be used for treating

XX e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,

XX asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.

XX They can also be used to inhibit platelet aggregation, cause

XX vasodilation, lower cholesterol levels, inhibit proliferation of vessel

XX wall smooth muscle, and fibrous tissue, reduce or prevent

XX gastro-intestinal bleeding and other side effects caused by non-steroidal

CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual  
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after  
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory  
 CC syndrome, hypertension and inflammatory skin disorders.

XX Sequence 746 AA;

Query Match 79.4%; Score 1935; DB 20; Length 746;  
 Best Local Similarity 81.9%; Pred. No. 1.3e-202;  
 Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;

QY 19 PT---PSWEIQTCKNLRTDGLVDRKVNITKWSICHGQGVHGYHAGEDATDAFRF 75

Db 3 PTPRYFTWDEVAQSGCEERWLVIDRKVINISEPTRHPGGSRVISHYAGQDATDPVAF 62

QY 76 HPDLEFVGKFLKPLLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLKTNHVFLL 135

Db 63 HINKGLVKVMNSLLIGELSPQSPFETKNKELTDSFRELRTATVERMGLMKANHVFFLL 122

QY 136 LLAHIIALESIAETVTFVFGNGWITPLITAFVL-ATSOAAGWLQHDYGHLSVYRKPKWN 194

Db 123 YLLHILLDDGAAMUTLWVFGTSFPLLCVLLSAVQAQAGWLQHDYGHLSVYRKPKWN 182

QY 195 HLVKFVIGHLKASANWNNHRHFQHHAKNIFHKDPDVMNLHVFLGEPQIEYGGKKL 254

Db 183 HLVKFVIGHLKASANWNNHRHFQHHAKNIFHKDPDVMNLHVFLGEPQIEYGGKKL 242

QY 255 KYLPVNHCHYEFFLIGPPLIPMFYQIQITMIVHKNVDLAWAVSYIRFITIPFY 314

Db 243 KYLPVNHCHYEFFLIGPPLIPMFYQIQITMIVHKNVDLAWAVSYIRFITIPFY 302

QY 315 GILGALLFLNFRFLESHFVWVQVNHVMEIDQAYRDWFFSSOLTATCNVEQSFNDW 374

Db 303 GILGALLFLNFRFLESHFVWVQVNHVMEIDQAYRDWFFSSOLTATCNVEQSFNDW 362

QY 375 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSG 434

Db 363 FSGHLNFQIEHLFPPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSG 422

QY 435 KLWLDAYLHK 444

Db 423 KLWLDAYLHK 432

## RESULT 17

AA92618  
 ID AA92618 standard; Protein; 752 AA.

XX AC AA92618;

XX 10-AUG-2000 (first entry)

XX Human desaturase homologue encoded by DNA contig 2535.

XX delta-6 desaturase; gamma-linolenic acid; biosynthesis;

XX transgenic insect cell; polyunsaturated long chain fatty acid;

XX antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;

XX osteopathic; cytostatic; antidiabetic; dermatological; gynecological;

XX anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;

XX antiaggregant; vasotropic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 433 /note= "encoded by TAA"

FT Misc-difference 459 /note= "encoded by TAA"

FT Misc-difference 596 /note= "encoded by TGA"

FT Misc-difference 629 /note= "encoded by TGA"

FT Misc-difference 655 /note= "encoded by TGA"

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FT      /note= "encoded by TAA"
FT      Misc-difference 673
FT      /note= "encoded by TGA"
FT      Misc-difference 688
FT      /note= "encoded by TGA"
XX      WO200020602-A2.
XX      13-APR-2000.
XX      29-SEP-1999; 99WO-US22686.
XX      05-OCT-1998; 98US-0103110.
XX      (ABBO ) ABBOTT LAB.
XX      Mukerji P, Huang Y, Parker-barnes JW, Das T;
XX      WPI; 2000-328935/28.
XX      N-PSDB; AAA09453.
XX      Novel transgenic insect cells comprising a nucleotide sequences which
XX      encode delta-6-desaturase or delta-12-desaturase, useful for producing
XX      poly-unsaturated long chain fatty acids, e.g. arachidonic acid
XX      Example 13; Page 168-169; 170pp; English.
XX      AAY92612-18 are identified based on homology to Mortierella alpina
XX      delta-5 and delta-6 desaturase genes. The human DNA's were aligned
XX      based on areas of homology to form a contig. Consensus sequences were
XX      assembled. A contig, 251178 overlaps with contig.3506132, and this new
XX      contig was called 2535 (AAA09453).
XX      The fatty acid desaturases are able to catalyse the conversion of oleic
XX      acid to linoleic acid, linoleic acid to gamma-linolenic acid or of
XX      alpha-linolenic acid to stearidonic acid. Transgenic insect cells
XX      comprising a nucleotide sequence which encodes a polypeptide comprising
XX      residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6
XX      desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are
XX      claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated
XX      from the recombinant insect cells are also claimed. Production of
XX      polyunsaturated long chain fatty acids (PUFAs) in insect cells has many
XX      advantages, as insect cells have greatly simplified lipid compositions,
XX      are not subject to external variable fluctuations, and can easily be
XX      maintained and manipulated. The oils are used in pharmaceutical
XX      compositions, infant formulas, dietary supplements or substitutes, and
XX      cosmetics (all claimed). The PUFA supplements have anti-inflammatory,
XX      antirheumatic, antiasthmatic, antipsoriatic, osteopathic, cytostatic,
XX      antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,
XX      hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic
XX      activity.
XX      SQ      Sequence 752 AA;
XX      Query Match 79.4%; Score 1935; DB 21; Length 752;
XX      Best Local Similarity 81.9%; Pred. No. 1.3e-202;
XX      Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;
XX      QY      19 PT---PSWEIQKHNRTSGLVIDRKVYNITKWSIQHGGORVIGHVAGEDATAPRAF 75
XX      Db      3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHFGSGSRVISHVAGQDAPPVAF 62
XX      QY      76 HPDLEFVGKFLPLILGELAPBEPSSODHGKNGSKITDFRALRKTAEEDMMLFKTNHVFLL 135
XX      Db      63 HINKGLVKVYMSLLIGELSPQSPFEPKTKNELTDFELRATVVRGLMCAHVPFLL 122
XX      QY      136 LLAHIIALSLIAFTVYFGNWIPTLITAFVL-ATSOQAQWLQHDYGHLSVYRKPKWN 194
XX      Db      123 YLLHILLDGAWLTLVWFSTGFLPELLCAVLLSAVQQAQWLQHDYGHLSVYRKPKWN 182
XX      QY      195 HLVHKFVIGHLKGASANNWNHRRHFQHAKPNIFHKDPDVNMLHFVLGEWQPIEGKKKL 254
XX      Db      183 HLVHKFVIGHLKGASANNWNHRRHFQHAKPNIFHKDPDVNMLHFVLGEWQPIEGKKKL 242
XX      QY      255 KYLPYNHQHYFFLIGPPLLIIPMYFOYQIIMTWIVHKWVVDLAWAVSYIRFITIPFY 314
XX      Db      243 KYLPYNHQHYFFLIGPPLLIIPMYFOYQIIMTWIVHKWVVDLAWAVSYIRFITIPFY 302
XX      QY      315 GILGALLFLNFIREFSHWFVWTQNMHIWVEIDQAYRDWFSQSQTATCNVQSPFNW 374
XX      Db      303 GILGALLFLNFIREFSHWFVWTQNMHIWVEIDQAYRDWFSQSQTATCNVQSPFNW 362
XX      QY      375 PSGLNFIQIEHHLFPTMPRNHLKIAPLVKSLCAKGIIEYQEKPLLRALLDIIRSLKKS 434
XX      Db      363 PSGLNFIQIEHHLFPTMPRNHLKIAPLVKSLCAKGIIEYQEKPLLRALLDIIRSLKKS 422
XX      QY      435 KLWLDAYLHK 444
XX      Db      423 KLWLDAYLHK 432
XX      RESULT 18
XX      AAW95514
XX      ID AAW95514 standard; Protein; 753 AA.
XX      AC AAW95514;
XX      DT 26-MAR-1999 (first entry)
XX      DE Amino acid sequence of human desaturase gene contig 253538a.
XX      KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
XX      KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
XX      KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
XX      KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
XX      KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
XX      KW diabetes; cosmetic; animal feed; human.
XX      OS Homo sapiens.
XX      FH Key Location/Qualifiers
XX      FT Misc-difference 433 /note= "encoded by TGA"
XX      FT Misc-difference 459 /note= "encoded by TGA"
XX      FT Misc-difference 596 /note= "encoded by TGA"
XX      FT Misc-difference 629 /note= "encoded by TGA"
XX      FT Misc-difference 655 /note= "encoded by TAA"
XX      FT Misc-difference 673 /note= "encoded by TAG"
XX      FT Misc-difference 688 /note= "encoded by TGA"
XX      FT Misc-difference 753 /note= "encoded by TGA"
XX      FT Misc-difference 753 /note= "encoded by TG"
XX      WO9846764-A1.
XX      22-OCT-1998.
XX      10-APR-1998; 98WO-US07421.
XX      24-OCT-1997; 97US-0956995.
XX      11-APR-1997; 97US-0833610.
XX      11-APR-1997; 97US-0834033.
XX      11-APR-1997; 97US-0834655.
XX      (ABBO ) ABBOTT LAB.
XX      (CALJ ) CALGENE LLC.
XX      Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
XX      Thurmond J;
XX      WPI; 1999-080739/07.
XX      N-PSDB; AAX00910.

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XX Nucleic acid construct able to express fatty acid desaturase in  
PT plants - useful in human or animal nutrition, as cosmetics and  
PT therapeutically, e.g. for restenosis, cancer and diabetes  
XX  
XX Claim 48; Page 169-171; 210pp; English.  
XX  
XX The invention relates to a nucleic acid construct that contains at least  
CC one of the nucleotide sequences (AA00889 to AA00891) encoding  
CC Mortierella alpina delta 6, delta 12 and delta 5 desaturases (AA095504 to  
CC AA095506) respectively, coupled to an expression control sequence  
CC functional in plants. Recombinant plant cells containing at least one DNA  
CC encoding a M. alpina fatty acid desaturase (FAD), can be used for the  
CC production of polyunsaturated fatty acid (PUFA). These recombinant cells  
CC or plants containing them are used to produce oils such as linoleic  
CC acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic  
CC acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils  
CC are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or  
CC dietary supplements or substitutes, for use in humans or animals; (iii)  
CC for treating disorders associated with inadequate consumption or  
CC production of PUFA (or their metabolites such as prostaglandins), e.g.  
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,  
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics,  
CC and (v) as animal feeds. Fragments of the DNA are used as probes to  
CC isolate related coding sequences. Recombinant plants can produce high  
CC yields of PUFA, since new pathways can be created and unwanted ones  
CC suppressed. Plants can be engineered to express oils of particular PUFA  
CC composition, e.g. one similar to that in human milk, and product recovery  
CC is simpler than with e.g. fish. Sequences AA095508-514 represent amino  
CC acid sequences of various contigs of human desaturase genes which are  
CC similar to the M. alpina desaturase sequences.  
XX  
XX Sequence 753 AA;

Query Match 79.4%; Score 1935; DB 20; Length 753;  
Best Local Similarity 81.9%; Pred. No. 1.3e-202;  
Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;

QY 19 PT---FSWEIQKLNRTDGLVDRKVNITKSIQHPGQGVIGHYAGEDATDAPRAF 75  
Db 3 PTPRYFTWDEVAQSGCEERWLVDRKVNISFTRHPGGSRVISHYAGQDATDFVAF 62  
QY 76 HPDLFVKGFLKPLLIGELAPEEPSODHGNKSKITDFRALRKTAEKMDNLFKNHVFLL 135  
Db 63 HINKGLVKYVNSLLIGELSPQSPFPTKNTKELTDFRELATVERMGLMKANHYVFFLL 122  
QY 136 LLAHIIALESTANETVYFGNGWPTLITAFVL-ATSOAGWLQHDYGHLSYVRPKWN 194  
Db 123 YLLHILLDGAALTLWVFGTSFLLCAVLLSAVQQAQGLQHDYGHLSYVRPKWN 182  
QY 195 HLVKHFGVIGHLKGASANNWNRHFRQHEAKPNIHKPDVNNLHVFLGWEQPIEYGGKLL 254  
Db 183 HLVKHFGVIGHLKGASANNWNRHFRQHEAKPNIHKPDVNNLHVFLGWEQPIEYGGKLL 242  
QY 255 KYPYNHCHYEYFFLIGPPLIPMYFOYCIINTMIVHKNWDLAWNSYIRFETITIPFY 314  
Db 243 KYPYNHCHYEYFFLIGPPLIPMYFOYCIINTMIVHKNWDLAWNSYIRFETITIPFY 302  
QY 315 GILGALLFLNIRFLESHWFVWVTQNMHIVMEIQEAYRDWFFSQLTATCNVQSPENDW 374  
Db 303 GILGALLFLNIRFLESHWFVWVTQNMHIVMEIQEAYRDWFFSQLTATCNVQSPENDW 362  
QY 375 FSGHNFQIEHLLPTPRNHLKIAPLVKSCLAKHIEQEKELLIRALLDIIRSLKSG 434  
Db 363 FSGHNFQIEHLLPTPRNHLKIAPLVKSCLAKHIEQEKELLIRALLDIIRSLKSG 422  
QY 435 KLWLDAYLHK 444  
Db 423 KLWLDAYLHK 432

RESULT 19  
AA094703

ID XX AAY84703 standard; Protein; 753 AA.  
AC AAY84703;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Amino acid sequence of a contig of a human desaturase enzyme.  
XX  
KW Delta5-desaturase; poly-unsaturated long chain fatty acid; PUFA;  
KW arachidonic acid; infant formula; dietary supplement; dietary substitute;  
KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;  
KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;  
KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;  
KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;  
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
KW acute respiratory syndrome; hypertension; inflammatory skin disorder;  
KW blood score; platelet aggregation; vasodilatation;  
KW gastro-intestinal bleeding.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
XX Misc-difference 1..752  
FT /note= "Xaa is an unspecified residue encoded by  
FT stop codons"  
FT  
FT Misc-difference 753  
FT /note= "encoded by TG"  
FT  
FN WO200020603-A1.  
XX  
PD 13-APR-2000.  
XX  
XX 29-SEP-1999; 99WO-US22692.  
XX  
XX 05-OCT-1998; 98US-0103109.  
XX  
PA (AB00 ) ABBOTT LAB.  
XX  
PI Mukerji P, Huang Y, Parker-Barnes JH, Das T;  
XX  
XX WPI: 2000-364599/31.  
DR N-PSDB; AAA14594.  
XX  
XX Novel transgenic insect cell with modified delta-5-desaturase  
PT production, useful for altering fatty acid biosynthesis -  
PT  
XX Example 9; Page 154-155; 161pp; English.  
XX  
CC AAY84697-Y84703 are encoded by contigs of a human desaturase. The  
CC specification describes a Mortierella alpina delta5-desaturase. The  
CC protein is involved in the biosynthesis of poly-unsaturated long chain  
CC fatty acids (PUFAs). The polynucleotide is to produce PUFAs, especially  
CC arachidonic acid. The oils produced by the invention are used in  
CC pharmaceutical compositions, infant formulas, dietary supplements,  
CC dietary substitutes, and cosmetics. The nutritional compositions can be  
CC used to treat normal individuals temporally exposed to stress, or  
CC individuals having specialized needs due to chronic or acute diseases  
CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or  
CC malabsorption, and other disorders such as restenosis after angioplasty,  
CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,  
CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated  
CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,  
CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,  
CC acute respiratory syndrome, hypertension, inflammatory skin disorders,  
CC as well as reduce blood score, inhibit platelet aggregation, cause  
CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and  
CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for  
CC geriatric treatments).  
XX  
XX Sequence 753 AA;

Query Match 79.4%; Score 1935; DB 21; Length 753;  
Best Local Similarity 81.9%; Pred. No. 1.3e-202;

Matches 352; Conservative 30; Mismatches 44; Indels 4; Gaps 2;  
Qy 19 PT---FSWBIQKHNLRTDGLVIDRKVYNIITKWSIQHGGQRVIGHYAGEDATDAFRAP 75  
Db 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNIISFTREHPGSRVISHYAGQDATDFVAP 62  
Qy 76 HPDLFVKGKLLPILGELAPEPSQDHGNSKITDFRALRTADDMNLFKTNHVFLL 135  
Db 63 HINKGLVKYKNSLLIGELSPQSPFTKNTKELTDFRELRTATVERMGLMKANHVFFLL 122  
Qy 136 LLAHIIALESIAFTVYFGNGWIPITLITAFVL-ATSQAQAGWLOHDYGHLSVYRKPKN 194  
Db 123 YLLHILLDGAAMLTLWVFTSFLPFLLCVLLSAVQAQAGWLOHDYGHLSVYRKPKN 182  
Qy 195 HLHVKFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLGEWQPIEYKKKL 254  
Db 183 HLHVKFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLGEWQPIEYKKKL 242  
Qy 255 KYLPYNHQHVEYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIRRPITVIFY 314  
Db 243 KYLPYNHQHVEYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIRRPITVIFY 302  
Qy 315 GILGALLFLNFIPLSHWVFWVTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFNDW 374  
Db 303 GILGALLFLNFIPLSHWVFWVTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFNDW 362  
Qy 375 FSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKHGIEYQEKPLRALDIIIRSLKSG 434  
Db 363 FSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKHGIEYQEKPLRALDIIIRSLKSG 422  
Qy 435 KLMLDAYLHK 444  
Db 423 KLMLDAYLHK 432

RESULT 20  
AA93456  
ID AA93456 standard; Protein; 322 AA.  
AC AA93456;  
DT 06-NOV-2001 (first entry)  
DE Human polypeptide, SEQ ID NO: 3112.  
XX Human; full length cDNA; cDNA synthesis; oligo-capping.  
XX Homo sapiens.  
XX EP1130094-A2.  
XX 05-SEP-2001.  
XX 07-JUL-2000; 2000EP-0114089.  
XX 08-JUL-1999; 99JP-0194486.  
XX 11-JAN-2000; 2000JP-0118774.  
XX 02-MAY-2000; 2000JP-0183785.  
XX (HELI-) HELIX RES INST.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
XX N-PSDB; AAK94377.  
XX 830 Primers useful for synthesizing full length cDNA clones and their  
XX use in genetic manipulation -  
XX Claim 8; SEQ ID NO 3112; 1380pp + sequence listing; English.  
XX The invention relates to primers for synthesizing full length cDNA

clones. 830 cDNA molecules encoding a human protein have been  
isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
molecules have been determined. Primers for synthesizing the full length  
cDNA are useful for clarifying the function of the protein encoded by  
the cDNA. The full length clones were obtained by construction of full  
length enriched cDNA libraries that were synthesised by the oligo-capping  
method. The primers enable the production of the full length cDNA easily  
without any special methods. The present sequence is a polypeptide  
encoded by a full length human cDNA of the invention.  
Note: The sequence data for this patent did not form part of the printed  
specification, but was obtained in CD-ROM format directly from EPO.  
XX  
SQ Sequence 322 AA;  
Query Match 73.4%; Score 1790; DB 22; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3e-187;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 123 MNLKTNHVFLLLAHIIALESIAFTVYFGNGWIPITLITAFVLATSQAQAGWLOHDY 182  
Db 1 MNLKTNHVFLLLAHIIALESIAFTVYFGNGWIPITLITAFVLATSQAQAGWLOHDY 60  
Qy 183 GHLSVYRKPKNHVLHVKFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLG 242  
Db 61 GHLSVYRKPKNHVLHVKFVIGHLKGASANNWHRHFOHAKENIFHKDPDVNMLHVFVLG 120  
Qy 243 EWQPIEYKKKLKYL PYNHQHVEYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSY 302  
Db 121 EWQPIEYKKKLKYL PYNHQHVEYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSY 180  
Qy 303 YIRFFITYIPFYGILGALLFLNFIPLSHWVFWVTQNNHIVMEIDQAYRDWFSQLT 362  
Db 181 YIRFFITYIPFYGILGALLFLNFIPLSHWVFWVTQNNHIVMEIDQAYRDWFSQLT 240  
Qy 363 TCNVEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKLAPLVKSLCAKHGIEYQEKPLRA 422  
Db 241 TCNVEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKLAPLVKSLCAKHGIEYQEKPLRA 300  
Qy 423 LLDIIRSLKSGKLWLDAYLHK 444  
Db 301 LLDIIRSLKSGKLWLDAYLHK 322  
RESULT 21  
AA95448  
ID AA95448 standard; Protein; 294 AA.  
XX AA95448;  
XX 10-OCT-2000 (first entry)  
XX Human delta-5-desaturase-related contig 2535-encoded protein.  
XX Delta-5-desaturase; human; polyunsaturated fatty acid;  
XX arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;  
XX docosahexaenoic acid; nutrition; feedstuff.  
XX Homo sapiens.  
XX WO200040705-A2.  
XX 13-JUL-2000.  
XX 29-DEC-1999; 99WO-US31163.  
XX 08-JAN-1999; 99US-0227613.  
XX (ABBO ) ABBOTT LAB.  
XX Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;  
XX WPI; 2000-465975/40.  
XX N-PSDB; AAA49938.

|           |   |
|-----------|---|
| PD        | 22-OCT-1998.  |
| XX        |   |
| XX        | 10-APR-1998; 98WO-US07126.  |
| PR        |   |
| XX        | 11-APR-1997; 97US-0834655.  |
| XX        | (ABBO ) ABBOTT LAB.   |
| PA        | (CALJ ) CALGENE LLC.  |
| XX        |   |
| XX        | Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;                   |
| PI        | Thurmond J;   |
| XX        |   |
| DR        | WPI: 1998-594582/50.  |
| DR        | N-PSTB; AA63642.  |
| XX        |   |
| PT        | New isolated fatty acid desaturase enzymes - used for the production      |
| PT        | of polyunsaturated fatty acids for use in, e.g. pharmaceutical            |
| PT        | compositions, nutritional compositions, cosmetics or animal feed          |
| XX        |   |
| PS        | Example 12; Pages 123-124; 165pp; English.                                |
| XX        |   |
| CC        | The present sequence is a human desaturase enzyme. The cDNA sequence was  |
| CC        | identified based on homology between human cDNA sequences and Mortierella |
| CC        | alpina desaturase gene sequences. The specification describes methods for |
| CC        | desaturating a fatty acid and for producing a desaturated fatty acid by   |
| CC        | expressing increased levels of a desaturase. The enzyme can be used for   |
| CC        | desaturating fatty acids. The enzyme can be used to produce               |
| CC        | polyunsaturated fatty acids, which can be used for treating malnutrition, |
| CC        | in pharmaceutical compositions, in cosmetics or in animal feed. The       |
| CC        | polyunsaturated fatty acids can be used for treating e.g. xeroderma       |
| CC        | after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, |
| CC        | cancer, diabetes or eczema or reduce blood pressure. They                 |
| CC        | can also be used to inhibit platelet aggregation, cause vasodilation,     |
| CC        | lower cholesterol levels, inhibit proliferation of vessel wall smooth     |
| CC        | muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding   |
| CC        | and other side effects caused by non-steroidal anti-inflammatory drugs,   |
| CC        | prevent or treat endometriosis and premenstrual syndrome, treat myalgic   |
| CC        | encephalomyelitis and chronic fatigue after viral infections, treat       |
| CC        | AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and    |
| XX        | inflammatory skin disorders.  |
| XX        |   |
| SQ        | Sequence 608 AA;  |
|           |   |
|           | Query Match 67.5%; Score 1646; DB 19; Length 608;                         |
|           | Best Local Similarity 100.0%; Pred.No. 4.6e-171;                          |
|           | Matches 294; Conservative 0; Mismatched 0; Indels 0; Gaps 0;              |
|           |   |
| OY        | 151 VFYFGNGWIPLLITAFVLATSOACAGWLQHDYGHLSVVRKPKNNHLVHKFVIGHLKASA 210       |
| DB        | 1 VFYPGNGWIPLLITAFVLATSOACAGWLQHDYGHLSVVRKPKNNHLVHKFVIGHLKASA 60          |
|           |   |
| OY        | 211 NWNHRRHFQHAKPNI FHKDPDVMNLHVFLVGEPWI EYGKKKLKYLPYNHQHEYFFLIG 270      |
| DB        | 61 NWNHRRHFQHAKPNI FHKDPDVMNLHVFLVGEPWI EYGKKKLKYLPYNHQHEYFFLIG 120       |
|           |   |
| OY        | 271 PLLIIPMYFOYQIIMTWIVHKWVDLAWAVSYVIRFFITYIPFYGLGALLFLNFIREFLE 330       |
| DB        | 121 PLLIIPMYFOYQIIMTWIVHKWVDLAWAVSYVIRFFITYIPFYGLGALLFLNFIREFLE 180       |
|           |   |
| OY        | 331 SHWFVVWTQNHHVIWEIDQEAYEDWFSQSQTATCNVEQSFNDPFSGHNFQIEHHLFPT 390        |
| DB        | 181 SHWFVVWTQNHHVIWEIDQEAYEDWFSQSQTATCNVEQSFNDPFSGHNFQIEHHLFPT 240        |
|           |   |
| OY        | 391 MPRNLHKAIPLVKSLCAKGIEYQSKPLLRALLDIIRSLKKSGLMLDAYLHK 444               |
| DB        | 241 MPRNLHKAIPLVKSLCAKGIEYQSKPLLRALLDIIRSLKKSGLMLDAYLHK 294               |
|           |   |
| RESULT 23 |   |
| AAW85134  |   |
| ID        | AAW85134 standard; Protein; 608 AA.                                       |
| XX        |   |
| AC        | AAW85134.   |



XX 11-FEB-1999 (first entry)  
 XX A desaturase enzyme encoded by contig 2535.  
 XX Fatty acid; desaturase; polyunsaturated fatty acid;  
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 608  
 FT /note= "not specified"  
 XX  
 XX WO9846765-A1.  
 XX  
 XX 22-OCT-1998.  
 XX  
 XX 10-APR-1998; 98WO-US07422.  
 XX  
 XX 11-APR-1997; 97US-0833610.  
 XX (ABBO ) ABBOTT LAB.  
 XX (CALJ ) CALGENE LLC.  
 XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 XX  
 XX WPI; 1999-009334/01.  
 DR N-PSDB; AAV82641.  
 XX  
 XX New nucleic acid encoding delta5 and other desaturase enzymes -  
 PT useful in production of oils of increased arachidonic acid content,  
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics  
 XX  
 XX Claim 87; Pages 117-119, 153pp; English.  
 XX  
 XX The present sequence represents a human desaturase enzyme. The enzyme  
 CC sequence is used in the methods of the invention. The specification  
 CC describes methods for desaturating a fatty acid and for producing a  
 CC desaturated fatty acid by expressing increased levels of a desaturase.  
 CC The enzyme can be used for desaturating fatty acids. The enzyme can be  
 CC used to produce polyunsaturated fatty acids, which can be used for  
 CC treating malnutrition, in pharmaceutical compositions, in cosmetics or  
 CC in animal feed. The polyunsaturated fatty acids can be used for treating  
 CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,  
 CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.  
 CC They can also be used to inhibit platelet aggregation, cause  
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel  
 CC wall smooth muscle and fibrous tissue, reduce or prevent  
 CC gastro-intestinal bleeding and other side effects caused by non-steroidal  
 CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual  
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after  
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory  
 CC syndrome, hypertension and inflammatory skin disorders.  
 XX  
 XX Sequence 608 AA;  
 XX  
 XX Query Match 67.5%; Score 1646; DB 20; Length 608;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-171;  
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 151 VFYFGNGWIPLTIAFVATLSQAQAGWLQHDYGHLSVYRKPKWNLVHKFVIGHLKASA 210  
 XX  
 XX 1 VFYFGNGWIPLTIAFVATLSQAQAGWLQHDYGHLSVYRKPKWNLVHKFVIGHLKASA 60  
 XX  
 XX 211 NWNHRRHFQHHAKENIFHKDPDVNMLHVFVGEWQPIEYQKKLKYLPYNHQHEYFFLIG 270  
 XX  
 XX 61 NWNHRRHFQHHAKENIFHKDPDVNMLHVFVGEWQPIEYQKKLKYLPYNHQHEYFFLIG 120  
 XX

QY 271 PPLLPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRELE 330  
 DB 121 PPLLPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRELE 180  
 QY 331 SHWFVVTOMNHVMEIQEAYRDWFSSQLTATCNVEQSFNDWFSGHLPQIEHLLPPT 390  
 DB 181 SHWFVVTOMNHVMEIQEAYRDWFSSQLTATCNVEQSFNDWFSGHLPQIEHLLPPT 240  
 QY 391 MPRHNLKTIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKLDAYLHK 444  
 DB 241 MPRHNLKTIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKLDAYLHK 294  
 RESULT 24  
 AAY92617  
 ID AAY92617 standard; Protein; 614 AA.  
 XX  
 XX AC AAY92617;  
 XX  
 XX DT 10-AUG-2000 (first entry)  
 XX  
 XX Human desaturase homologue encoded by partial DNA contig sequence.  
 XX  
 XX delta-6 desaturase; gamma-linolenic acid; biosynthesis;  
 KW transgenic insect cell; polyunsaturated long chain fatty acid;  
 KW antiinflammatory; antirheumatic; antidiabetic; dermatological; gynecological;  
 KW osteopathic; cytostatic; antidiabetic; hypotensive; nephrotropic; vasodilator;  
 KW anti-HIV; neuroprotective; vasotrophic.  
 KW antiaggregant; vasotrophic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 295 /note= "encoded by TAA"  
 FT Misc-difference 321 /note= "encoded by TAA"  
 FT Misc-difference 458 /note= "encoded by TGA"  
 FT Misc-difference 491 /note= "encoded by TGA"  
 FT Misc-difference 517 /note= "encoded by TAA"  
 FT Misc-difference 535 /note= "encoded by TGA"  
 FT Misc-difference 550 /note= "encoded by TGA"  
 FT  
 XX WO2000020602-A2.  
 XX  
 XX 13-APR-2000.  
 XX  
 XX 29-SEP-1999; 99WO-US22686.  
 XX  
 XX 05-OCT-1998; 98US-0103110.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Mukerji P, Huang Y, Parker-barnes JM, Das T;  
 XX  
 XX WPI; 2000-328935/28.  
 DR N-PSDB; AAY9452.  
 XX  
 XX Novel transgenic insect cells comprising a nucleotide sequences which  
 PT encode delta-6-desaturase or delta-12- desaturase, useful for producing  
 PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid  
 XX  
 XX Example 13; Page 166-167; 170pp; English.  
 PS  
 XX AAY92612-18 are identified based on homology to Mortierella alpina  
 CC delta-5 and delta-6 desaturase genes. The human DNA's were aligned  
 CC based on areas of homology to form a contig. Consensus sequences were

| Key                 | Location/Qualifiers     |
|---------------------|-------------------------|
| Misc-difference 295 | /note= "encoded by TGA" |
| Misc-difference 321 | /note= "encoded by TGA" |
| Misc-difference 458 |                         |

|     |    |          |         |                       |         |          |     |
|-----|----|----------|---------|-----------------------|---------|----------|-----|
| XX. | SQ | Sequence | 615 AA; | Query Match           | 67.5%;  | Score    | 164 |
|     |    |          |         | Best Local Similarity | 100.0%; | Pred. No |     |

151 VYFNGWIPTLITAFVLATSOAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKASA 210  
 VYFNGWIPTLITAFVLATSOAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKASA  
 1 VYFNGWIPTLITAFVLATSOAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKASA 60  
 VYFNGWIPTLITAFVLATSOAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKASA

QY 211 NWNHRHFQHAKENIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 270  
 DB 61 NWNHRHFQHAKENIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 120  
 QY 271 PPLIIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFIYIPYIGLALLFNIRFLE 330  
 DB 121 PPLIIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFIYIPYIGLALLFNIRFLE 180  
 QY 331 SHWFWVTQNMHIWMEIDQAYRDWFSQSQTATCNVEQSFNDWFSCHLNFOIEHHLFPT 390  
 DB 181 SHWFWVTQNMHIWMEIDQAYRDWFSQSQTATCNVEQSFNDWFSCHLNFOIEHHLFPT 240  
 QY 391 MPRNLHKAIPVKSICAKGIEYQKPLRALDIIIRSLKSGKWLMDAYLHK 444  
 DB 241 MPRNLHKAIPVKSICAKGIEYQKPLRALDIIIRSLKSGKWLMDAYLHK 294

## RESULT 26

AA84702  
 ID AAY84702 standard; Protein; 615 AA.

AC AAY84702;

DT 08-AUG-2000 (first entry)

DE Amino acid sequence of a contig of a human desaturase enzyme.

XX Delta5-desaturase; poly-unsaturated long chain fatty acid; PUFA;  
 KW arachidonic acid; infant formula; dietary supplement; dietary substitute;  
 KW cosmetic; stress; metabolic disorder; gastrointestinal difficulty;  
 KW malabsorption; restenosis; angioplasty; inflammation; kidney stone;  
 KW rheumatoid arthritis; asthma; psoriasis; osteoporosis; tract stone;  
 KW cancer; cachexia; diabetes; eczema; endometriosis; premenstrual syndrome;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder;  
 KW blood score; platelet aggregation; vasodilatation;  
 KW gastro-intestinal bleeding.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..614 /note= "Xaa is an unspecified residue encoded by stop codons"

FT Misc-difference 615 /note= "encoded by TG"

XX WO200020603-A1.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US22692.

XX 05-OCT-1998; 98US-0103109.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-Barnes JH, Das T;

XX WPI; 2000-364599/31.

XX N-PSDB; AAA14593.

XX Novel transgenic insect cell with modified delta-5-desaturase  
 FT production, useful for altering fatty acid biosynthesis -

XX Example 9; Page 153-154; 161pp; English.

XX AAY84697-Y84703 are encoded by contigs of a human desaturase. The  
 CC specification describes a Mortierella alpina delta5-desaturase. The  
 CC protein is involved in the biosynthesis of poly-unsaturated long chain  
 CC fatty acids (PUFAs). The polynucleotide is to produce PUFAs, especially  
 CC arachidonic acid. The cils produced by the invention are used in  
 CC pharmaceutical compositions, infant formulas, dietary supplements,

CC dietary substitutes, and cosmetics. The nutritional compositions can be  
 CC used to treat normal individuals temporality exposed to stress, or  
 CC individuals having specialized needs due to chronic or acute diseases  
 CC (e.g. metabolic disorders such as gastrointestinal difficulties and/or  
 CC malabsorption, and other disorders such as restenosis after angioplasty,  
 CC symptoms of inflammation, rheumatoid arthritis, asthma, psoriasis,  
 CC osteoporosis, kidney stones, tract stones, cancer, cachexia associated  
 CC with cancer, diabetes, eczema, endometriosis, premenstrual syndrome,  
 CC myalgic encephalomyelitis, chronic fatigue, AIDS, multiple sclerosis,  
 CC acute respiratory syndrome, hypertension, inflammatory skin disorders,  
 CC as well as reduce blood score, inhibit platelet aggregation, cause and  
 CC vasodilatation, inhibit proliferation of vessel wall smooth muscle and  
 CC fibrous tissue, prevent or reduce gastro- intestinal bleeding, and for  
 CC geriatric treatments).

XX Sequence 615 AA;

Query Match 67.5%; Score 1646; DB 21; Length 615;

Best Local Similarity 100.0%; Pred. NO. 4.7e-171; Indels 0; Gaps 0;  
 Matches 294; Conservative 0; Mismatches 0;

QY 151 VFYFGNGWIPITLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKASA 210

DB 1 VFYFGNGWIPITLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKASA 60

QY 211 NWNHRHFQHAKENIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 270

DB 61 NWNHRHFQHAKENIFHKDPDYNMLHVFVLGEWQPIEYKXKKLKYLPYNHQHEYPFLIG 120

QY 271 PPLIIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFIYIPYIGLALLFNIRFLE 330

DB 121 PPLIIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFIYIPYIGLALLFNIRFLE 180

QY 331 SHWFWVTQNMHIWMEIDQAYRDWFSQSQTATCNVEQSFNDWFSCHLNFOIEHHLFPT 390

DB 181 SHWFWVTQNMHIWMEIDQAYRDWFSQSQTATCNVEQSFNDWFSCHLNFOIEHHLFPT 240

QY 391 MPRNLHKAIPVKSICAKGIEYQKPLRALDIIIRSLKSGKWLMDAYLHK 444

DB 241 MPRNLHKAIPVKSICAKGIEYQKPLRALDIIIRSLKSGKWLMDAYLHK 294

## RESULT 27

ABG94699

ID ABG94699 standard; Protein; 356 AA.

AC ABG94699;

XX 02-DEC-2002 (first entry)

XX Human delta5-desaturase #9.

XX Human; delta5-desaturase; polyunsaturated fatty acid; DGLA;

XX dihomo-gamma-linolenic acid; arachidonic acid; 20:4n-3; cosmetic;

XX eicosapentaenoic acid; EPA; pharmaceutical; nutritional; animal feed;

XX enzyme.

XX Homo sapiens.

XX US6432684-B1.

XX 13-AUG-2002.

XX 08-JAN-1999; 99US-0227613.

XX 11-APR-1997; 97US-0833610.

XX 10-APR-1998; 98WO-US07422.

XX (ABBO ) ABBOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Das T;

XX WPI; 2002-689761/74.

XX Nucleic acids encoding human DELTA5-desaturase, useful for catalysing  
PT the conversion of dihomogamma-linolenic acid to arachidonic acid and  
PT in the conversion of 20:4n-3 to eicosapentaenoic acid -  
XX  
XX  
XX Example 1; Figure 18; 88pp; English.  
XX  
XX The invention relates to an isolated human delta5-desaturase nucleotide  
CC sequence (I) which desaturates polyunsaturated fatty acids at  
CC carbon 5. The nucleotide sequence (I) may be used in the recombinant  
CC production of vectors and host cells for the production of delta5-  
CC desaturase. Delta5-desaturase may be utilised in the conversion of  
CC dihomogamma-linolenic acid (DGLA) to arachidonic acid (AA) and in the  
CC conversion of 20:4n-3 to eicosapentaenoic acid (EPA). AA or  
CC polyunsaturated fatty acids produced from it may be added to  
CC pharmaceutical compositions, nutritional compositions, animal feeds, as  
CC well as other products such as cosmetics. ABG94691-ABG94708 represent  
CC human delta5-desaturase amino acid sequences of the invention.  
XX  
SQ Sequence 356 AA;  
Query Match 66.8%; Score 1628.5; DB 23; Length 356;  
Best Local Similarity 99.7%; Pred. No. 1.8e-169;  
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 151 VFYFGNGWIPITLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 210  
DB 1 VFYFGNGWIPITLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 60  
QY 211 NWNHHRHFQHAKENIFHKDPDVMHLVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 270  
DB 61 NWNHHRHFQHAKENIFHKDPDVMHLVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 120  
QY 271 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 330  
DB 121 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 179  
QY 331 SHWFVWVTQNMHIVMEIDQAYRDWFSSQLTATCNVQSFENDFSGHLNFQIEHLFPT 390  
DB 180 SHWFVWVTQNMHIVMEIDQAYRDWFSSQLTATCNVQSFENDFSGHLNFQIEHLFPT 239  
QY 391 MPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRLSKSGKMLDAYLHK 444  
DB 240 MPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRLSKSGKMLDAYLHK 293  
RESULT 28  
ABG96517  
ID ABG96517 standard; Protein; 356 AA.  
XX  
XX ABG96517;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human partial desaturase protein from contig 2535.  
XX  
KW Human; enzyme; delta5 desaturase; polyunsaturated fatty acid;  
KW PUFA; nutritional; animal feed; cosmetic; skin aging; burn; angioplasty;  
KW inflammation; rheumatoid arthritis; asthma; psoriasis; osteoporosis;  
KW kidney stone; urinary tract stone; cancer; cachexia; diabetes; eczema;  
KW AIDS; multiple sclerosis; blood pressure; cancer; cachexia; diabetes;  
KW vasodilation; cholesterol; proliferation of fibrous tissue;  
KW endometriosis; myalgic encephalomyelitis; human breast milk;  
KW dietary supplement; chromosome 11q12.  
XX  
OS Homo sapiens.  
PN US6428990-B1.  
XX  
XX 06-AUG-2002.  
XX  
XX 12-NOV-1999; 99US-0439261.  
XX

PR 11-APR-1997; 97US-0833610.  
PR 10-APR-1998; 98WO-US07422.  
PR 08-JAN-1999; 99US-0227613.  
XX  
XX (ABBO) ABBOTT LAB.  
XX  
XX Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;  
XX WPI; 2002-730518/79.  
XX  
XX Producing a polyunsaturated fatty acid (PUFA), useful in dietary  
PT supplements and in treating diseases e.g., cancer, comprises expressing  
PT human delta 5-desaturase enzyme and exposing enzyme to substrate PUFA  
PT to convert to product PUFA -  
XX  
XX Example 1; Fig 18; 104pp; English.  
XX  
XX The invention relates to producing (M1) a polyunsaturated fatty acid  
CC (PUFA), comprising: (i) isolating a fully defined human Delta5-desaturase  
CC gene sequence (I); (ii) constructing a vector comprising (I);  
CC (iii) introducing the vector into a host cell for expression of the  
CC human Delta5-desaturase enzyme (II); and (iv) exposing (II) to a  
CC substrate PUFA (III) such that it is converted to a product PUFA (IV).  
CC The method is useful for producing a polyunsaturated fatty acid  
CC such as arachidonic acid (AA), eicosapentaenoic acid (EPA), adrenic  
CC acid, (n-3)-docosapentaenoic acid, (n-6)-docosapentaenoic acid and/or  
CC docosahexaenoic (DHA) acid. The PUFAs produced by the method, such  
CC as arachidonic acid (AA), eicosapentaenoic acid (EPA) and/or  
CC docosahexaenoic (DHA) acid, are useful for replicating the PUFA content  
CC of human breast milk or to alter the presence of PUFAs normally found  
CC in a non-human mammal's milk. PUFAs produced by (M1) may be added to a  
CC dietary substitute or supplement, particularly an infant formula, for  
CC patients undergoing intravenous feeding or for preventing or treating  
CC malnutrition or other conditions or disease states. The PUFAs are  
CC useful for producing nutritional compositions e.g., any food or  
CC preparation for human consumption including for enteral or parenteral  
CC consumption, which when taken into the body serve to nourish or build  
CC up tissues or supply energy and/or maintain, restore or support  
CC adequate nutritional status or metabolic function. The PUFAs are also  
CC useful in animal feed supplements to alter an animal tissue or milk  
CC fatty acid composition to one or more desirable for human or animal  
CC consumption, in animal feed substitutes, animal vitamins or in animal  
CC topical ointments. The PUFAs produced by this method are useful in  
CC producing pharmaceutical compositions for treating rough or aging skin,  
CC injured or burnt skin, angioplasty, inflammation, rheumatoid arthritis,  
CC asthma, psoriasis, osteoporosis, kidney or urinary tract stone, cancer,  
CC cachexia associated with cancer, diabetes, eczema, AIDS, multiple  
CC sclerosis. PUFAs are also useful in reducing blood pressure, inhibiting  
CC platelet aggregation, inducing vasodilation, reducing cholesterol  
CC levels, inhibiting proliferation of fibrous tissue, treating  
CC endometriosis, and myalgic encephalomyelitis. The gene for delta5  
CC desaturase is located on chromosome 11q12. The present sequence  
XX is a partial human delta5 desaturase protein.  
XX  
SQ Sequence 356 AA;  
Query Match 66.8%; Score 1628.5; DB 23; Length 356;  
Best Local Similarity 99.7%; Pred. No. 1.8e-169;  
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 151 VFYFGNGWIPITLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 210  
DB 1 VFYFGNGWIPITLITAFVLATSAQAQGLQHDYGHLSVYRKPKNHVLVHKFVIGHLKGASA 60  
QY 211 NWNHHRHFQHAKENIFHKDPDVMHLVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 270  
DB 61 NWNHHRHFQHAKENIFHKDPDVMHLVFLVGEWQPIEYGGKKLKYLPYNHQHEYFFLIG 120  
QY 271 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 330  
DB 121 PPLIPMYFOYQIIMTVHKWVDLAWAVSYIRFFITIPFYIGLALLFLNFRFLE 179  
QY 331 SHWFVWVTQNMHIVMEIDQAYRDWFSSQLTATCNVQSFENDFSGHLNFQIEHLFPT 390

Db 180 SHFWVVTQMNHIVMEIDQEAIRDFSSQLTATCNVEQSFDFNDFSGHNFQIEHLPPT 239  
 QY 391 MPRHNLKIAPLVKSICAKHG:EYQEKPLLRALLDIIRSLKSGKMLDAYLHK 444  
 Db 240 MPRHNLKIAPLVKSICAKHG:EYQEKPLLRALLDIIRSLKSGKMLDAYLHK 293

RESULT 29  
 AAB58942  
 ID AAB58942 standard; Protein; 286 AA.  
 XX  
 AC AAB58942;  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 650.  
 XX  
 KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KW neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 KW antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;  
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20005173-A1.  
 XX  
 FD 21-SEP-2000.  
 XX  
 XX 08-MAR-2000; 2000WO-US05881.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 FI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-611515/59.  
 DR N-PSDB; AAF21845.  
 XX

New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention,  
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
 PT disorders and neurological diseases -  
 XX  
 PS Claim 11; Page 1091-1092; 1299pp; English.  
 XX

Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
 CC neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 CC antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;  
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The  
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
 CC particularly breast and ovarian cancer. The nucleic acid sequences,  
 CC proteins, agonists and antagonists may also be used in the diagnosis,  
 CC prevention and treatment of immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; cardiovascular disorders such as  
 CC myocardial ischaemias; wound healing; neurological diseases such as  
 CC cerebral anoxia and epilepsy; and infectious diseases.  
 XX  
 SQ Sequence 286 AA;

Query Match 65.4%; Score 1594; DB 21; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-166;  
 Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 IPTLITAFVLTSAQAGWLOHDYGHLSVYRKPKNNHLYVHKFVIGHLKGSANWNNRRHF 218  
 Db 1 IPTLITAFVLTSAQAGWLOHDYGHLSVYRKPKNNHLYVHKFVIGHLKGSANWNNRRHF 60

QY 219 QHEAKPNIFHKDPDNNMLHVFVLGEWQPIEYGGKKLKYLPYNNHQHBYFFLIGPPLIPMY 278  
 Db 61 QHEAKPNIFHKDPDNNMLHVFVLGEWQPIEYGGKKLKYLPYNNHQHBYFFLIGPPLIPMY 120

QY 279 FOYQIIMTLMVHKNNVDLAWAVSYIRFTIYIPFYIGLALLFLNFIFLSESHFWVWT 338  
 Db 121 FOYQIIMTLMVHKNNVDLAWAVSYIRFTIYIPFYIGLALLFLNFIFLSESHFWVWT 180

QY 339 QMNHVMEIDQEAIRDFSSQLTATCNVEQSFDFNDFSGHNFQIEHLPPTMPRNLHK 398  
 Db 181 QMNHVMEIDQEAIRDFSSQLTATCNVEQSFDFNDFSGHNFQIEHLPPTMPRNLHK 240

QY 399 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKMLDAYLHK 444  
 Db 241 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKMLDAYLHK 286

RESULT 30  
 AAY97540  
 ID AAY97540 standard; Protein; 445 AA.  
 XX  
 AC AAY97540;  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human fatty acid desaturase 3 protein sequence.  
 XX  
 KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;  
 KW liver disease; coronary artery disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI035207-A1.  
 XX  
 FD 13-SEP-2000.  
 XX  
 PF 09-MAR-1999; 99EP-0104664.  
 XX  
 PR 09-MAR-1999; 99EP-0104664.  
 XX  
 PA (MULT-) MULTIGENE BIOTECH GMBH.  
 XX  
 FI Weber BHF, Marquardt A;  
 XX  
 DR WPI; 2000-559875/52.  
 DR N-PSDB; AAA90954.  
 XX

Novel cDNA molecules encoding three human fatty acid desaturases,  
 PT FADS1, FADS2 and FADS3, useful in the treatment of liver disease,  
 PT coronary artery disease and cancer -  
 XX  
 PS Claim 1; Page 44-46; 72pp; English.  
 XX

This sequence is the human fatty acid desaturase, FADS-3, of the  
 CC invention. An antibody directed against the 3 FADS molecule of the  
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or  
 CC therapeutic purposes. The FADS coding sequences are useful in gene  
 CC therapy. The polypeptide and antibodies are also useful in screening for  
 CC modulating drugs. The polypeptides are also useful in screening for  
 CC disease, coronary artery disease and cancer.  
 CC Note: Two copies of the sequence listing are present within this  
 CC patent, which contain different sequences. AAA90952 and AAA90955 are  
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are  
 CC stated as being SEQ ID's 7-22.  
 XX

SQ Sequence 445 AA;

Query Match 64.0%; Score 1560.5; DB 21; Length 445;  
 Best Local Similarity 62.3%; Pred. No. 6.9e-162;  
 Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGGNQG--EGAAAREVSVPTFSWEEIQKHLRTDGLVIDRKVYNITKWSIQHPGQOR 58  
 DB 1 MGVGEPGREGPAQGPALPTFCWEQIRAHQPGDKMLVIERRVYDISRWAQRHFGGSR 60

QY 59 VIGHYAGEDATDAFRAPHQDLNFKVFLKPLIGELAPEPSQDHGKSKITEDFRALK 118  
 DB 61 LIGHGAEDATDAFRAPHQDLNFKVFLKPLIGELAPEPSQDHGKSKITEDFRALK 120

QY 119 TAEDMNLFTNHFVFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL 178  
 DB 121 AEDMKLFDASPTFFAFLLGHILAMEVLAWLLIYLLGPGWPSALAAFIASQAQSWCL 180

QY 179 QHDYGHLSVYRKPKWNHVKFVGHKLGASANNWHRHFOHAKPNIFHKDPDVNMLHV 238  
 DB 181 QHDLGHASIFPKSWMNHVAKFVNGQLKGFSAHWNFRHFOHAKPNIFHKDPDVTVAPV 240

QY 239 FVLGEWQPIEYKKKLYLPYNHOFYFFLIGPPLIPMYFOYQIIMTVHKNWDLAW 298  
 DB 241 FLIGE--SSVEYKKKRRYLPYNQOHLYFFLIGPPLITLVNFEVENLAYMLVCMQWADLLM 299

QY 299 AVSYIRFFITYIPYIGILGALLFNPIRPLESHWVWVTOMNHVWEIDQAYRDWPS 358  
 DB 300 AASFYARFFLSYLPFYGVGLLFFVAVRVLESHEWVWVTOMNHVWEIDQAYRDWPS 359

QY 359 QLTATCNVEQSPFNDWFSGLNFQIEHLLFPTMPRHNLHAKIAPLVKSLCAKHGLSYEVKP 418  
 DB 360 QLAATCNVEPSLFTNWFSGHLNFQIEHLLFPRMPRHNSRVAPLVKSLCAKHGLSYEVKP 419

QY 419 LLRALLDIIRSLKSGKMLDAYLHK 444  
 DB 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 31  
 AAY83229  
 ID AAY83229 standard; Protein; 445 AA.  
 AC AAY83229;  
 DT 16-AUG-2000 (first entry)  
 DE CYB5RP fatty acid desaturase.  
 KW CYB5RP; fatty acid desaturase; cytochrome b5; macular degeneration;  
 KW skin disease; diabetes; inflammation; autoimmune disease;  
 KW cardiovascular disease; viral infection; virus; identification;  
 KW human.  
 OS Homo sapiens.  
 FH Key  
 FT Domain /label= Cytochrome b5 domain  
 FT Region 182..186  
 FT Region /label= His box 1  
 FT Region 219..223  
 FT Region /label= His box 2  
 FT Region 383..387  
 FT Region /label= His box 3  
 PN WO200021557-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23253.  
 XX  
 XX 09-OCT-1998; 98US-0103760.  
 PR

XX PA (MERI ) MERCK & CO INC.  
 XX PI Petrukhin K, Caskey CT;  
 XX DR WPI; 2000-317847/27.  
 XX DR N-PSDB; AAZ93706.  
 XX  
 PT Novel cytochrome b5-related protein useful for identifying modulators  
 PT useful for treating retinal dysfunction such as macular degeneration,  
 PT skin diseases, diabetic complications and cardiovascular disorders  
 XX  
 PS Claim 3; Figure 3; 44pp; English.  
 XX  
 CC CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.  
 CC Pharmaceutical compositions comprising an activator or an inhibitor of  
 CC CYB5RP protein are useful for treating macular degeneration. The  
 CC CYB5RP protein is useful for identifying its activators or inhibitors  
 CC which are useful for treating abnormal conditions associated with  
 CC CYB5RP protein activity such as skin disease, diabetic complications,  
 CC inflammatory and autoimmune disorders, cardiovascular disorders and  
 CC complications of viral infection. Large amounts of valuable essential  
 CC fatty acids can be produced by the expression of CYB5RP protein.  
 XX  
 SQ Sequence 445 AA;

Query Match 64.0%; Score 1560.5; DB 21; Length 445;  
 Best Local Similarity 62.3%; Pred. No. 6.9e-162;  
 Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGGNQG--EGAAAREVSVPTFSWEEIQKHLRTDGLVIDRKVYNITKWSIQHPGQOR 58  
 DB 1 MGVGEPGREGPAQGPALPTFCWEQIRAHQPGDKMLVIERRVYDISRWAQRHFGGSR 60

QY 59 VIGHYAGEDATDAFRAPHQDLNFKVFLKPLIGELAPEPSQDHGKSKITEDFRALK 118  
 DB 61 LIGHGAEDATDAFRAPHQDLNFKVFLKPLIGELAPEPSQDHGKSKITEDFRALK 120

QY 119 TAEDMNLFTNHFVFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL 178  
 DB 121 AEDMKLFDASPTFFAFLLGHILAMEVLAWLLIYLLGPGWPSALAAFIASQAQSWCL 180

QY 179 QHDYGHLSVYRKPKWNHVKFVGHKLGASANNWHRHFOHAKPNIFHKDPDVNMLHV 238  
 DB 181 QHDLGHASIFPKSWMNHVAKFVNGQLKGFSAHWNFRHFOHAKPNIFHKDPDVTVAPV 240

QY 239 FVLGEWQPIEYKKKLYLPYNHOFYFFLIGPPLIPMYFOYQIIMTVHKNWDLAW 298  
 DB 241 FLIGE--SSVEYKKKRRYLPYNQOHLYFFLIGPPLITLVNFEVENLAYMLVCMQWADLLM 299

QY 299 AVSYIRFFITYIPYIGILGALLFNPIRPLESHWVWVTOMNHVWEIDQAYRDWPS 358  
 DB 300 AASFYARFFLSYLPFYGVGLLFFVAVRVLESHEWVWVTOMNHVWEIDQAYRDWPS 359

QY 359 QLTATCNVEQSPFNDWFSGLNFQIEHLLFPTMPRHNLHAKIAPLVKSLCAKHGLSYEVKP 418  
 DB 360 QLAATCNVEPSLFTNWFSGHLNFQIEHLLFPRMPRHNSRVAPLVKSLCAKHGLSYEVKP 419

QY 419 LLRALLDIIRSLKSGKMLDAYLHK 444  
 DB 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

RESULT 32  
 ABU08788  
 ID ABU08788 standard; Protein; 445 AA.  
 AC ABU08788;  
 XX  
 XX 09-JUN-2003 (first entry)  
 DT  
 XX Human delta 6 desaturase D6DH-1.  
 DE  
 XX

|   |   |
|---|---|
| Human; enzyme; D6DH-1; delta 6 desaturase-1; fatty acid desaturase; cardiovascular disease; angina pectoris; atheroma embolism; hypertension; atherosclerosis; arteriosclerosis; cardiac ischaemia; hyperlipidaemia; hypercholesterolaemia; hypertriglyceridaemia; gangrene; decubitus ulcer; mesenteric ischaemia; renal artery stenosis; stroke; nephrosclerosis; aging; Alzheimer's disease; angioimmunoblastic lymphadenopathy; anorexia; basal cell carcinoma; cardiac amyloidosis; cerebral amyloidosis; goiter; chronic lymphatic leukaemia; degenerative osteoarthritis; delirium; dementia; depression; dyskinesia; diabetic hyperosmolar nonketotic coma; glaucoma; hypercholesterolaemia; hypothermia; metabolic bone disease; osteoporosis; normal pressure hydrocephalus; diabetes; Reye's syndrome; Parkinson's disease; polymyalgia; rheumatism; prostatic carcinoma; renal amyloidosis; tuberculosis; urinary incontinence; galactosaemia; fatty acid metabolism disorder; Addison's disease; cystic fibrosis; fatty hepatocirrhosis; hyperadrenalism; hypoadrenalism; hyperlipaemia; hyperparathyroidism; hypoparathyroidism; lipid myopathy; obesity; lipodystrophy; phenylketonuria; cancer. |   |
| Homo sapiens.   |   |
| Key   | Location/Qualifiers   |
| Region  | 183..187  |
| FT  | /label= Histidine_box   |
| FT  | 219..223  |
| FT  | /label= Histidine_box   |
| FT  | 351..354  |
| FT  | /label= Histidine_box   |
| XX  |   |
| XX  | US6492108-B1.   |
| XX  |   |
| XX  | 10-DEC-2002.  |
| XX  |   |
| XX  | 26-MAR-1999; 98US-0048888.  |
| XX  |   |
| XX  | 26-MAR-1999; 98US-0048888.  |
| XX  |   |
| XX  | (INCY) INCYTE GENOMICS INC.   |
| XX  |   |
| XX  | Hillman JL, Guegler KJ, Corley NC, Shah P;  |
| XX  |   |
| XX  | WPI: 2003-327308/31.  |
| XX  | N-PSDB; ABX93651.   |
| XX  |   |
| XX  | New isolated polynucleotide encoding polypeptide having delta-6 desaturase activity for use in diagnosis, treatment and prevention of cardiovascular diseases, disorders of aging, disorders of fatty acid metabolism, and cancer -   |
| XX  |   |
| XX  | Claim 2; Fig 1; 39pp; English.  |
| XX  |   |
| XX  | The invention relates to an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence given in the specification. The polypeptide has fatty acid desaturase activity or delta-6 desaturase activity. For use in the diagnosis, treatment and prevention of cardiovascular diseases (e.g. angina pectoris, atheroma embolism, atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension, hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene, mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis), disorders of ischaemia, renal artery stenosis, stroke, nephrosclerosis), disorders of aging (e.g. Alzheimer's disease, stroke, angioimmunoblastic lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia, diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia, hypothermia, metabolic bone disease including osteoporosis, normal pressure hydrocephalus, Parkinson's disease, Reye's syndrome, polymyalgia, rheumatism, prostatic carcinoma, renal amyloidosis, tuberculosi, urinary incontinence), disorders of fatty acid metabolism (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis, galactosaemia, goiter, hyperadrenalism, hypoadrenalism, obesity, hyperparathyroidism, hypoparathyroidism, hyperlipaemia, lipid myopathics, lipodystrophies, phenylketonuria) and cancer. The present sequence represents the amino acid sequence of human delta 6 desaturase-1, D6DH-1. |

|    |   |   |     |
|----|---|---|-----|
| 1  | MGKGGNQG--EGAAEREVSVPTEGWEIEIOKHNLTDSGLVIDRKVYNIITKKSIOHPGGOR | 58  |     |
| 2  | 1   | MGVGEFGPREGPAQCAPPTFCWEQIRAHQDQDKWLVIERRVYDISRWQAQRHPGGS                  | 60  |
| 3  | 59  | VIGHYAGEDATDAFRAHPDLFEVGVKFLKPLLIGELAPEEPSQHGKNSKITEDFRALRK               | 118 |
| 4  | 61  | LIGHGGAEDATDAFRAHQDLNFKVKELQPLLIGELAPEEPSQDGLNAQLVEDFRALHQ                | 120 |
| 5  | 119   | TAEDMNLFTKNHVFLLLLLAHI IALESIAMFTVYFGNGWTPTLITAFVLATSOAAGWL               | 178 |
| 6  | 121   | AAEDMKLFDASPTFFAFLGHILANEVLMLIYLLGPGWVPSALAAFI LAISQAQSWCL                | 180 |
| 7  | 179   | QHDYGHLSVTRKPKNHLVHKFVIGHI KGASANNWNRHFRQHAHPNI FHKDPDVMNLHV              | 238 |
| 8  | 181   | QHDILGHASIFKKSWMNVVAQKFVNGQLKGFSAHWNFRFHQHAHPNIFHKDPDVTVA                 | 240 |
| 9  | 239   | FVLGEWQPIEYGGKKLXLPYNHQHEFFYFLIGPPLLIPMVFOYQI IMTMIVHKWVDLAW              | 298 |
| 10 | 241   | FLLGE--SSVEYGGKKRYLPLVNOQHLFFLIGPPLLITVNFVEVLA YMLVCMQADLLW               | 299 |
| 11 | 299   | AVSYIIRFFTYIPFYIGLALLFLNIRFLESWFVVTOMNHIWMEIDOEARDWPS                     | 358 |
| 12 | 300   | AA SFYARFFLSYLPFYGVPGLLFFVAVRVLESWFVNI TOMNHI PKI GHEKRDWVSS              | 359 |
| 13 | 359   | QLTATCNVEQSFENDWPSGHLNFOI EHLHFTPMRHLNHLKIAPLVKSLCAKHGLEYOKP              | 418 |
| 14 | 360   | QLAATCNVEPSLFTNFWPSGHLNFOI EHLHFPMPRHNSYRVAPLVKSLCAKHGLESYVKP             | 419 |
| 15 | 419   | LLRALLDIIRSLKSKGLWLDAYLHK   | 444 |
| 16 | 420   | FLTALVDIVRSLKSKGDIWLDAYLHQ  | 445 |
| 17 | RESULT 33   |   |     |
| 18 | AAAM25786   |   |     |
| 19 | ID  | AAAM25786 standard; Protein; 490 AA.                                      |     |
| 20 | XX  | AAAM25786;  |     |
| 21 | XX  |   |     |
| 22 | XX  | 16-OCT-2001 (first entry)   |     |
| 23 | XX  | Human protein sequence SEQ ID NO:1301.                                    |     |
| 24 | XX  | Human; cancer; ulcer; HIV infection; human immunodeficiency virus;        |     |
| 25 | XX  | antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;        |     |
| 26 | XX  | antibacterial; endocrine; cardiant; central nervous system; vitruide;     |     |
| 27 | XX  | anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;   |     |
| 28 | XX  | antiagregant; haemostatic; vulnerary; antilucer; osteopathic; eczema;     |     |
| 29 | XX  | dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;    |     |
| 30 | XX  | immunoprotective; antidepressant; nootropic; antiparkinsonian; infection; |     |
| 31 | XX  | immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;  |     |
| 32 | XX  | anti-anaphylactic; rheumatoid arthritis; septic shock; pancreatitis;      |     |
| 33 | XX  | cardiac dysfunction; neuropathology, cardiac anaphylaxis; autoimmunity;   |     |
| 34 | XX  | genetic disease; haematopoietic disorder; platelet disorder; asthma;      |     |
| 35 | XX  | thrombocytopaenia; diabetosis; severe combined immunodeficiency;          |     |
| 36 | XX  | allergic rhinitis; diabetes; multiple sclerosis; depression;              |     |
| 37 | XX  | Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;     |     |
| 38 | XX  | neurological disorder.  |     |
| 39 | OS  | Homo sapiens.   |     |
| 40 | XX  |   |     |
| 41 | PN  | WO200153455-A2.   |     |
| 42 | XX  |   |     |
| 43 | PD  | 26-JUL-2001.  |     |
| 44 | XX  |   |     |
| 45 | XX  | 22-DEC-2000; 2000WO-US35017.  |     |
| 46 | PF  |   |     |



PR 23-DEC-1999; 99US-0471275.  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-457603/49.  
DR N-PSDB; AAH99727.  
XX  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX  
XX Claim 20; Page 270; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
XX AAM25963. The proteins can have activities based on the tissues and  
XX cells they are expressed in, such as: antiinflammatory; antirheumatic;  
XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;  
XX cardiovascular; antianaemic; antidiabetic; antihypertensive; antitumor;  
XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
XX antitumor; antidiabetic; dermatological; antiallergic; antiasthmatic;  
XX antitumor; osteoprotective; neuroprotective; antidepressant; neurotropic;  
XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
XX encoding them can be used in gene therapy, antisense therapy and vaccine  
XX production. The proteins and polynucleotides are useful for screening for  
XX agonists or antagonists of a protein and for the treatment and diagnosis  
XX of disorders associated with the activity of a protein e.g. inflammation,  
XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
XX infections, autoimmunity, genetic diseases, haematopoietic disorders,  
XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
XX osteoporosis, severe combined immunodeficiency, eczema, allergic  
XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
XX Alzheimer's disease, Parkinson's disease, neurodegenerative and  
XX neurological disorders.  
XX  
XX Sequence 490 AA;

Query Match 64.0%; Score 1560.5; DB 22; Length 490;  
Best Local Similarity 62.3%; Pred. No. 8e-162;  
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;  
QY 1 MGKGNQ--EQAAREVSVPTFSWEEIQKHLNRTSGLVDRKVNITKWSIQHPGQR 58  
DB 46 MGGVGPBPREGPAQPGAPLFTFCWEQIRAHQDQGDKWLVIERRVYDISRWAQRHPGGR 105  
QY 59 VIGHYAGEDATDAFRAHFDLEFVGKFLPLIGELAPEPSODHGKNGKITEDFRALRK 118  
DB 106 LIGHGAGEDATDAFRAHFDLEFVGKFLPLIGELAPEPSODGFLNQLVEDFRALHQ 165  
QY 119 TAEDMNLKTNHVFLLALLAHILALIESIAWFTVYFGNGWIPFLITAFVLATSOAQAGWL 178  
DB 166 AAEEDMLKFDASPTFFAFLGHILAMEVLAWLLYLLPGWVPSALAAFTLAISQAOSWCL 225  
QY 179 OHYGHLSVVRKPNWHLVHKFVGHILKGSANWNRHFRHFOHAKENIFHKPDVNMHLV 238  
DB 226 QHDLGHASIFKSGWNNHVAQVNGKLGSAHWNRFRHFOHAKENIFHKPDVNTVAVP 285  
QY 239 FVLGEMQFIYGGKKLKYLPYNHQHEYFFLIGPFLIPMYFQYQIIMTVHKNQWVDLAW 298  
DB 286 FLLGE-SSVEYGGKKRYLPYNQCHLYFFLIGPFLITLVNFEVNEAYMLVCNQWADLLW 344  
QY 299 AVSYIIRFFTYTPFYGILGALLFLNPIRELSHFWVWVTONNHVMEIDQEARWESS 358  
DB 345 AASYARAFFLSYLPFYGVPGVLLFFVAVRVLESHFWVWVTONNHVMEIDQEARWESS 404  
QY 359 QLATCNVEQSFNDWFSGHNLFOIEHLLFPTMPRHNLHKAIPLVKSLCAKGIIEYQKRP 418  
DB 405 QLATCNVEPSLFTNWFSGHNLFOIEHLLFPRFRHNSRVAVLVKSLCAKGLSYEVKRP 464  
QY 419 LLRALLDIIRSLKSKGLWLDAYLHK 444

DB 465 FLTALYDIVRSEKSGDILWLDAYLHQ 490  
RESULT 34  
ABG10281  
ID ABG10281 standard; Protein; 446 AA.  
XX  
XX AC ABG10281;  
XX  
XX DT 13-FEB-2002 (first entry)  
XX  
XX DE Novel human diagnostic protein #10272.  
XX  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200175067-A2.  
XX  
XX PD 11-OCT-2001.  
XX  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX  
XX PA (HYSE-) HYSEQ INC.  
XX  
XX FI Drmanac RT, Liu C, Tang YT;  
XX  
XX DR WPI; 2001-639362/73.  
XX DR N-PSDB; AAS74468.  
XX  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity -  
XX  
XX Claim 20; SEQ ID No 40640; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences, (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG0010-ABG30377 represent novel human  
XX diagnostic amino acid sequences of the invention.  
XX Note: the sequence data for this patent did not appear in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 446 AA;  
Query Match 62.6%; Score 1527; DB 22; Length 446;  
Best Local Similarity 61.7%; Pred. No. 3.3e-158;  
Matches 276; Conservative 61; Mismatches 106; Indels 4; Gaps 3;  
QY 1 MGKGNQ--EQAAREVSVPTFSWEEIQKHLNRTSGLVDRKVNITKWSIQHPGQR 58  
DB 1 MGGVGPBPREGPAQPGAPLFTFCWEQIRAHQDQGDKWLVIERRVYDISRWAQRHPGGR 60



26-OCT-2000; 2000US-243009P.  
(XENO-) XENON GENETICS INC.  
Winther MD, Knickle LC, Haardt M, Allen SJ, Ponton A;  
De Antueno RJ, Jenkins DK, Nwaka SO;  
WPI; 2002-454647/48.  
Novel control region of delta-5-desaturase gene useful as a target for  
screening compounds useful in the treatment of diseases involving  
abnormal lipid metabolism including diabetic neuropathy  
Disclosure; Fig 4; 93pp; English.  
The invention relates to human delta-5-desaturase (hDSD) gene control  
region used as a target for screening drugs useful in treatment of  
diseases involving abnormal lipid metabolism including diabetic  
neuropathy, arterial hypertension, hypercholesterolaemia, atherosclerotic  
heart disease, chronic inflammatory disorders, autoimmune disorders, such  
as rheumatoid arthritis, diminished lymphocyte proliferation,  
T-cell-mediated cytotoxicity, natural killer cell activity,  
macrophage-mediated cytotoxicity, monocyte and neutrophil chemotaxis,  
major histocompatibility class II expression and antigen presentation,  
production of pro-inflammatory cytokines (interleukins 1 and 6, tumour  
necrosis factor) and adhesion molecule expression, eczema, psoriasis,  
acute respiratory distress syndrome (ARDS), articular cartilage  
degradation (ACD) and cancer. Host cell containing the control  
region of DSD gene is useful for screening for a modulator capable  
of regulating the expression of a mammalian DSD gene, especially for  
identifying modulators that modulate lipid metabolism or diabetic  
neuropathy. The screening method is an assay for identifying modulators  
that modulate the n-3 lipid metabolic pathway, conversion of  
18:3n3-22:6n3, or n-9 lipid metabolic pathway, conversion of  
16:0-22:4n9 or n-6 lipid metabolic pathway, conversion of 18:2n6-22:5n6.  
The human DSD control region provides a powerful tool for dissecting the  
role of DSD gene expression and inducing modifications, which eliminate  
or control alterations associated with metabolic disorders. The  
present sequence is C-terminal tagged human delta-5-desaturase  
(hDSD) enzyme.

PR 26-OCT-2000; 2000US-243009P.  
XX (XENO-) XENON GENETICS INC.  
XX Winther MD, Knickle LC, Haardt M, Allen SJ, Ponton A;  
XX De Antueno RJ, Jenkins DK, Nwaka SO;  
XX WPI; 2002-454647/48.  
XX Novel control region of delta-5-desaturase gene useful as a target for  
XX screening compounds useful in the treatment of diseases involving  
XX abnormal lipid metabolism including diabetic neuropathy  
XX  
XX Disclosure; Fig 4; 93pp; English.  
XX The invention relates to human delta-5-desaturase (hDSD) gene control  
XX region used as a target for screening drugs useful in treatment of  
XX diseases involving abnormal lipid metabolism including diabetic  
XX neuropathy, arterial hypertension, hypercholesterolaemia, atherosclerotic  
XX heart disease, chronic inflammatory disorders, autoimmune disorders, such  
XX as rheumatoid arthritis, diminished lymphocyte proliferation,  
XX T-cell-mediated cytotoxicity, natural killer cell activity,  
XX macrophage-mediated cytotoxicity, monocyte and neutrophil chemotaxis,  
XX major histocompatibility class II expression and antigen presentation,  
XX production of pro-inflammatory cytokines (interleukins 1 and 6, tumour  
XX necrosis factor) and adhesion molecule expression, eczema, psoriasis,  
XX acute respiratory distress syndrome (ARDS), articular cartilage  
XX degradation (ACD) and cancer. Host cell containing the control  
XX region of DSD gene is useful for screening for a modulator capable  
XX of regulating the expression of a mammalian DSD gene, especially for  
XX identifying modulators that modulate lipid metabolism or diabetic  
XX neuropathy. The screening method is an assay for identifying modulators  
XX that modulate the n-3 lipid metabolic pathway, conversion of  
XX 18:3n3-22:6n3, or n-9 lipid metabolic pathway, conversion of  
XX 16:0-22:4n9 or n-6 lipid metabolic pathway, conversion of 18:2n6-22:5n6.  
XX The human DSD control region provides a powerful tool for dissecting the  
XX role of DSD gene expression and inducing modifications, which eliminate  
XX or control alterations associated with metabolic disorders. The  
XX present sequence is C-terminal tagged human delta-5-desaturase  
XX (hDSD) enzyme.

XX SQ Sequence 473 AA;  
Query Match 62.2%; Score 1516; DB 23; Length 473;  
Best Local Similarity 62.0%; Pred. No. 5.7e-157;  
Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;  
QY 11 AAREVSVPT---PSWEEIQKHNLRDGLVIDRKVYNITKWSIQHPGGORVIGHYAGED 67  
DB 7 AAEATAAGPTFRYFTWDEVAQRSCERWLVDRKVTNISEFTFRHPGSRVISHVAGQD 66  
QY 68 ATDAFRAPHPDLFVGVKFLKPLLIGELAPEEPSQDHGKSKITEDFRALKTAEDNLFK 127  
DB 67 ATDFVFAFHINKGLVKYMSLLIGELSPQSPSEPTKNEKLTDFELRATVVERMLMK 126  
QY 128 TNHVPFLLLLAHIALSIAFTVFYFGNGHPIPLITAFVLATSOAAGWLQHDYGLSLV 187  
DB 127 ANHVFFLLYLLHLLDGAALTLTWFTGTSFLPCLCAVLLSAVQAAGWLQHDYGLSLV 186  
QY 188 YRKPKNVHLVKFVIGHLKASANNWNRHFRHQHAKPNIHFKDPDNNMLH--VFLVGEWQ 245  
DB 187 FSTSKWNHLLHHFVIGHLKAPASNNWNRHFRHQHAKPNIHFKDPDNNMLH--VFLVGEWQ 245  
QY 246 PIEVKKLKYLPYNHQQEYFFLGPPLLIPIYQYQIIMTIVKQWVLAWSVYIR 305  
DB 246 SVELGQKKYKYPYNHQQEYFFLGPPLLIPIYQYQIIMTIVKQWVLAWSVYIR 305  
QY 306 PFITVPIYGLGALLFLNFIRESHFWVMTQNNHIVMEIDQAYEDWFFSSOLTATCN 365  
DB 306 PFITVPIYGLGALLFLNFIRESHFWVMTQNNHIVMEIDQAYEDWFFSSOLTATCN 365  
QY 366 VEQSPFNDFWFSGLHNFQIEHLLFPPTMPRNLHKLAPLVKSLCAKGEYQEKPLLRALLD 425

CC atherosclerosis, arteriosclerosis, cardiac ischaemia, hypertension,  
 CC hypercholesterolaemia, hyperlipidaemia, hypertriglyceridaemia, gangrene,  
 CC mesenteric ischaemia, renal artery stenosis, stroke, nephrosclerosis,  
 CC disorders of aging (e.g. Alzheimer's disease, angioimmunoblastic  
 CC lymphadenopathy, anorexia, basal cell carcinoma, cardiac or cerebral  
 CC amyloidosis, chronic lymphatic leukaemia, decubitus ulcers, degenerative  
 CC osteoarthritis, delirium, dementia, depression, diabetes, dyskinesia,  
 CC diabetic hyperosmolar nonketotic coma, glaucoma, hypercholesterolaemia,  
 CC hypothermia, metabolic bone disease including osteoporosis, normal  
 CC pressure hydrocephalus, Parkinson's disease, Reye's syndrome,  
 CC polymyalgia, rheumatics, prostatic carcinoma, renal amyloidosis,  
 CC tuberculosis, urinary incontinence), disorders of fatty acid metabolism  
 CC (e.g. Addison's disease, cystic fibrosis, fatty hepatocirrhosis,  
 CC galactosaemia, goiter, hyperadrenism, hypoadrenalism, obesity,  
 CC hyperparathyroidism, hyperparathyroidism, hyperlipaemia, lipid myopathies,  
 CC lipodystrophies, phenylketonuria) and cancer. The present sequence  
 CC represents the amino acid sequence of human delta 6 desaturase-2, D6D-2.  
 XX  
 SQ Sequence 444 AA;  
 Query Match 62.1%; Score 1515; DB 24; Length 444;  
 Best Local Similarity 62.0%; Pred. No. 6.7e-157;  
 Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;  
 QY 11 AAREVSVPT---FSWBEIOKHNLRTDGLVIDRKVYNTKWSIQHPGQGVIGHVAGED 67  
 DB 7 AAEATAAQGPTRYFTWDEVAQSGCEERWLVIDRKVYNISEFTRRHGGSRVISHVAGQD 66  
 QY 68 ATDAFRAHPDLEFVGKPLKPLIGELAPEPSQDHGKNSKITEDFRLAKRTAEDMNLFK 127  
 DB 67 ATDPPVAFHINKGLVKYMNLSLIGELSPQSPPTNKELTDFEFLRATVERMGLMK 126  
 QY 128 TNHVFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAAGWLQHDYGLSV 187  
 DB 127 ANHVFLLYLHLILLEGAAWLTWVFGTSLFELLCVALLSAVQAQGLQHDYGLSV 186  
 QY 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFFQHHAKPNI FHKDPDVMNLH--VFVLGEWQ 245  
 DB 187 FSTSKWNHLHFFVIGHLKGAPASWWSHMHFOHAKPNCFRKDPDINN-HPFFSFGALGKIL 245  
 QY 246 PIEYKGGKLYLPYNHGHVEFLGPPLLIPMYFOYQIIMTVHKNWDLAWAVSYIR 305  
 DB 246 SVELGKQKKYMPYNHGHVEFLGPPALLPYFQWIFVTVQRKKWDLAWMTFYVR 305  
 QY 306 FFITYIPYIGLGLALLFNIRFLESNFWVVTQNNHIVMEIDQAYRDWFSQLTATCN 365  
 DB 306 FFLLTVPLGLKAFGLFFIVRLESNFWVVTQNNHIVMEIDQAYRDWFSQLTATCN 365  
 QY 366 VEQSFNDWFSGLHNFQIEHHLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLD 425  
 DB 366 VHKSAFNDWFSGLHNFQIEHHLFPTMPRHNYHKVAPLVQSLCAKHGIEYQSKPLLSAFAD 425  
 QY 426 IIRSLKSGKWLDAYLHK 444  
 DB 426 IHSKESQQLWLDAYLHQ 444  
 RESULT 38  
 AAM93314  
 ID AAM93314 standard; Protein; 501 AA.  
 XX  
 AC AAM93314;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 2827.  
 XX  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 FN EP1130094-A2.  
 XX

PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114089.  
 XX  
 PR 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR MPI; 2001-524355/58.  
 DR N-P8DB; AAX94234.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 2827; 1380pp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesising the full length  
 CC cDNA are useful for cloning the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX  
 SQ Sequence 501 AA;  
 Query Match 62.1%; Score 1515; DB 22; Length 501;  
 Best Local Similarity 62.0%; Pred. No. 8e-157;  
 Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;  
 QY 11 AAREVSVPT---FSWBEIOKHNLRTDGLVIDRKVYNTKWSIQHPGQGVIGHVAGED 67  
 DB 64 AAEATAAQGPTRYFTWDEVAQSGCEERWLVIDRKVYNISEFTRRHGGSRVISHVAGQD 123  
 QY 68 ATDAFRAHPDLEFVGKPLKPLIGELAPEPSQDHGKNSKITEDFRLAKRTAEDMNLFK 127  
 DB 124 ATDPPVAFHINKGLVKYMNLSLIGELSPQSPPTNKELTDFEFLRATVERMGLMK 183  
 QY 128 TNHVFLLLAHIIALESIAFTVFYFGNGWIPTLITAFVLATSOAAGWLQHDYGLSV 187  
 DB 184 ANHVFLLYLHLILLEGAAWLTWVFGTSLFELLCVALLSAVQAQGLQHDYGLSV 243  
 QY 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFFQHHAKPNI FHKDPDVMNLH--VFVLGEWQ 245  
 DB 244 FSTSKWNHLHFFVIGHLKGAPASWWSHMHFOHAKPNCFRKDPDINN-HPFFSFGALGKIL 302  
 QY 246 PIEYKGGKLYLPYNHGHVEFLGPPLLIPMYFOYQIIMTVHKNWDLAWAVSYIR 305  
 DB 303 SVELGKQKKYMPYNHGHVEFLGPPALLPYFQWIFVTVQRKKWDLAWMTFYVR 362  
 QY 306 FFITYIPYIGLGLALLFNIRFLESNFWVVTQNNHIVMEIDQAYRDWFSQLTATCN 365  
 DB 363 FFLLTVPLGLKAFGLFFIVRLESNFWVVTQNNHIVMEIDQAYRDWFSQLTATCN 422  
 QY 366 VEQSFNDWFSGLHNFQIEHHLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLD 425  
 DB 423 VHKSAFNDWFSGLHNFQIEHHLFPTMPRHNYHKVAPLVQSLCAKHGIEYQSKPLLSAFAD 482  
 QY 426 IIRSLKSGKWLDAYLHK 444  
 DB 483 IHSKESQQLWLDAYLHQ 501



CC comprising a human delta-5-desaturase nucleotide sequence (see  
CC AAA49932). Transgenic plants capable of producing polyunsaturated  
CC fatty acids (PUFAs) in their seeds, and transgenic mammals are also  
CC claimed. AA and EPA can be converted into other PUFAs, especially  
CC docosapentaenoic acid and docosahexaenoic acid, using additional  
CC desaturase enzymes. The PUFA products are used in nutritional,  
CC veterinary and pharmaceutical compositions that can be administered  
CC to animals or humans as a dietary substitute/supplement.  
XX

|     |                       |   |  |
|-----|-----------------------|---|--|
| Seq | Sequence              | 444   | AA;  |
| QY  | Query Match           | 61.9%;  | Score 1508; DB 21; Length 444;                       |
| QY  | Best Local Similarity | 61.7%;  | Pred. No. 3.9e-156;                                  |
| QY  | Matches 271;          | Conservative 62;  | Mismatches 100; Indels 6; Gaps 3;                    |
| QY  | 11                    | AAEREVSVP   | ---PSWEIOKHNLRDTSGLVIDRKVYNITKWSIOHPCGQGVIGHYAGED 67 |
| DB  | 7                     | AAETAACQPTPRYFTWDEVAQRSGCEERWLVDRKVNISEFTRRHFGGSRVISHYAGQD 66     |  |
| QY  | 68                    | ATDAFRAHPDLEFVGKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNMLFX 127 |  |
| DB  | 67                    | ATDPFVAHINKGLVKKYNNLSLIGELSPQSPSFPTKKNKELTDEFRELKATVERMGLMK 126   |  |
| QY  | 128                   | TNHPVFLLLAHIIALESIAWFTVYFCNGWIPITLITAFVLATSQAQAGMLQHDYGHLSV 187   |  |
| DB  | 127                   | ANHVFLLYLLHILLDGAAMLTLWVGTSTFPFLCAVLLSAVQAQAGMLQHDYGHLSV 186      |  |
| QY  | 188                   | YRKPKNHLVHKFVIGHUKGASAKWNNHRHFOHIAKPNIFHKDPDVNMLH--VFVLGEWQ 245   |  |
| DB  | 187                   | FSTKWNHLLHFFVIGHUKGAPASWNNHMFQHEAKNCFKRPDINN-HPFFPALGKIL 245      |  |
| QY  | 246                   | PIEYKKLKYLPVNHQHEVFFLIGPPLLIPIWFOYQIIMTMIVHKNWDLAWAVSYIR 305      |  |
| DB  | 246                   | SVELGKQKKYPNYHGHYFLLIGPALLPLYPQWIFVFIQKKNVDLAWMITFYR 305          |  |
| QY  | 306                   | PFITIPYIGILGALLFLNFIREFLESHWVWVTQNNHIVMEIDQAYRDWFSSOLTATCN 365    |  |
| DB  | 306                   | FLTYVPLGLKAFGLFFIVREFLESNNWVWVTQNNHIPMHIDHNDNDWVSTOLLATCN 365     |  |
| QY  | 366                   | VEQSFNDWFSGLNLFQIEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLRLALD 425    |  |
| DB  | 366                   | VHKSANFNDWFSGLNLFQIEHHLFPTMPRHNTKVPVLOSICAKRGIEYQSKPLLSAFAD 425   |  |
| QY  | 426                   | IIRSLKSGKWLDAYLHK 444   |  |
| DB  | 426                   | IHSLSKESGOWLDAYLHQ 444  |  |

Search completed: December 9, 2003, 10:17:39  
Job time : 49 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 10:08:11 ; Search time 17 Seconds  
(without alignments)  
1228.227 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

Sequence: 1 MGKGNQGEBAEREVSPT.....DIIRSLKSKGLMDAYLHK 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 1646  | 67.5        | 444    | 1 FADS_BRARE | Qdex7 brachydanio   |
| 2          | 210   | 8.6         | 359    | 1 LUCD_SYNY3 | Q8871 synecocyst    |
| 3          | 173   | 7.1         | 133    | 1 CYB5_BOVIN | P00171 bos taurus   |
| 4          | 172   | 7.1         | 133    | 1 CYB5_PIG   | P00172 sus scrofa   |
| 5          | 169.5 | 7.0         | 133    | 1 CYB5_RABIT | P00169 oryctolagus  |
| 6          | 162   | 6.6         | 133    | 1 CYB5_HORSE | P00170 equus caball |
| 7          | 160   | 6.6         | 133    | 1 CYB5_RAT   | P00173 rattus norv  |
| 8          | 159.5 | 6.5         | 447    | 1 FDC3_SESIN | P48620 sesamum ind  |
| 9          | 159   | 6.5         | 133    | 1 CYB5_HUMAN | P00167 homo sapien  |
| 10         | 158   | 6.5         | 573    | 1 CYB2_HANAN | P09437 hansecula a  |
| 11         | 157   | 6.4         | 133    | 1 CYB5_MOUSE | P56395 mus musculu  |
| 12         | 155.5 | 6.4         | 351    | 1 DESA_SPIPL | Q54794 spirulina p  |
| 13         | 153.5 | 6.3         | 881    | 1 NIA1_PHAVU | P39865 phaseolus v  |
| 14         | 151.5 | 6.2         | 87     | 1 CYB5_ALOSE | P00168 alouatta se  |
| 15         | 149   | 6.1         | 131    | 1 CYB5_RHIST | Q3hf1 rhizopus st   |
| 16         | 148.5 | 6.1         | 146    | 1 CYB5_RAT   | P04166 rattus norv  |
| 17         | 148.5 | 6.1         | 383    | 1 FDC3_BRANA | P48624 brassica na  |
| 18         | 147.5 | 6.1         | 139    | 1 CYB5_NEUCR | Q9p510 neurospora   |
| 19         | 147.5 | 6.1         | 460    | 1 FDC3_RICCO | P48619 ricinus com  |
| 20         | 146.5 | 6.0         | 146    | 1 CYB5_HUMAN | Q43169 homo sapien  |
| 21         | 146   | 6.0         | 447    | 1 FDC6_SPIOL | P48629 spinacia ol  |
| 22         | 145.5 | 6.0         | 379    | 1 FDC3_TOBAC | P48626 nicotiana t  |
| 23         | 144.5 | 5.9         | 138    | 1 CYB5_CHICK | P00174 gallus gall  |
| 24         | 143.5 | 5.9         | 400    | 1 FDC1_MORIS | P59688 mortierella  |
| 25         | 142.5 | 5.8         | 400    | 1 FDC1_MORAP | Q9y815 mortierella  |
| 26         | 141   | 5.8         | 134    | 1 CYB5_ARATH | O48845 arabidopsis  |
| 27         | 141   | 5.8         | 384    | 1 SCS7_YEAST | Q03529 saccharomyc  |
| 28         | 139.5 | 5.7         | 917    | 1 NIA2_ARATH | P11035 arabidopsis  |
| 29         | 137.5 | 5.6         | 386    | 1 FDC3_ARATH | P48623 arabidopsis  |
| 30         | 137.5 | 5.6         | 918    | 1 NIA2_GUCNA | P17563 cucurbita m  |
| 31         | 137   | 5.6         | 448    | 1 FDC6_ARATH | P46312 arabidopsis  |
| 32         | 136.5 | 5.6         | 124    | 1 CYB1_SCHPO | O94391 schizosacch  |
| 33         | 135   | 5.5         | 435    | 1 FDC3_ARATH | P48622 arabidopsis  |

|    |       |     |     |              |                    |
|----|-------|-----|-----|--------------|--------------------|
| 34 | 134.5 | 5.5 | 134 | 1 CYB1_ARATH | Q42342 arabidopsis |
| 35 | 133.5 | 5.5 | 134 | 1 CYB5_DROME | Q9v4n3 drosophila  |
| 36 | 132   | 5.4 | 380 | 1 FDC3_PHAU  | P32291 phaseolus a |
| 37 | 131.5 | 5.4 | 443 | 1 FDC6_BRANA | P48627 brassica na |
| 38 | 131.5 | 5.4 | 911 | 1 NIA1_BRANA | P39867 brassica na |
| 39 | 131   | 5.4 | 135 | 1 CYB5_TOBAC | P49099 nicotiana t |
| 40 | 131   | 5.4 | 920 | 1 NIA2_GICIN | P43101 cichorium i |
| 41 | 130.5 | 5.4 | 351 | 1 DESA_SYNY3 | P20388 synecocyst  |
| 42 | 130.5 | 5.4 | 414 | 1 CYB5_DROME | P19967 drosophila  |
| 43 | 130.5 | 5.4 | 446 | 1 FDC3_ARATH | P46310 arabidopsis |
| 44 | 130.5 | 5.4 | 911 | 1 NIA2_BRANA | P39868 brassica na |
| 45 | 129.5 | 5.3 | 911 | 1 NIA2_LYCES | P17570 lycopersico |

## ALIGNMENTS

|  |  |           |      |         |  |
|--|--|-----------|------|---------|--|
| RESULT 1   |  |           |      |         |  |
| FADS_BRARE                                       |  |           |      |         |  |
| ID   | FADS_BRARE   | STANDARD; | PRT; | 444 AA. |  |
| AC   | QDEX7;   |           |      |         |  |
| DT   | 28-FEB-2003 (Rel. 41, Created)   |           |      |         |  |
| DT   | 28-FEB-2003 (Rel. 41, Last sequence update)                                |           |      |         |  |
| DT   | 28-FEB-2003 (Rel. 41, Last annotation update)                              |           |      |         |  |
| DE   | Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).                      |           |      |         |  |
| GN   | FADS2 OR FADS06  |           |      |         |  |
| OS   | Brachydanio rerio (Zebrafish) (Danio rerio).                               |           |      |         |  |
| OC   | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                    |           |      |         |  |
| OC   | Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;       |           |      |         |  |
| OC   | Cyprinidae; Danio.   |           |      |         |  |
| OX   | NCBI_TaxID=7955;   |           |      |         |  |
| RN   | [1]  |           |      |         |  |
| RP   | SEQUENCE FROM N.A.   |           |      |         |  |
| RC   | TISSUE=Liver;  |           |      |         |  |
| RX   | MEDLINE=21592990; PubMed=11724940;   |           |      |         |  |
| RA   | Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,                |           |      |         |  |
| RA   | Sargent J.R., Teale A.J.;  |           |      |         |  |
| RT   | "A vertebrate fatty acid desaturase with delta5 and delta6                 |           |      |         |  |
| RT   | activities.";  |           |      |         |  |
| RL   | Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).                        |           |      |         |  |
| CC   | !- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6           |           |      |         |  |
| CC   | activities. May represent a component of the polyunsaturated fatty         |           |      |         |  |
| CC   | acid biosynthesis pathway.   |           |      |         |  |
| CC   | !- PATHWAY: Polyunsaturated fatty acid biosynthesis.                       |           |      |         |  |
| CC   | !- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.                |           |      |         |  |
| CC   | !- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.               |           |      |         |  |
| CC   | This SWISS-PROT entry is copyright. It is produced through a collaboration |           |      |         |  |
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| CC   | use by non-profit institutions as long as its content is in no way         |           |      |         |  |
| CC   | modified and this statement is not removed. Usage by and for commercial    |           |      |         |  |
| CC   | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |           |      |         |  |
| CC   | or send an email to license@isb-sib.ch).                                   |           |      |         |  |
| CC   | -----  |           |      |         |  |
| CC   | EMBL; AF309556; AAC5710.1; -;  |           |      |         |  |
| DR   | HSSP; P00173; IJEX.  |           |      |         |  |
| DR   | ZFIN; ZDB-GENE-011212-1; fads2.  |           |      |         |  |
| DR   | InterPro; IPR001199; Cyt B5.   |           |      |         |  |
| DR   | InterPro; IPR005804; FA desat fam.   |           |      |         |  |
| DR   | Pfam; PF00487; FA desaturase; 1.   |           |      |         |  |
| DR   | Pfam; PF00173; heme; 1; 1.   |           |      |         |  |
| DR   | ProDom; PD000812; Cyt B5; 1.   |           |      |         |  |
| DR   | ProDom; PD001081; FA desat fam; 2.   |           |      |         |  |
| DR   | PROSITE; PS00191; CYTOCHROME B5; 1; FALSE NEG.                             |           |      |         |  |
| DR   | PROSITE; PS0255; CYTOCHROME B5; 2; 1.                                      |           |      |         |  |
| KW   | Fatty acid biosynthesis; Oxidoreductase; Heme.                             |           |      |         |  |
| FT   | DOMAIN 18 95   |           |      |         |  |
| FT   | IRON (HEME AXIAL LIGAND) (BY SIMILARITY).                                  |           |      |         |  |
| FT   | METAL 53 53  |           |      |         |  |
| FT   | METAL 76 76  |           |      |         |  |
| SQ   | SEQUENCE 444 AA; 52032 MW; 6AA25AIDCIDCF65 CRC64;                          |           |      |         |  |
| Query Match 67.5%; Score 1646; DB 1; Length 444; |  |           |      |         |  |



```

Best Local Similarity 64.6%; Pred. No. 3.6e-129;
Matches 287; Conservative 63; Mismatches 94; Indels 0; Gaps 0;
QY 1 MGKGNGQGEAAREVSVPTSWETIQKHLRTDSGLVIDRKVYNITKWSIQHGGQORVI 60
Db 1 MGKGNGQGEAAREVSVPTSWETIQKHLRTDSGLVIDRKVYNITKWSIQHGGQORVI 60
QY 61 GHYAGEDATAPRAHPDLEFVGKLPKLLIGELAPESPQDHGKNSKITDFPALAKTA 120
Db 61 GHYAGEDATAPRAHPDLEFVGKLPKLLIGELAPESPQDHGKNSKITDFPALAKTA 120
QY 121 EDNMFKNHVFLLLAHIIAIESIAWFTVYFNGMIPTLITAFVLATSOAAGMLQOH 180
Db 121 EDNMFKNHVFLLLAHIIAIESIAWFTVYFNGMIPTLITAFVLATSOAAGMLQOH 180
QY 181 DYGHLSVTRKPKNHLVHKFVGHKASAGNWNHRHFQHAKEPIFKDPDVMNLHV 240
Db 181 DYGHLSVTRKPKNHLVHKFVGHKASAGNWNHRHFQHAKEPIFKDPDVMNLHV 240
QY 241 LGEMOPIEXGKCKLVLPYNHOFYFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAV 300
Db 241 LGEMOPIEXGKCKLVLPYNHOFYFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAV 300
QY 301 SYIIRFFTYIPYIGLALLFLNIRFLESFVWVTQMHIVMEIDQAYRDFWFSQOL 360
Db 301 SYIIRFFTYIPYIGLALLFLNIRFLESFVWVTQMHIVMEIDQAYRDFWFSQOL 360
QY 361 TATCNVQSFDFWFSGLNFOIEHLLPPTMPRHNLHIAPIVKSCLAKHGIEYQEKPLL 420
Db 361 TATCNVQSFDFWFSGLNFOIEHLLPPTMPRHNLHIAPIVKSCLAKHGIEYQEKPLL 420
QY 421 RALLDIIRSLKXSGKLWLDAYLHK 444
Db 421 RALLDIIRSLKXSGKLWLDAYLHK 444

RESULT 2
LLCD_SINY3 STANDARD; PRT; 359 AA.
AC Q08871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Linoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
DE DES6 OR SL0262.
GN Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93283633; PubMed=8389613;
RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RA Miyajima N., Hiroseawa M., Sugita M., Saeamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -I- CATALYTIC ACTIVITY: Linoleoyl-CoA + AH(2) + O(2) = gamma-
CC linolenoyl-CoA + A + 2 H(2)O.
CC -I- COFACTOR: IRON.
CC -----
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CC -----
CC EMBL; L11421; AAA27286.1; --
CC EMBL; D90914; BAA18502.1; --
CC InterPro; IPR005804; FA_desat_fam.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD001081; FA_desat_fam; 1.
CC Oxidoreductase; Iton; Complete proteome.
CC SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;

Query Match 8.6%; Score 210; DB 1; Length 359;
Best Local Similarity 23.5%; Pred. No. 4.3e-10;
Matches 85; Conservative 53; Mismatches 135; Indels 88; Gaps 18;
QY 127 KTNHVFLLLAHIIAIESIAWFTVYFNGMIPTLITAFVLATSOAAGMLQHDY 182
Db 35 RDNPSMYLKTLLIIVLWLPs-ANAFVLFAVPVFPVLLGCMVLAIALAASFNVG--HDA 90
QY 183 GHLSVTRKPKNHN---LVHKFVGHKASAGNWNHRHFQHAKEPIFKDPDVMNLHV 238
Db 91 NNNAYSGNPHNRVLGMYTFV-----GLSSFLMRYRHHYLLHTYTNILGHDFEI--- 140
QY 239 FVLGEWQPIEYGGKCLKLPLYN-----HOHEFFFLIGPPLIPMY-FOYQIIMTIVHKN 292
Db 141 -----HGDGAVMSPEQEHVGIYRFOFYIWLGLYLFIPFYWFLYDVVLNKGKY 190
QY 293 -----WDLAWAVSYIIRFFI-----TIPYIGLALL 321
Db 191 HDHKIPFPQFLELASLLGKLLMLGYVGLPGLALGFSIPEVLIGASVTYMT-YGIWVCTI 249
QY 322 FLNFIREFSHWFWVTQMHIVMEIDQAYRDFWFSQOLATCN-VEQSFFDNFSGHL 379
Db 250 FM-LAHVLESTBELTPDGESG---ALDDE-----WAICQIETTANFATNPFVN-WFCGL 300
QY 380 NFOIEHLLPPTMPRHNLHIAPIVKSCLAKHGIEYQEKPLLALLDIIRSLKXSGKLWLD 439
Db 301 NHQVTHLFPNICHHPOLENIIDKVCQFGEYKVPYTFKAAI-----ASNYRWLE 353
QY 440 A 440
Db 354 A 354

RESULT 3
CYB5_BOVIN STANDARD; PRT; 133 AA.
AC P00171; Q27947; Q28837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128451; PubMed=2915932;
RA Cristiano R.J., Steggle A.W.;
RT "The complete nucleotide sequence of bovine liver cytochrome b5
RT mRNA."
RL Nucleic Acids Res. 17:799-799(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94010928; PubMed=8406485;

```

RA Cristiano R.J., Giordano S.J., Steggle A.W.;  
 RT "the isolation and characterization of the bovine cytochrome b5 gene,  
 RL and a transcribed pseudogene.";  
 RN Genomics 17:348-354(1993).  
 RN (3)  
 RN SEQUENCE OF 1-97.  
 RP TISSUE=ERYTHROCYTE;  
 RX MEDLINE=85299161; PubMed=4030743;  
 RA Abe K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;  
 RT "Amino acid sequences of cytochrome b5 from human, porcine, and  
 RL bovine erythrocytes and comparison with liver microsomal cytochrome  
 RN b5.";  
 RN J. Biochem. 97:1659-1668(1985).  
 RN (4)  
 RN SEQUENCE OF 1-10 AND 130-133.  
 RP MEDLINE=74080219; PubMed=4810060;  
 RA Ozols J.;  
 RT "Cytochrome b5 from microsomal membranes of equine, bovine, and  
 RL porcine livers. Isolation and properties of preparations containing  
 RN the membranous segment.";  
 RN Biochemistry 13:426-434(1974).  
 RN (5)  
 RN SEQUENCE OF 5-96.  
 RP MEDLINE=70067001; PubMed=5391285;  
 RA Ozols J., Strittmatter P.;  
 RT "Correction of the amino acid sequence of calf liver microsomal  
 RL cytochrome b5.";  
 RN J. Biol. Chem. 244:6617-6618(1969).  
 RN (6)  
 RN SEQUENCE OF 5-95.  
 RP MEDLINE=70289989; PubMed=5273224;  
 RA Tsugita A., Kobayashi M., Tan S., Kyo S., Rashid M.A., Yoshida Y.,  
 RA Kajihara T., Hagihara B.;  
 RT "Comparative study of the primary structures of cytochrome b5 from  
 RL four species.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 67:442-447(1970).  
 RN (7)  
 RN SEQUENCE OF 91-133.  
 RP MEDLINE=78218214; PubMed=670203;  
 RA Fleming P.J., Dailey H.A., Corcoran D., Strittmatter P.;  
 RT "The primary structure of the nonpolar segment of bovine cytochrome  
 RL b5.";  
 RN J. Biol. Chem. 253:5369-5372(1978).  
 RN (8)  
 RN SEQUENCE OF 1-10.  
 RP MEDLINE=89323209; PubMed=2752049;  
 RA Ozols J.;  
 RT "Structure of cytochrome b5 and its topology in the microsomal  
 RL membrane.";  
 RN Biochim. Biophys. Acta 997:121-130(1989).  
 RN (9)  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF OXIDIZED FORM.  
 RA Mathews F.S., Argos P., Levine M.;  
 RT "The structure of cytochrome b-5 at 2.0-A resolution.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 37:387-395(1971).  
 RN (10)  
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF REDUCED FORM.  
 RP MEDLINE=75095526; PubMed=1167544;  
 RA Argos P., Mathews F.S.;  
 RT "The structure of ferriocytchrome b5 at 2.8-A resolution.";  
 RL J. Biol. Chem. 250:747-751(1975).  
 RN (11)  
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RP Durley R.C.E., Mathews F.S.;  
 RT "Refinement and structural analysis of bovine cytochrome b5 at 1.5-A  
 RL resolution.";  
 RN Acta Crystallogr. D 52:65-76(1996).  
 RN (12)  
 RN X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 7-88, AND MUTAGENESIS.  
 RP MEDLINE=20303064; PubMed=10842340;  
 RA Wu J., Gan J.-H., Xia Z.-X., Wang Y.-H., Wang W.-H.,  
 RA Xue L.-L., Xie Y., Huang Z.-X.;  
 RT "Crystal structure of recombinant trypsin-solubilized fragment of

cytochrome b5 and the structural comparison with Val61His mutant.";  
 RL Proteins 40:249-257(2000).  
 RN (13)  
 RN STRUCTURE BY NMR.  
 RP MEDLINE=96200988; PubMed=8613986;  
 RA Muskett F.W., Kelly G.P., Whitford D.;  
 RT "The solution structure of bovine ferricytochrome b5 determined using  
 RL heteronuclear NMR methods";  
 RN J. Mol. Biol. 258:172-189(1996).  
 RN (14)  
 RN STRUCTURE BY NMR OF 7-88, AND MUTAGENESIS.  
 RP MEDLINE=21145463; PubMed=11248680;  
 RA Wu Y., Wang Y., Qian C., Lu J., Li E., Wang W., Lu J., Xie Y.,  
 RA Wang J., Zhu D., Huang Z., Tang W.;  
 RT "Solution structure of cytochrome b5 mutant (E44/48/56A/D60A) and its  
 RL interaction with cytochrome c.";  
 RN Eur. J. Biochem. 268:1620-1630(2001).  
 RN (15)  
 RN STRUCTURE BY NMR OF 7-88, AND MUTAGENESIS.  
 RP MEDLINE=21571982; PubMed=11714912;  
 RA Qian C., Yao Y., Ye K., Wang J., Tang W., Wang Y., Wang W., Lu J.,  
 RA Xie Y., Huang Z.;  
 RT "Effects of charged amino-acid mutation on the solution structure of  
 RL cytochrome b5 and binding between cytochrome b5 and cytochrome c.";  
 CC Protein Sci. 10:2451-2459(2001).  
 CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
 CC OXYGENASES.  
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE  
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X13617; CAA31949.1; -  
 DR EMBL; M63328; AAC14455.1; ALT SEQ.  
 DR EMBL; M63326; AAC14455.1; JOINED.  
 DR EMBL; M63327; AAC14455.1; JOINED.  
 DR EMBL; L22966; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A47215; CEBOS.  
 DR PDB; 1CYO; 15-MAR-00.  
 DR PDB; 1HKO; 25-MAR-03.  
 DR PDB; 1FO3; 23-MAY-01.  
 DR PDB; 1FO4; 23-MAY-01.  
 DR PDB; 1SHB; 15-NOV-00.  
 DR PDB; 1ES1; 15-NOV-00.  
 DR PDB; 115U; 31-DEC-02.  
 DR PDB; 1LQX; 04-SEP-02.  
 DR PDB; 1LR6; 04-SEP-02.  
 DR PDB; 1M20; 11-SEP-02.  
 DR InterPro; IPR001199; Cyt\_B5.  
 DR Pfam; PF00173; heme\_1; 1.  
 DR ProDom; PD000612; Cyt\_B5; 1.  
 DR PROSITE; PS00191; CYTOCHROME\_B5\_1; 1.  
 DR PROSITE; PS02555; CYTOCHROME\_B5\_2; 1.  
 KW Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;  
 KW 3D-structure.  
 FT INIT MET 0 0  
 FT MOD\_RES 1 1  
 FT DOMAIN 1 90  
 FT DOMAIN 91 133  
 FT METAL 43 43  
 FT METAL 67 67  
 FT METAL 67 67  
 FT CONFLICT 1 4  
 FT CONFLICT 15 17  
 FT CONFLICT 61 61  
 FT CONFLICT 97 97  
 FT S -> SES (IN REF. 2).  
 FT S -> SES (IN REF. 2).  
 FT ACETYLATION  
 FT HEME-BINDING.  
 FT MEMBRANE-BINDING.  
 FT IRON (HEME AXIAL LIGAND).  
 FT IRON (HEME AXIAL LIGAND).  
 FT ARES -> ZS2ZBA (IN REF. 5).  
 FT BIC -> QIE (IN REF. 5).  
 FT N -> D (IN REF. 5 AND 6).  
 FT S -> SES (IN REF. 2).

PT CONFLICT 133 133 N -> D (IN REF. 4).

PT STRAND 10 11

PT HELIX 13 16

PT TURN 17 18

PT TURN 20 21

PT TURN 22 23

PT TURN 24 29

PT TURN 30 31

PT TURN 32 35

PT TURN 37 42

PT TURN 44 45

PT TURN 48 53

PT TURN 54 55

PT STRAND 57 57

PT HELIX 59 64

PT TURN 65 66

PT HELIX 69 75

PT TURN 76 78

PT STRAND 79 80

PT HELIX 85 90

SQ SEQUENCE 133 AA; 15198 MW; E27B600B61E0BC43 CRC64;

Query Match 7.1%; Score 173; DB 1; Length 133;

Best Local Similarity 32.0%; Pred. No. 1.6e-07;

Matches 47; Conservative 26; Mismatches 48; Indels 26; Gaps 4;

QY 11 AAREVSVPTSEWEIOKHNLRDTSGLVIDRKYNITKWSIOHPGGORVIGHAGEDATD 70

DB 1 ABEESKAVKYTLBEEIOKHNSKTWLTLYHYVDLTKFLEHPGGBEVLRQAGGATE 60

QY 71 AFRAFHPDLEFVG-----KELKPLLIGELAPEPSQDHGKNSKITEDFALRKRTARDMN 124

DB 61 NF-----EDVGHSSTDARELSKTFIIGELHPDD-----RSKITPSSIIITIDSNP 106

QY 125 LFKTN-----HVFLLLLAHIALES 145

DB 107 SWWTNWLIPALSALEVALIYHLYTSEN 133

RESULT 4

CYB5\_PIG STANDARD; PRT; 133 AA.

AC P00172; O18813;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome b5.

GN CYB5.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]\_

RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Blood, and Liver;

RX MEDLINE=98042520; PubMed=9367886;

RA Vandermark P.K.; Steggles A.W.;

RT "The isolation and characterization of the soluble and membrane-bound porcine cytochrome b5 cDNAs."

RL Biochem. Biophys. Res. Commun. 240:80-83 (1997).

RN [2]

RP SEQUENCE.

RC TISSUE=Erythrocyte, and Liver;

RX MEDLINE=85289161; PubMed=4030743;

RA Abe K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;

RT "Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythrocytes and comparison with liver microsomal cytochrome b5."

RL J. Biochem. 97:1659-1668 (1985).

RN [3]

RP SEQUENCE OF 1-6.

RX MEDLINE=74060219; PubMed=4810060;

RA Ozols J.;

"Cytochrome b5 from microsomal membranes of equine, bovine, and porcine livers. Isolation and properties of preparations containing the membranous segment.";

Biochemistry 13:426-434 (1974).

[4]

RP SEQUENCE OF 7-88.

RX MEDLINE=71134790; PubMed=4993957;

RA Nobrega F.G., Ozols J.;

RT "Amino acid sequences of tryptic peptides of cytochromes b5 from microsomes of human, monkey, porcine, and chicken liver.";

J. Biol. Chem. 246:1706-1717 (1971).

[5]

RP SEQUENCE OF 89-133, AND REVISIONS TO 14; 15 AND 61.

RX MEDLINE=78012290; PubMed=289425;

RA Ozols J., Gerard C.;

RT "Primary structure of the membranous segment of cytochrome b5.";

Proc. Natl. Acad. Sci. U.S.A. 74:3725-3729 (1977).

[6]

RP SEQUENCE OF 1-10.

RX MEDLINE=89323209; PubMed=2752049;

RA Ozols J.;

RT "Structure of cytochrome b5 and its topology in the microsomal membrane.";

Biochim. Biophys. Acta 997:121-130 (1989).

RL Biochim. Biophys. Acta 997:121-130 (1989).

CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES.

CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE (LIVER FORM). BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM. OR CYTOPLASMIC (ERYTHROCYTE FORM).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=Liver, Membrane-bound;

CC IsoId=P00172-1; Sequence=Displayed;

CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;

CC IsoId=P00172-2; Sequence=VSP 001242, VSP 001243;

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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EMBL; AF016388; AAC48779.1; -.

EMBL; AF016389; AAC48780.1; -.

PIR; JCS782; CBPGS.

PIR; JCS783; JCS783.

HSP; P00171; ICYO.

InterPro; IPR001199; Cyt\_B5.

ProDom; PD000612; Cyt\_B5; 1.

Pfam; PF00173; heme\_1; 1.

ProSite; PS00191; CYTOCHROME B5\_1; 1.

ProSite; PS0255; CYTOCHROME B5\_2; 1.

Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;

Alternative splicing.

INIT\_MET 0 0

MOD\_RES 1 1

DOMAIN 1 90

DOMAIN 91 133

FT METAL 43 43

FT METAL 67 67

FT VARSPIC 97 97

FT VARSPIC 98 133

FT CONFLICT 61 61

FT SEQUENCE 133 AA; 15179 MW; 986FE1150BF30C4C CRC64;

SQ

Query Match 7.1%; Score 172; DB 1; Length 133;

Best Local Similarity 31.3%; Pred. No. 1.9e-07;

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Matches 47; Conservative 28; Mismatches 47; Indels 28; Gaps 4;
QY 11 AAEVSVPTFSWEIEQKHNRTDSGLVDRKVNITKWSIQHGGQGVIGHYAGEDATD 70
DB 1 AEQSDKAVKYVTLSEIKHNKSKTWLILHHKVDLTFLBEHPGGEVLEQAGGDATE 60
QY 71 AFRAHPDLEFVG-----KFLKPLLIGELAPEEPQSDHGKNSKITEDFRALRKTAEDMN 124
DB 61 NP-----EDVGHSTDAEELSKTIIIGELHPDD-----RSKIAPSELIITVSNS 106
QY 125 LFKTNHVPFLLLAHIALESIAWPTVFYF 154
DB 107 SWNTNW-----IPASIALVWSLMYHF 128

RESULT 5
CYB5_RABIT
ID CYB5_RABIT STANDARD; PRT; 133 AA.
AC P00169; Q28726;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]_TaxID:9986;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89128816; PubMed=322252;
RA Darius N., Fisher C.W., Steggle A.W.;
RT "The nucleotide sequence of rabbit liver cytochrome b5 mRNA.";
RN Protein Seq. Data Anal. 1:351-353(1988).
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=New Zealand white;
RA Takamatsu H., Kozutsumi Y., Suzuki A., Kawasaki T.;
RT "Molecular cloning of rabbit cytochrome b5 genes: evidence for the
RT occurrence of two separate genes encoding the soluble and microsomal
RT forms.";
RN Biochem. Biophys. Res. Commun. 185:845-851(1992).
RP SEQUENCE OF 8-45 AND 49-90.
RX MEDLINE=69108787; PubMed=5709273;
RA Tsugita A., Kobayashi M., Kajihara T., Hagihara B.;
RT "Primary structure of rabbit liver cytochrome b5.";
RN J. Biochem. 64:727-730(1968).
RP SEQUENCE OF 6-7 AND 46-48.
RX MEDLINE=70289899; PubMed=5272324;
RA Tsugita A., Kobayashi M., Tani S., Kyo S., Rashid M.A., Yoshida Y.,
RA Kajihara T., Hagihara B.;
RT "Comparative study of the primary structures of cytochrome b5 from
RT four species.";
RN Proc. Natl. Acad. Sci. U.S.A. 67:442-447(1970).
RP SEQUENCE OF 4-97.
RX MEDLINE=71001482; PubMed=5506260;
RA Ozols J.;
RT "Amino acid sequence of rabbit liver microsomal cytochrome b5.";
RN J. Biol. Chem. 245:4863-4874(1970).
RP SEQUENCE OF 91-133.
RX MEDLINE=80049603; PubMed=500581;
RA Kondo K., Tajima S., Sato R., Narita K.;
RT "Primary structure of the membrane-binding segment of rabbit
RT cytochrome b5.";
RN J. Biochem. 86:1119-1128(1979).
RP SEQUENCE OF 98-133.
RX MEDLINE=80115672; PubMed=7354043;

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RA Takagaki Y., Gerber G.E., Nibei K., Khorana H.G.;
RT "Amino acid sequence of the membranous segment of rabbit liver
RT cytochrome b5. Methodology for separation of hydrophobic peptides.";
RN J. Biol. Chem. 255:1536-1541(1980).
RP SEQUENCE OF 1-10.
RX MEDLINE=89323209; PubMed=2752049;
RA Ozols J.;
RT "Structure of cytochrome b5 and its topology in the microsomal
RT membrane.";
RN Biochim. Biophys. Acta 997:121-130(1989).
RP STRUCTURE BY NMR OF 6-99.
RX MEDLINE=20117684; PubMed=10651812;
RA Banci L., Bertini I., Rosato A., Scacchieri S.;
RT "Solution structure of oxidized microsomal rabbit cytochrome b5
RT factors determining the heterogeneous binding of the heme.";
RN Eur. J. Biochem. 267:755-766(2000).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
CC -1- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Liver, Membrane-bound;
CC IsoId=P00169-1; Sequence=Displayed;
CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;
CC IsoId=P00169-2; Sequence=VSP 001244, VSP 001245;
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M24844; AAB03878.1; -
CC EMBL; D10901; BAA01712.1; -
CC PIR; JN0316; JN0316.
CC PIR; S03373; CBRB5.
CC PDB; 1DO9; 20-MAR-00.
CC InterPro: IPR001199; Cyt_B5.
CC Pfam; PF00173; heme_1_1.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;
CC Alternative splicing; 3D-structure.
CC INIT MET 0 0
CC MOD_RES 1 1 ACETYLATION.
CC DOMAIN 1 90 HEME-BINDING.
CC DOMAIN 91 133 MEMBRANE-BINDING.
CC METAL 43 43 IRON (HEME AXIAL LIGAND).
CC METAL 67 67 IRON (HEME AXIAL LIGAND).
CC VARSPPLIC 97 97 T -> P (in isoform 2).
CC /FTid=VSP 001244.
CC VARSPPLIC 98 133 Missing (in isoform 2).
CC /FTid=VSP 001245.
CC CONFLICT 61 61 N -> D (IN REF. 3 AND 5).
CC CONFLICT 103 103 D -> N (IN REF. 6).
CC SEQUENCE 133 AA; 15218 MW; 2E48AEC20BC39720 CRC64;
Query Match 7.0%; Score 169.5; DB 1; Length 133;
Best Local Similarity 33.1%; Pred. No. 3.1e-07;
Matches 46; Conservative 27; Mismatches 45; Indels 21; Gaps 4;
QY 11 AAEVSVPTFSWEIEQKHNRTDSGLVDRKVNITKWSIQHGGQGVIGHYAGEDATD 70
DB 1 AAQSDKAVKYVTLSEIKHNKSKTWLILHHKVDLTFLBEHPGGEVLEQAGGDATE 60

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QY 71 AFRAHPDLFVVG-----KFLKPLLIIGELAPESPQDHGKNSKITEPFRALRKTAEDMN 124  
 Db 61 NF-----EDVGHSDARELSKTFIIGELHPDD-----RSKSKPMETLITITVDSNS 106  
 QY 125 LFKTNHVFFLLLAHIAL 143  
 Db 107 SWTNVW-IPAISALIVAL 124

## RESULT 6

CYB5\_HORSE  
 ID CYB5\_HORSE STANDARD; PRT; 133 AA.  
 AC P00170;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome b5.  
 GN CYB5.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE OF 1-98.  
 RX MEDLINE=7028943; PubMed=977596;  
 RA Ozols J., Gerard C., Nobrega F.G.;  
 RT "Proteolytic cleavage of horse liver cytochrome b5. Primary structure  
 of the heme-containing moiety."  
 RL J. Biol. Chem. 251:6767-6774 (1976).  
 RN [2]  
 RP SEQUENCE OF 89-133.  
 RX MEDLINE=78045981; PubMed=562879;  
 RA Ozols J., Gerard C.;  
 RT "Covalent structure of the membranous segment of horse cytochrome b5.  
 Chemical cleavage of the native hemoprotein."  
 RL J. Biol. Chem. 252:8549-8553 (1977).  
 RN [3]  
 RP SEQUENCE OF 1-10.  
 RX MEDLINE=89323209; PubMed=2752049;  
 RA Ozols J.;  
 RT "Structure of cytochrome b5 and its topology in the microsomal  
 membrane."  
 RL Biochim. Biophys. Acta 997:121-130 (1989).  
 CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
 FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
 OXYGENASES.  
 CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE  
 CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 DR HSP; P00171; ICYO.  
 DR InterPro; IPR001199; Cyt B5.  
 DR Pfam; PF00173; heme\_1; 1.  
 DR ProDom; PD000612; Cyt B5; 1.  
 DR PROSITE; PS00191; CYTOCHROME B5; 1.  
 DR PROSITE; PS00255; CYTOCHROME\_B5; 2; 1.  
 KW Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation.  
 FT MOD\_RES 1 1  
 FT DOMAIN 1 90  
 FT HEME-BINDING.  
 FT DOMAIN 91 133  
 FT IRON (HEME AXIAL LIGAND).  
 FT METAL 43 43  
 FT IRON (HEME AXIAL LIGAND).  
 FT METAL 57 57  
 FT CONFLICT 1 5  
 FT AEOQSD -> ZEDAS (IN REF. 1).  
 SQ SEQUENCE 133 AA; 15140 MW; 85E50818D8CF4247 CRC64;

Query Match 6.6%; Score 162; DB 1; Length 133;  
 Best Local Similarity 27.3%; Pred. No. 1.3e-06;  
 Matches 45; Conservative 28; Mismatches 44; Indels 48; Gaps 5;  
 QY 11 AAREVSVPTFWSEIQHNLTDSGLVIDRKVYNITKWSIQHPGQGVICHYAGEDATD 70  
 Db 1 AEQSKAVKXYLTLEIKKHNSKSTWLILHHKVYDLTFLDHPGGEVLEQQAGGDATE 60

QY 71 AFRAHPDLFVVG-----KFLKPLLIIGELAPESPQDHGKNSKITEPFRALRKTAEDMN 124  
 Db 61 NF-----EDIGHSTDAEELSRTFIIGELHPDD-----RSKIAPVETLITITVD--- 103  
 QY 125 LFKTNHVFFLLLAHIALAESIAWFTVFYFGNGWIPTLITAFVLA 169  
 Db 104 -----SNSSWWT-----NWNIPASAVVA 123

## RESULT 7

CYB5\_RAT  
 ID CYB5\_RAT STANDARD; PRT; 133 AA.  
 AC P00173; O35768;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cytochrome b5.  
 GN CYB5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93011015; PubMed=1396500;  
 RA Mitoma J.-Y., Ito A.;  
 RT "The carboxy-terminal 10 amino acid residues of cytochrome b5 are  
 necessary for its targeting to the endoplasmic reticulum."  
 RL EMBO J. 11:4197-4203 (1992).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX STRAIN=Sprague-Dawley; TISSUE=Brain;  
 MEDLINE=97396150; PubMed=9245704;  
 RA Yoo M.;  
 RT "Identification of two homologous cytochrome b5s in rat brain."  
 RL Biochem. Biophys. Res. Commun. 236:641-642 (1997).  
 RN [3]  
 RP SEQUENCE.  
 RX MEDLINE=82232110; PubMed=7093287;  
 RA Ozols J., Heinemann F.S.;  
 RT "Chemical structure of rat liver cytochrome b5. Isolation of peptides  
 by high-pressure liquid chromatography."  
 RL Biochim. Biophys. Acta 704:163-173 (1982).  
 RN [4]  
 RP SEQUENCE OF 1-10.  
 RX MEDLINE=89323209; PubMed=2752049;  
 RA Ozols J.;  
 RT "Structure of cytochrome b5 and its topology in the microsomal  
 membrane."  
 RL Biochim. Biophys. Acta 997:121-130 (1989).  
 RN [5]  
 RP SEQUENCE OF 6-88.  
 RX MEDLINE=83182449; PubMed=6840088;  
 RA Lederer F., Ghir R., Guillard B., Cortial S., Ito A.;  
 RT "Two homologous cytochromes b5 in a single cell."  
 RL Eur. J. Biochem. 132:95-102 (1983).  
 RN [6]  
 RP STRUCTURE BY NMR OF 1-98.  
 RX MEDLINE=96234953; PubMed=8639599;  
 RA Falzone C.J., Mayer M.R., Whitman E.L., Moore C.D., Lecomte J.T.J.;  
 RT "Design challenges for hemoproteins: the solution structure of  
 apocytochrome b5."  
 RL Biochemistry 35:6519-6526 (1996).  
 RN [7]  
 RP STRUCTURE BY NMR OF 5-98.  
 RX MEDLINE=98028409; PubMed=9363779;  
 RA Banci L., Bertini I., Ferroni F., Rosato A.;  
 RT "Solution structure of reduced microsomal rat cytochrome b5."  
 RL Eur. J. Biochem. 249:270-279 (1997).  
 RN [8]  
 RP STRUCTURE BY NMR OF 5-98.  
 RX MEDLINE=98067675; PubMed=9425037;  
 RA Arnesano F., Banci L., Bertini I., Felli I.C.;

RT "The solution structure of oxidized rat microsomal cytochrome b5."; Biochemistry 37:173-184 (1998).

RN [9].  
RP STRUCTURE BY NMR OF 5-98.  
RX MEDLINE=9828557; PubMed=9622481;  
RA Dangi B., Sarma S., Van C., Banville D.L., Guiles R.D.;  
RT "The origin of differences in the physical properties of the  
RT equilibrium forms of cytochrome b5 revealed through high-resolution  
RT NMR structures and backbone dynamic analyses."; Biochemistry 37:8289-8302 (1998).

RN [10].  
RP STRUCTURE BY NMR OF 1-98.  
RX MEDLINE=21191748; PubMed=11294656;  
RA Falzone C.J., Wang Y., Vu B.C., Scott N.L., Bhattacharya S.,  
RA Leconte J.T.J.;

RT "Structural and dynamic perturbations induced by heme binding in  
RT cytochrome b5."; Biochemistry 40:4879-4891 (2001).

CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
CC OXYGENASES. IT IS ALSO INVOLVED IN SEVERAL STEPS OF THE STEROL  
CC BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE C-5 DOUBLE BOND  
CC INTRODUCTION DURING THE C-5 DESATURATION.

CC -!- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE. BOUND TO THE  
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.

CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long;  
CC IsoId=P00173-1; Sequence=Displayed;

CC Name=Short;  
CC IsoId=P00173-2; Sequence=VSP\_001246, VSP\_001247;

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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CC -----  
CC EMBL; D13205; BAA02492.1; -  
CC EMBL; AF007107; AAB67609.1; -  
CC EMBL; AF007108; AAB67610.1; -  
CC PIR; JC5596; JCS596.

CC PIR; S28404; CBRT5.  
CC PDB; 1LET; 21-APR-97.  
CC PDB; 1IEU; 21-APR-97.  
CC PDB; 1AQA; 17-SEP-97.  
CC PDB; 1AW3; 04-FEB-98.  
CC PDB; 1AXX; 04-MAR-98.  
CC PDB; 2AXX; 04-MAR-98.

CC PDB; 1B5A; 17-JUN-98.  
CC PDB; 1B5B; 17-JUN-98.  
CC PDB; 1BPX; 12-AUG-98.  
CC PDB; 1BLV; 29-JUL-98.  
CC PDB; 1187; 16-MAY-01.  
CC PDB; 118C; 16-MAY-01.  
CC PDB; 11B7; 04-APR-01.

CC PDB; 1JEX; 11-JUL-01.  
CC PDB; 1MNY; 13-NOV-02.  
CC InterPro; IPR001199; Cyt\_B5.

CC Pfam; PF00173; Heme\_1; 1.  
CC ProDom; PD006612; Cyt\_B5; 1.  
CC PROSITE; PS00191; CYTOCHROME B5\_1; 1.

CC PROSITE; PS0255; CYTOCHROME B5\_2; 1.  
CC KEGG; Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;

KW Alternative splicing; 3D-structure.  
FT INIT\_MET 0

FT MOD\_RES 0  
FT DOMAIN 1 1 ACETYLATION.

FT DOMAIN 1 90 HEME-BINDING.

FT DOMAIN 91 133 MEMBRANE-BINDING.

FT METAL 43 43 IRON (HEME AXIAL LIGAND).

FT METAL 67 67 IRON (HEME AXIAL LIGAND).  
FT VASPLIC 96 99 ETLL -> HSAL (in isoform Short).  
FT VASPLIC 100 133 /FTId=VSP\_001246.  
Missing (in isoform Short).  
Q -> E (IN REF. 5).

FT CONFLICT 17 17  
FT STRAND 11 11  
FT HELIX 13 18  
FT TURN 19 20  
FT TURN 22 23  
FT STRAND 26 29  
FT TURN 30 31  
FT STRAND 32 35  
FT TURN 37 38  
FT HELIX 39 42  
FT TURN 44 45  
FT HELIX 47 53  
FT TURN 54 55  
FT STRAND 57 57  
FT HELIX 59 65  
FT TURN 69 70  
FT HELIX 71 78  
FT STRAND 79 83  
FT HELIX 85 90

SQ SEQUENCE 133 AA; 15224 MW; AE568036F3B105B4 CRC64;

Query Match 6.6%; Score 160; DB 1; Length 133;  
Best Local Similarity 27.9%; Pred. No. 1.9e-06;  
Matches 46; Conservative 26; Mismatches 45; Indels 48; Gaps 5;

QY 11 AAREVSVPTFSWEEIOKHLRTDSGLVIDRKVYNITKWSIQHPGQGVIGHVAGEDATD 70  
DB 1 AEQSDKDKVYLTLEIQKHDKSKTWTLLHKVYDLTKFLEHPGGEVLREQAGDATE 60

QY 71 AFRAFHDPDLFVG-----KFLKLLIGELAPEPSQDHGKNSKITDFALRKTIADMN 124  
DB 61 NF-----EDVGSHTDARELSKTYIIGELHPDD-----RSKIAPSETLTIVT-- 103

QY 125 LFKTNHVFLLLAHIALSIAWFTVYFGNGWIPITLITAFVLA 169  
DB 104 -----SNSSWWT-----NWVIFALSALVVA 123

RESULT 8  
FD3C SESIN STANDARD; PRT; 447 AA.

AC P49620;  
DI 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).

GN FAD7.  
OS Sesamum indicum (Oriental sesame) (Gingelly).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
OC Asteridae; Lamiales; Pedaliaceae; Sesamum.

OX NCBI\_TaxID=4182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV\_4294; TISSUE=Cotyledon;

RA Shoji K.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES  
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY  
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT  
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
CC AND/ OR BE INVOLVED IN METAL ION BINDING.

CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

CC EMBL; U25817; AAA70334.1; --  
CC InterPro; IPR005804; FA\_Gesat\_fam.  
CC Pfam; PF00487; FA\_desaturase; 1.  
CC ProDom; PD01081; FA\_desat\_fam; 2.  
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
KW Transit peptide.  
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
FT CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE.  
FT DOMAIN 167 171 HISTIDINE BOX-1.  
FT DOMAIN 203 207 HISTIDINE BOX-2.  
FT DOMAIN 370 374 HISTIDINE BOX-3.  
SQ SEQUENCE 447 AA; 51116 MW; 4576250DDSDAGB1 CRC64;

Query Match 6.5%; Score 159.5; DB 1; Length 447;  
Best Local Similarity 20.6%; Pred. No. 8.6e-06;  
Matches 94; Conservative 70; Mismatches 164; Indels 129; Gaps 23;

Qy 32 RTD-----SGLVIDRKVNITKWSIQHPGQGVICHYAGEDATDAFRPHDLEFVGKFLK 87  
Db 39 RTDLGSSCLSGILREKRWALVSAPLRLVVEEENKESGERVINGEESDFGAPP 98  
Qy 88 PLLIGELAPEPSODHGKNSKITEDFRALRKTAEEDNNLFTNHFVLLLAHIALESTIA 147  
Db 99 PFKLSIDREATP-----KHCVKDPWRSMSGVVVRD-----VAVVFGLAAVA 139  
Qy 148 WFTVYFNGWIPLTITAFVLATSOAQAGWLOHDYGHLSVVRKPKNHLVHKFVIGHLKG 207  
Db 140 -----AYF--NNWVWVPLVFAQSTFWALFVLGCHDCHGSGSNPKLNS-----VVGHLH 199  
Qy 208 ASA-----NNWNRHFQHAKENIPFKDPDNNMLHVFVLGEMQP-----IEYGGKKLK 255  
Db 190 SSILVPVHGWRISHRTH--QNHGIVENDES-----WHPLSEKIYKNLDTATKKLR 238  
Qy 256 Y-LPNHGHQHEFFLIGPPLLIPMYF-----OYQIMTMIIVHK 291  
Db 239 FTLP-----PLALPVLVMSRSPQKQSHPHSDLDLFPVNEKDVITSTVCWT 287  
Qy 292 NVDLAWAVSVYIRFFITYIPYGI--LGALLFLNFIREFLESH-----WFWVVTOMNH 342  
Db 288 AMIALVGLSFVIG-PVQLLKLYGIPYLGVMWLDLVLYLHHGHGDKLPWY----- 338  
Qy 343 IWEIDQAYRDW--FSSQLTATCNVEQSFNDWFSGLNFQIEHLLFPTMPRHNLKIA 400  
Db 339 -----RGKWSVYLRGLT-TLDRDYGVINN-IHHDIGTHVTHLHFQIPHYHLIEAT 388  
Qy 401 PLVKSICAKHGTEYQE-----KPLRALLDIIRSLKK 432  
Db 389 EAAKPVLGKY-----YREPKSAPLPHLLGDLTSLR 422

## RESULT 9

CYB5\_HUMAN  
ID CYB5\_HUMAN STANDARD; PRT; 133 AA.  
AC P00167;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome b5.  
GN CYB5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Liver;  
RX MEDLINE=89025904; PubMed=3178851;  
RA Yoo M., Steggle A.W.;  
RT "The complete nucleotide sequence of human liver cytochrome b5 mRNA.";  
RL Biochem. Biophys. Res. Commun. 156:576-580(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Li X.R., Giordano S.J., Yoo M., Steggle A.W.;  
RN Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-97 FROM N.A.  
RC TISSUE=Erythrocyte;  
RX MEDLINE=91298976; PubMed=1712589;  
RA Giordano S.J., Steggle A.W.;  
RT "The human liver and reticulocyte cytochrome b5 mRNAs are products  
RL from a single gene.";  
RN Biochem. Biophys. Res. Commun. 178:38-44(1991).  
RN [4]  
RP SEQUENCE OF 1-97.  
RC TISSUE=Erythrocyte;  
RX MEDLINE=85289161; PubMed=4030743;  
RA Abe K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;  
RT "Amino acid sequences of cytochrome b5 from human, porcine, and  
RL bovine erythrocytes and comparison with liver microsomal cytochrome  
RN b5.";  
RN J. Biochem. 97:1659-1668(1985).  
RN [5]  
RP SEQUENCE OF 1-90.  
RX MEDLINE=71134790; PubMed=4993957;  
RA Nobrega F.G., Ozols J.;  
RT "Amino acid sequences of tryptic peptides of cytochromes b5 from  
RL microsomes of human, monkey, porcine, and chicken liver.";  
RN J. Biol. Chem. 246:1706-1717(1971).  
RN [6]  
RP SEQUENCE OF 1-90.  
RX MEDLINE=72154531; PubMed=5062820;  
RA Ozols J.;  
RT "Cytochrome b5 from a normal human liver. Isolation and the partial  
RL amino acid sequence.";  
RN J. Biol. Chem. 247:2242-2245(1972).  
RN [7]  
RP SEQUENCE OF 1-90.  
RX MEDLINE=74074962; PubMed=4770377;  
RA Rashid M.A., Hagihara B., Kobayashi M., Tani S., Teugita A.;  
RT "Structural studies of cytochrome b5. 3. Sequential studies on human  
RL liver cytochrome b5.";  
RN J. Biochem. 74:985-1002(1973).  
RN [8]  
RP SEQUENCE OF 1-35 AND 83-133.  
RX MEDLINE=89323209; PubMed=2752049;  
RA Ozols J.;  
RT "Structure of cytochrome b5 and its topology in the microsomal  
RL membrane.";  
RN Biochim. Biophys. Acta 997:121-130(1989).  
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
CC OXYGENASES.  
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE (LIVER FORM). BOUND TO  
CC THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM. OR CYTOPLASMIC  
CC (ERYTHROCYTE FORM).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=Liver, Membrane-bound;  
CC IsoId=P00167-1; Sequence=Displayed;  
CC Name=2; Synonyms=Erythrocyte, Cytoplasmic;  
CC IsoId=P00167-2; Sequence=VSP 001240, VSP 001241;  
CC -1- DISEASE: DEFECTS IN CYB5 ARE THE CAUSE OF TYPE IV HEREDITARY  
CC METHEMOGLOBINEMIA.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
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CC -----  
 CC EMBL; M22865; AAA35729.1; ALT SEQ.  
 CC EMBL; L39945; AAA63169.1; JOINED.  
 CC EMBL; L39792; AAA63169.1; JOINED.  
 CC EMBL; L39941; AAA63169.1; JOINED.  
 CC EMBL; L39944; AAA63169.1; JOINED.  
 CC EMBL; L39943; AAA63169.1; JOINED.  
 CC EMBL; L39944; AAA63169.1; JOINED.  
 CC EMBL; M60174; AAA52165.1; --  
 CC PIR; A28936; CBHUS.  
 CC PIR; JN0075; CBHUS.  
 CC HSPSP; P00171; 1BHB.  
 CC HSPSP; P00171; 1BHB.  
 CC HSPSP; HGN2570; CYB5.  
 CC GO; M250790; --  
 CC GO; GO:0004129; F:cytochrome c oxidase activity; TAS.  
 CC InterPro; IPR001199; Cyt B5.  
 CC Pfam; PF00173; heme\_1; 1  
 CC PRINTS; PR00363; CYTOCHROME B5.  
 CC PRODOM; PD000612; Cyt B5; 1.  
 CC PROSITE; PS00191; CYTOCHROME B5\_2; 1.  
 CC PROSITE; PS00255; CYTOCHROME B5\_2; 1.  
 CC Electron transport; Transmembrane; Heme; Iron; Microsome; Acetylation;  
 CC Alternative splicing.  
 CC INIT MET 0  
 CC MOD RES 1 1  
 CC DOMAIN 1 90  
 CC DOMAIN 91 133  
 CC METAL 43 43  
 CC METAL 67 67  
 CC VARSPLIC 97 97  
 CC VARSPLIC 98 133  
 CC MISSING (in isoform 2).  
 CC /FtId=VSP\_001240.  
 CC Missing (in isoform 2).  
 CC /FtId=VSP\_001241.  
 CC MISSING (IN REF. 5).  
 CC Q -> E (IN REF. 8).  
 CC EBIQ -> QBIQ (IN REF. 5, 6 AND 7).  
 CC MISSING (IN REF. 7).  
 CC N -> D (IN REF. 5, 6 AND 7).  
 CC RPK -> KPR (IN REF. 4, 5, 6 AND 7).  
 CC A -> V (IN REF. 8).  
 CC CONFLICT 121 121  
 CC SEQUENCE 133 AA; 15199 MW; 2FAD2AE87B6C992E CRC64;  
 CC  
 CC Query Match 6.5%; Score 159; DB 1; Length 133;  
 CC Best Local Similarity 30.8%; Pred. No. 2.3e-06;  
 CC Matches 44; Conservative 27; Mismatches 44; Indels 28; Gaps 4;  
 CC  
 CC 11 AAREVSVPTFSEWEEKLNRLTDSGLVIDRKVYNTKSIQHPGGORVIGHVAGEDATD 70  
 CC 1 AEQDEAVKYTLEIQKHHSKSTWILHKKYVDLTKFLEHPGGEEVLRQAGGDATE 60  
 CC 71 AFRAHPDLPFVG-----KFLKELLIGELAPEEPSQDHGKNSKITEDFALRKTAEDMN 124  
 CC 61 NF-----EDVGHSTDAEMSKTFIIGELHPDD-----RPLKPKPTLTITIDSSS 106  
 CC 125 LFKTNHVFLLLAHLIALESIA 147  
 CC 107 SWTNWV-----IPASAVA 121  
 CC  
 CC RESULT 10  
 CC CYB2 HANAN  
 CC ID CYB2 HANAN STANDARD; PRT; 573 AA.  
 CC AC P09437;  
 CC DT 01-MAR-1999 (Rel. 10, Created)  
 CC DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Cytochrome B2, mitochondrial precursor (EC 1.1.2.3) (L-lactate  
 CC dehydrogenase [cytochrome]) (L-lactate ferricytochrome C  
 CC oxidoreductase) (L-LCR).

GN CYB2.  
 OS Hansenula anomala (Yeast) (Candida pelliculosa).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Pichia.  
 CC NCBI\_TaxID=4927;  
 CC  
 CC (1)  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=90045973; PubMed=2813072;  
 CC Riser Y., Tegoni M., Gervais M.;  
 CC "Nucleotide sequence of the Hansenula anomala gene encoding  
 CC flavocytochrome b2 (b<sub>2</sub>-lactate:cytochrome c oxidoreductase).";  
 CC Nucleic Acids Res. 17:8381-8391(1989).  
 CC (2)  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=9008451; PubMed=2688640;  
 CC Black M.T., Gunn F.J., Chapman S.K., Reid G.A.;  
 CC "Structural basis for the kinetic differences between  
 CC flavocytochromes b2 from the yeasts Hansenula anomala and  
 CC Saccharomyces cerevisiae.";  
 CC Biochem. J. 263:973-976(1989).  
 CC (3)  
 CC SEQUENCE OF 80-163.  
 CC MEDLINE=88082787; PubMed=3319613;  
 CC Haumont P.-Y., Thomas M.-A., Labeyrie F., Lederer F.;  
 CC "Amino-acid sequence of the cytochrome-b5-like heme-binding domain  
 CC from Hansenula anomala flavocytochrome b2.";  
 CC Eur. J. Biochem. 169:539-546(1987).  
 CC -!- CATALYTIC ACTIVITY: (S)-lactate + 2 ferricytochrome c = pyruvate +  
 CC 2 ferrocyclochrome c.  
 CC -!- SUBUNIT: Homotetramer.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.  
 CC -!- MISCELLANEOUS: THIS ENZYME BINDS FMN AND PROTOHEME IX PROSTHETIC  
 CC GROUPS.  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
 CC B5 FAMILY.  
 CC -!- SIMILARITY: TO SPINACH GLYOXALATE OXIDASE (33% IDENTITY), TO  
 CC P. PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M.SMEGMATIS LACTATE  
 CC 2-MONOOXYGENASE.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

Query Match 6.5%; Score 158; DB 1; Length 573;

```
Best Local Similarity 23.7%; Pred. No. 1.5e-05;
Matches 52; Conservative 40; Mismatches 73; Indels 54; Gaps 8;

QY 13 EREVSVTFWSWEIQ-----KXNLTDSGLVIDRKVNITKWSIQHFGQGVIGHYAG 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 DKFISDVPHWKQTELTPEIVSQHNKXDDLWVLNGQVYDLTDFLPHGQKIIIRYAG 127

QY 66 EDATDAFRAHPDLEFVGKFLKP-----LLIGELAPEPSQDGHGKSKI----- 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 KQAKIFVPHPP-DTIEKIPPEKHGLPIVGPEQEELSDEBIDRLRIERKPLSQ 186

QY 110 ---TEDFRALK-----TAEDMNLFKTNH-----VFELLLAHIIALSIAW 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 MINLHDPETIARQLPPALAVYCSAADDEVTLENHAYHRIFFENPKI--LIDVKDVI 244

QY 149 FTVYFNGMPTLITAFVLATSQAQGLQHDYGHLSV 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 STEFFGKTSAPFYISATALAK-----LGHPEGEVAI 276

RESULT 11
CYB5_MOUSE
ID _CYB5_MOUSE STANDARD; PRT; 133 AA.
AC P56395;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
RA Schellenberg K., Steptoe M., Tan P., Underwood K., Moore B.,
RA Theising B., Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases
CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES. IT IS ALSO INVOLVED IN SEVERAL STEPS OF THE STEROL
CC BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE C-5 DOUBLE BOND
CC INTRODUCTION DURING THE C-5 DESATURATION.
CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AA107504; -; NOT ANNOTATED CDS.
CC DR EMBL; W62851; -; NOT ANNOTATED CDS.
CC DR EMBL; AA106561; -; NOT ANNOTATED CDS.
CC DR EMBL; AA107511; -; NOT ANNOTATED CDS.
CC DR EMBL; AA086847; -; NOT ANNOTATED CDS.
CC DR EMBL; AA105541; -; NOT ANNOTATED CDS.
CC DR HSSP; P00173; 1AQA.
CC DR MGD; MG1:1926952; Cyb5.
CC DR SWISS-2DPAGE; P56395; MOUSE.
CC DR InterPro; IPR001199; Cyt B5.
CC DR Pfam; PF00173; heme b1;
CC DR PRINTS; PR00363; CYTOCHROMES.
CC DR ProDom; PD000612; Cyt B5; 1.
CC DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
CC KW Electron transport; Transmembrane; Heme; Iron; Microsome.

FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 90 HEME-BINDING (BY SIMILARITY).
FT DOMAIN 91 133 MEMBRANE-BINDING (BY SIMILARITY).
FT METAL 43 43 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 67 67 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 133 AA; 15110 MW; 58540A370B38CEAE CRC64;

Query Match 6.4%; Score 157; DB 1; Length 133;
Best Local Similarity 33.1%; Pred. No. 3.4e-06;
Matches 42; Conservative 22; Mismatches 43; Indels 20; Gaps 3;

QY 11 AAREVSVPTSWREIOKHNLRITDSGLVIDRKVNITKWSIQHFGQGVIGHYAGEDATD 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 AQSDKQVYVLEIEIQHKDSKTWILHHKVYDLTKFLEHFGGEBVLREQAGDATE 60

QY 71 AFRAFHPDLEFVG-----KFLKPLLIGELAPEPSQDGHGKSKITEDFRALRKTAEDMN 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 NP-----EDVGHSTDARELSKTYIIGELHPDD-----RSKIAKPSDTLITTVESNS 106

QY 125 LFKTNHV 131
   : : : : :
Db 107 SWWTNWV 113

RESULT 12
DESA_SPIPL
ID _DESA_SPIPL STANDARD; PRT; 351 AA.
AC Q54794;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fatty acid desaturase (EC 1.14.19.-) (Delta 12 desaturase).
GN DESA.
OS Spirulina platensis.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
OX NCBI_TaxID=1156;
RN [1]
RP SEQUENCE FROM N.A.
RA Murata N., Deshniun P., Tasaka Y.;
RL Submitted (APR-1995) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANES GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL; X86736; CAA60415.1; -
CC DR PIR; S54259; S54259.
CC DR InterPro; IPR005804; FA_desat_fam.
CC DR InterPro; IPR005803; FA_desaturase.
CC DR Pfam; PF00487; FA_desaturase; 1.
CC DR ProDom; PD001081; FA_desat_fam; 2.
CC DR PROSITE; PS00574; FATTY ACID DESATUR_2; FALSE NEG.
CC KW Oxidoreductase; Fatty acid biosynthesis; Membrane.
CC PT DOMAIN 89 93 HISTIDINE BOX-1.
CC DR DOMAIN 125 129 HISTIDINE BOX-2.
CC FT DOMAIN 286 290 HISTIDINE BOX-3.
CC SQ SEQUENCE 351 AA; 40928 MW; 125A9F1E07E5EE97 CRC64;

Query Match 6.4%; Score 155.5; DB 1; Length 351;
Best Local Similarity 24.0%; Pred. No. 1.4e-05;
Matches 74; Conservative 35; Mismatches 122; Indels 77; Gaps 16;

QY 147 ANFTVF-----YFGNGWIPILITAFVLA-----TSQAQAGW--LQHDYGHLSVYRPKWN 194
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Db 44 ANMTVIVNVVGLGWLGTALPWFLLPVVFTGTALTGFVVGHCGRSFSR-----N 99
QY 195 HLVKFVIGHLKGASAW-----WNHRFQHAKPNIFKHDPDNNMLHVFLGEWOP-----I 247
Db 100 VVNDVWV-GHILFLPIYFPFHSWRIGHNQHKYTNRMELD-----NANQFWRKE 147
QY 248 EY-GKKKLKYLPNHQHEVFFLIGPPELLIPMYFQOIIMTWIVHKWVDLAWAVSYIRF 306
Db 148 EYQNAKFWQVIYDLFRGAWLG-----SILHWSIHEDWTKFEGKQKQVXF 196
QY 307 -----FITVIPPYIGLALLFNIRFLESHWFV---WV---TQNNHIVMEID 348
Db 197 SLLLVIGAAAIAPTMILITIGWVG-----FVKFWIPLVLFHFWMTFTLLHHTIADIP 250
QY 349 QEAYRDWF--SSOLTATCNVEQSFNDWFSGLHNFQIEHHLFPTPRHNLHXIAPLVKSL 406
Db 251 FREPEQWHAESQSGTVCHNYSRWGEFLCHDINHVPHTAIPWYNLRFTFVYR--- 308
QY 407 CAKHGIEY 414
Db 309 --KIGGEY 314

RESULT 13
NIAL PHAVU STANDARD; PRT; 881 AA.
AC P39855;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR-1).
GN NIAL OR NRI.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Saxa; TISSUE=Shoot;
RA Hoff T., Stumman B.M., Henningsen K.W.;
RT "Cloning and expression of a gene encoding a root specific nitrate
RT reductase in bean (Phaseolus vulgaris).";
RL Physiol. Plantarum 82:197-204(1991).
CC -|- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -|- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -|- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -|- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -|- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC
CC EMBL; X513603; CAA37672.1; -;
CC PIR; S25445; S25445.
CC HSRP; P17571; 2CND.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR001834; Cyt B5_reductase.
DR InterPro; IPR000572; Euk MD oxred.
DR InterPro; IPR001709; FPN_Cyt_redctse.
DR InterPro; IPR005066; Mo-Co_dimer.

```

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DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxigored_molyb; 1.
DR PRINTS; PR00406; CYTBSRDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPCR.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 167 167 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 406 406 INTERCHAIN (POTENTIAL).
FT METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 881 AA; 99222 MW; A212A1288B4EE661 CRC64;

Query Match 6.3%; Score 153.5; DB 1; Length 881;
Best Local Similarity 25.2%; Pred No. 6e-05;
Matches 69; Conservative 40; Mismatches 78; Indels 87; Gaps 14;

QY 5 GNQEGAAERF-----VVP-----TFSWEIQKHNRRTDGLVIDR 41
Db 479 GNQSGWNAEKQLEKSESNPILKKSVPFMTATKSYSLSEVRHNRNDSAWIIVG 538
QY 42 KYVNTKWSIQHPGQGVIGHYAGEDATDAFRHPDLEFVGKFLKLLIGELAPESPQ 101
Db 539 HVYDCTFLKDPGEGESILLNAGTDCTEFEAIHSDK--AKWLEDYRIGELMTTDTYS 596
QY 102 D-----HGKN-----SKITEDFPALR--KTAED--M 123
Db 597 DSSSNNSNVHGNSETTHLAPIREVALNPKEIPCKILSKTSISHDVLLRALFALPAEDQVM 656
QY 124 NLFKTNHVPF-----LLLLAH--IIALESIAWF-----TVFY-----FGNGWIPFL-I 163
Db 657 GLPVGNVHFLCATVDEKLCMRAYTPTSSVDVEGFFDLVVKVYFGVHPNPNFGGIMSQHL 716
QY 164 TAFVLATISQAQAGWLQH-DY---GHLSVYVRPKW 193
Db 717 DSLPIGSVDVKGPIGLHIEYTGRCGNFLVHGKPRF 750

RESULT 14
CYB5_ALOSE
ID CYB5_ALOSE STANDARD; PRT; 87 AA.
AC P00168;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5 (fragment).
GN CYB5.
OS Alouatta seniculus (Red howler monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;
OC Alouatta;
OX NCBI_TaxID=9503;
RN [1]
RP SEQUENCE.
RX MEDLINE=71134790; PubMed=4993957;
RA Nobrega F.G.; Ozols J.;
RT "Amino acid sequences of tryptic peptides of cytochromes b5 from
RT microsomes of human, monkey, porcine, and chicken liver.";
RL J. Biol. Chem. 246:1706-1717(1971).
RN [2]
RP REVISIONS TO 11; 14; 85 AND 87.
RX MEDLINE=89323209; PubMed=2752049;
RA Ozols J.;

```

DR PRINTS; PR00363; CYTOCHROME<sub>B5</sub>.  
DR PRODom; PR000612; Cyt B5; 1.  
DR PROSITE; FS00191; CYTOCHROME<sub>B5</sub>\_1; 1.  
DR PROSITE; FS50255; CYTOCHROME<sub>B5</sub>\_2; 1.  
KW Electron transport; Heme; Iron; Membrane.  
KW METAL 38  
FT FT METAL 38  
FT FT METAL 62  
SQ SEQUENCE 131 AA; 14651 MW; 589D7413C768F2F0 CRC64;  
Query Match 6.1%; Score 149; DB 1; Length 131;  
Best Local Similarity 34.3%; Pred. No. 1.5e-05;  
Matches 36; Conservative 19; Mismatches 32; Indels 18; Gaps

| CYMS_RAT | CYMS_RAT  | STANDARD;                         | PRT; | 146 AA. |
|----------|---|-----------------------------------|------|---------|
| ID       | P04166  | Q9OWG1;                           |      |         |
| AC       | 20-MAR-1987   | (Rel. 04; Created)                |      |         |
| DT       | 16-OCT-2001   | (Rel. 40; Last sequence update)   |      |         |
| DT       | 15-SEP-2003   | (Rel. 42; Last annotation update) |      |         |
| DE       | Cytochrome b5 outer mitochondrial membrane isoform precursor. |                                   |      |         |
| GN       | CYB5B OR QNB5.  |                                   |      |         |

OS Eukaryoticus (Rat).  
 OS Eukaryotica; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxId=10116;  
 [1]\_SEQUENCE FROM N.A.  
 RP Kuroda R., Ikenoue T., Honsho M., Tujimoto S., Miroma J., Ito A.;  
 RA "Charged amino acids at the carboxy-terminal portions determine  
 RT intracellular locations of two isoforms of cytochrome b5.";  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases  
 EN

RX MEDLINE=83182449; PubMed=6840088;  
RA Lederer F., Girir R., Guizard B., Cortial S., Ito A.;  
RT "Two homologous cytochromes b5 in a single cell.";  
RL Eur. J. Biochem. 132:95-102(1983).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
RR MEDLINE=97128856; PubMed=89732114;  
RA Rodriguez-Waranon M.J., Qiu F., Stark R.E., Zhang X.,  
RA Founding S.I., Rodriguez V., Schilling C.L. III, Bunce R.A.,  
RA Ravera M.,  
RT "13C NMR spectroscopic and X-ray crystallographic study of the role  
RT played by mitochondrial cytochrome b5 heme propionates in the  
RT electrostatic binding to cytochrome c.";  
RL Biochemistry 35:16378-16390(1996).

RA Rivera M., Seetharaman R., Girdhar D., Wirtz M., Zhang X., Wang X.,  
PA White S.:  
RT "the reduction potential of cytochrome b5 is modulated by its exposed  
RL heme edge."; *RT Biochemistry* 37:1485-1494(1998).

2A Wirtz M., Oganesyan V., Zhang X., Studer J., Rivera M.;  
 RT "Modulation of redox potential in electron transfer proteins: effects  
 RT of complex formation on the active site microenvironment of cytochrome  
 RT bs.";  
 RL Faraday Discuss. 116:221-234 (2000).

[6]  
 RP X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS) OF 17-103.  
 RX MEDLINE=21468937; PubMed=11583146;  
 RA Altuve A., Silchenko S., Lee K.-H., Kucera K., Terzyan S., Zhang X.,  
 RA Benson D.R., Rivera M.;  
 RT "Probing the differences between rat liver outer mitochondrial  
 RL membrane cytochrome b5 and microsomal cytochromes b5";  
 RL Biochemistry 40:9469-9483(2001).  
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
 CC OXYGENASES.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial outer membrane.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
 CC  
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 CC  
 DR EMBL; Y12517; CAA73117.1; -;  
 DR PDB; 1BSM; 12-MAR-97.  
 DR PDB; 1AWP; 18-NOV-98.  
 DR PDB; 1EUB; 04-APR-01.  
 DR PDB; 1ICC; 19-SEP-01.  
 DR PDB; 1LJO; 20-NOV-02.  
 DR InterPro; IPR001199; Cyt B5.  
 DR Pfam; PF001173; heme 1; 1-  
 DR PRINTS; PR00363; CYTOCHROME B5.  
 DR PRODOM; PD000612; Cyt B5; 1.  
 DR PROSITE; PS00191; CYTOCHROME B5\_1; 1.  
 DR PROSITE; PS0285; CYTOCHROME B5\_2; 1.  
 DR Electron transport; Mitochondrion; Outer membrane; Transmembrane;  
 KW Heme; Iron; 3D-structure.  
 FT PROPEP 1 11  
 FT CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL  
 FT DOMAIN 12 103 MEMBRANE ISOPORM.  
 FT TRANSMEM 119 136 HEME-BINDING.  
 FT METAL 55 55 POTENTIAL.  
 FT METAL 79 79 IRON (HEME AXIAL LIGAND).  
 FT CONFLICT 12 12 IRON (HEME AXIAL LIGAND).  
 FT STRAND 22 23 N -> D (IN REF. 2).  
 FT HELIX 25 28  
 FT TURN 29 30  
 FT STRAND 32 33  
 FT TURN 34 35  
 FT STRAND 36 41  
 FT TURN 42 43  
 FT STRAND 44 47  
 FT HELIX 49 54  
 FT TURN 56 57  
 FT HELIX 60 63  
 FT TURN 64 67  
 FT STRAND 69 69  
 FT TURN 71 77  
 FT HELIX 78 78  
 FT HELIX 81 86  
 FT STRAND 87 90  
 FT STRAND 91 95  
 FT HELIX 97 99  
 SQ SEQUENCE 146 AA; 16265 MW; 1CA90DD3C81C412E CRC64;  
 Query Match 6.18; Score 148.5; DB 1; Length 146;  
 Best Local Similarity 32.78; Pred. No. 1.9e-05;  
 Matches 36; Conservative 24; Mismatches 37; Indels 13; Gaps 4;  
 QY 5 GNOGEAAAEVSYPTFSWEIQKHLNRDTSGLVIDRKVYNTKWSIQHPGQGVTHYVA 64  
 DB 10 GRNGQGS---DPAVTVYRLEEVAKRNTAEETWVHGRVYDITRFLSEHPGGSEVLEQA 66

QY 65 GEDATDAFR--AFHPDLFVGVKELKPLIG-----ELAPEPSQDHGKNS 107  
 DB 67 GADATESFEDVGHSPDAR---EMLKQYIGDVHPNDLKPKDGKDPKNN 113  
 RESULT 17  
 ID FD3E BRANA STANDARD; PRT; 383 AA.  
 AC P48624; P46311;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).  
 GN FAD3.  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 ON NCBI\_TaxID=3708;  
 RX MEDLINE=93088059; PubMed=1455229;  
 RA Somerville C.R.;  
 RA "Map-based cloning of a gene controlling omega-3 fatty acid  
 RT desaturation in Arabidopsis";  
 RL Science 258:1353-1355(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94302147; PubMed=8029334;  
 RA Yadav N.S., Wierzbicki A., Asgenter M., Caeter C.S., Perez-Grau L.,  
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,  
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,  
 RA Feldmann K.A., Pierce J., Browne J.;  
 RT "Cloning of higher plant omega-3 fatty acid desaturases";  
 RL Plant Physiol. 103:467-476(1993).  
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES  
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,  
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE  
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER  
 CC PHOSPHOLIPIDS.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.  
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; L01418; AAA32994.1; -;  
 DR EMBL; L22962; AAA61775.1; -;  
 DR PIR; A44227; A44227.  
 DR InterPro; IPR005804; FA desat. fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Prodom; PD001081; FA\_desat\_fam; 2.  
 DR Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;  
 KW Transmembrane.  
 FT TRANSMEM 53 73 POTENTIAL.  
 FT TRANSMEM 210 230 POTENTIAL.  
 FT TRANSMEM 234 254 POTENTIAL.  
 FT DOMAIN 98 102 HISTIDINE BOX-1.  
 FT DOMAIN 134 138 HISTIDINE BOX-2.  
 FT DOMAIN 301 305 HISTIDINE BOX-3.  
 FT CONFLICT 11 11 V -> A (IN REF. 2).  
 FT CONFLICT 15 22 SGARKEG -> ER (IN REF. 2).

```

FT CONFLICT 57 57 T -> A (IN REF. 2).
FT CONFLICT 64 64 A -> V (IN REF. 2).
FT CONFLICT 68 68 M -> V (IN REF. 2).
FT CONFLICT 78 78 L -> F (IN REF. 2).
FT CONFLICT 84 84 V -> A (IN REF. 2).
FT CONFLICT 113 114 SV -> TA (IN REF. 2).
FT CONFLICT 162 162 P -> S (IN REF. 2).
FT CONFLICT 181 181 I -> L (IN REF. 2).
FT CONFLICT 195 195 F -> Y (IN REF. 2).
FT CONFLICT 232 232 D -> G (IN REF. 2).
FT CONFLICT 264 264 E -> D (IN REF. 2).
FT CONFLICT 320 321 RA -> KS (IN REF. 2).
FT CONFLICT 383 383 AA; 43936 MW; DAD7C3AGFAI2826A CRC64;
SQ SEQUENCE 383 AA; 43936 MW; DAD7C3AGFAI2826A CRC64;

Query Match 6.1%; Score 148.5; DB 1; Length 383;
Best Local Similarity 22.5%; Pred. No. 5.9e-05;
Matches 92; Conservative 62; Mismatches 149; Indels 105; Gaps 25;

QY 65 GEDATDAFRAPHDPLEFVGKFLKPLLLGELAPEPSQDHGKNGKITEDPRLAKRTAEDMN 124
DB 13 GDSGARKEEGDPSAQ-----PFFKIGDTPAATP-----KHCWVKSPLRMS-----54
QY 125 LFKTNHVFLLLAHIALESIAWF--TVFVGNGWPTTITA-FVLATSOAQAGWLQHD 181
DB 55 -YVTRDI-FAVAALA-MAAVYFDSWFLWPLVWVAQG---TLFWAIFVLG-----HD 99
QY 182 YGHLVSVERKPNW---HLVHKFVIGHLKASANNHRHFQHHAKENIHKDPDVNMLH 237
DB 100 COHGSFSDIPLNVSUGHILHSFILVPYHG-----WISHRTH--QNHGHVENDES---149
QY 238 VFVLGEWQPIEYGGKKLKPYNHQHEVFFLIGPLIPMYFOQIIMTWIVHKN-----292
DB 150 -----WVPLP--EKLYKNLPHSTRMLRYTVPLPMLAYPIVLYWYRSPKSGSHENPYSSL 201
QY 293 -----WDLAVASVYIRFF---ITYIPFVIGLALLFLNFIRESLHWF 334
DB 202 PAPSERKUIASTTCW-SIMATLVLSFLVDPTVLKVGCV-----PYLIFVMWLD-----253
QY 335 VVWVTQNHVMEIDQAYR--DW--FSSQLTATCNVEQSPFNDFWFSGLHNFQIEHHLPPT 390
DB 254 -----VTVLHHGHDEKLPWYRGKWSYLRGLT-TIDRDYGIENN-IHHDIGTHVHHLFPQ 309
QY 391 MPRNLHKTAPIVSLCAKH-GIEYQEKPLLRAL-LDIIRSLKSGK 435
DB 310 IPHYHL-----VDTRAARKHVLGRYRBPKTSGAIPHLVESLVAISK 352

RESULT 18
CYB5_NEUCR STANDARD; PRT; 139 AA.
AC Q9P5L0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable cytochrome b5.
GN B23121.190.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSG 987;
RX PubMed=12655011;
RA Mannhaupt G., Monrone C., Haase D., Mewes H.-W., Aign V.,
RA Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
RA Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the
RT Neurospora genome sequence."
RL Nucleic Acids Res. 31:1944-1954(2003).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE

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CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL356172; CAB91687.2; -
CC InterPro; IPR001199; Cyt B5.
CC Pfam; PF00173; heme 1; 1.
CC PRINTS; PR00363; CYTOCHROME B5.
CC ProDom; PR000612; Cyt B5; 1.
CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC PROSITE; PS02055; CYTOCHROME B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome.
KW DOMAIN 1 78 HEME-BINDING.
FT TRANSMEM 105 125 POTENTIAL.
FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 139 AA; 14613 MW; 404BF3BAIDF5D575 CRC64;

Query Match 6.1%; Score 147.5; DB 1; Length 139;
Best Local Similarity 40.0%; Pred. No. 2.2e-05;
Matches 32; Conservative 19; Mismatches 16; Indels 13; Gaps 2;

QY 21 FSWERIQHNLTDSGLVIDRKVNITKWS:QHPGQQRVIGHYAGEDATDAFRAPHPDLE 80
DB 5 FTYQVVAENTKDLVYVHDKVYDITKVEDEHFGEEVLLDVAGQDSTEAF-----E 57
QY 81 FVG-----KFLKPLLLIGEL 94
DB 58 DVGHSDEAREALEPLLVGTL 77

RESULT 19
FD3C_RICCO STANDARD; PRT; 460 AA.
ID FD3C_RICCO
AC P48619;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
GN PAD7A-1.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Baker 296; TISSUE=Seed;
RC MEDLINE=94302177; PubMed=8029360;
RA van de Loo F.J., Somerville C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
RL Plant Physiol. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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EMBL; L25897; AAA73511.1; -;  
 PIR; T10063; T10063.  
 InterPro; IPR005804; FA\_desat\_fam.  
 Pfam; PF00487; FA\_desaturase; 1.  
 ProDom; PD001081; FA\_desat\_fam; 2.  
 Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
 Transit peptide.  
 TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
 CHAIN 177 460 OMEGA-3 FATTY ACID DESATURASE.  
 DOMAIN 177 181 HISTIDINE BOX-1.  
 DOMAIN 213 217 HISTIDINE BOX-2.  
 DOMAIN 380 384 HISTIDINE BOX-3.  
 SEQUENCE 460 AA; 52561 MW; 836592904EF3C7B0 CRC64;

Query Match 6.1%; Score 147.5; DB 1; Length 460;  
 Best Local Similarity 22.5%; Pred. No. 8.9e-05;  
 Matches 101; Conservative 59; Mismatches 176; Indels 113; Gaps 23;

40 DRKVN-----ITKWSICHPGQGV-----IGHVAGED--ATDAFAFHPDLEFVGK 84  
 41 DSKSYNLCSFKYSSNSKSNALNVAVPNVSTVSGEDDREREFGNIVNDSKGGE 100  
 85 FL-----KPLIGELAPEPSQDHGNSKITEFRAIRKTAEDMNLKTNHVPFLLLLAH 139  
 101 FFDAGAPPTFLADIRAAIP-----KHCWYNKPNRSNYSVLRVVV-----VFGLAAVA- 149  
 140 IIALESIAWTVFVFGNGWPTLITAFVLATSQAQAGLQHDYGHLSVYRKPKNHLVHK 199  
 150 -----AYP-----NNWVAPLYWFCQTFWALFVLGDCGSGFSNPNKLS- 192  
 200 FVGLHKGAGA-----NWNHRRHQHAKPNIHKPDVNMHMLFVLGEGQPIYGYKKLK 255  
 193 -VVGHLHSSILVPHYHGWRISHRTH--QNHGVENDES-----NHPL--SEKIFK 238  
 256 YLPYNHQHEVFFLIGPPLLIPMYF-----QYQIIMTVHKNVNDLAWAVSYIR 305  
 239 SLDNVTKLRLSPLFFMLAYPFYLNWSRSPGKSGHFPDGLFVPERKDI----- 289  
 306 FFITYIPFYGLGALL-FLNF-----IRFLESH-----WFWVTQNMHIWIDQEA 351  
 290 --ITSTACTWAMAALLVYLNFSMGPVQMLKLYGIPYMFVWMLDFVTVLHHGHEDKLWP 347  
 352 YRDWFSSQL---TATCNVQSFNDWFSCHLNQIEHLEPTWPRNLHKIALPLVKSICA 408  
 348 YRGKAWSYLRGLTLDYDGVINN--IHHDIGTHVHHLPFPQPHVHLVEATEAARPMVG 406  
 409 KHGIEYQEK-----PL-LRALDIDIRSLKK 432  
 407 KY---YREPKSGFLPLHLLGLSVRSME 432

RESULT 20  
 CYN5\_HUMAN STANDARD; PRT; 146 AA.  
 ID CYN5\_HUMAN  
 AC O43169;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome b5 outer mitochondrial membrane isoform precursor.  
 GN CYB5M OR OMB5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Ishibashi K.;

"Cytochrome b5 and aquaporins share the last transmembrane amino acids sequence".  
 Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH

FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND

OXYGENASES (BY SIMILARITY).

LOCUS: Mitochondrial outer membrane (By

similarity).

LOCUS: BELONGS TO THE CYTOCHROME B5 FAMILY.

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EMBL; AB009282; BAA23735.1; -;

HSP; P04166; 1BEM.

InterPro; IPR001199; Cyt\_B5.

Pfam; PF00173; heme\_1; 1.

PRINTS; PR00363; CYTOCHROMEBS.

ProDom; PD000612; Cyt\_B5; 1.

PROSITE; PS00191; CYTOCHROME\_B5\_1; 1.

PROSITE; PS00255; CYTOCHROME\_B5\_2; 1.

Electron transport; Mitochondrion; Outer membrane; Transmembrane;

Heme; Iron.

PROPEP 1 11 BY SIMILARITY.

CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL

MEMBRANE ISOFORM.

DOMAIN 12 103 HEME-BINDING.

TRANSMEM 119 136 POTENTIAL.

METAL 55 55 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

METAL 79 79 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

SEQUENCE 146 AA; 16332 MW; 2FF7DEA297124E19 CRC64;

Query Match 6.0%; Score 146.5; DB 1; Length 146;

Best Local Similarity 35.4%; Pred. No. 2.8e-05;

Matches 40; Conservative 20; Mismatches 34; Indels 19; Gaps 4;

5 GNOCEGAAREVSVPTFSWEIQLKHLRTSLGLVDRKVNITKWSIQHPGQGVIGHYA 64

8 GSDGKG-GEVTSVTVYKLEEVAKRSLKELWLVHGVYDVTRFNEHSGEVLLEQA 66

65 GEDATDAFRAHPDLEFVG-----KFLKPLLIG-----ELAPEPSQDHGKN 106

67 GVDASEP-----EDVGHSSDAREMLKQYVIGDIHPSDLKPSGSGKDPSON 112

RESULT 21

FD6C\_SPTOL

ID FD6C\_SPTOL STANDARD; PRT; 447 AA.

AC P48629;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).

GN FAD6.

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllales; Caryophyllaceae; Spinacia.

NCBI\_TaxID=3582;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.

RC STRAIN=cv. Subito; TISSUE=Leaf;

RX MEDLINE=95036044; PubMed=7948918;

RA Schmidt H.; Dresselhaus T.; Buck F.; Heinz E.;

RT "Purification and PCR-based cDNA cloning of a plastidial n-6

desaturase";

Plant Mol. Biol. 26:631-642(1994).

CC FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES



THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

!- PATHWAY: Polyunsaturated fatty acid biosynthesis.

!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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EMBL; X78311; CAA55121.1; -

PIR; S53309.

InterPro; IPR005804; FA desat. fam.

pfam; PF00487; FA desaturase; 1.

ProDom; PD001081; FA desat. fam; 2.

Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane; Transit peptide.

TRANSIT 1 65 CHLOROPLAST.

CHAIN 66 447 OMEGA-6 FATTY ACID DESATURASE.

DOMAIN 171 175 HISTIDINE BOX-1.

DOMAIN 207 211 HISTIDINE BOX-2.

DOMAIN 367 371 HISTIDINE BOX-3.

SEQUENCE 447 AA; 51306 MW; 2BA7C87PFF953508 CRC64;

Query Match 6.0%; Score 146; DB 1; Length 447;  
Best Local Similarity 20.4%; Pred. No. 0.00011;  
Matches 79; Conservative 60; Mismatches 142; Indels 106; Gaps 19;

QY 91 IGEAPEPSQDHGKNSKITEDEFRALRKTAEADNMNLFKTNHVFLLLAHIALESTIA--- 147  
D 97 IGEPLDDVT-----MRDIITSLPKQVPEINDTKAWGTVLISVTSYALGIFMIKAP 148

QY 148 WFTVFYFGNGWIPULTITAFVLATSOAGWLOHDIYGLSHLVYRKPKNHLVHKFVIGHLKG 207  
D 149 WY-LPLAWAWTGTGTAITFFV-----IGHCAHKSFSK-----NKLVED-IVGLTAP 193

QY 208 ASANW-----WNRHRHQHAKENIHKD-----PDVNMHLVFLYG---EWQP 246  
D 194 MPLIYVPEWPKDQHTKTWLEEDTAWLPIMKEDISSPGLRKALIVAYGRLTWMS 253

QY 247 IEYGGKKLYLPYNNQHEV-----FPLIGPPLLIPMYFOYQINTMIVHKWV 294  
D 254 IAHWLKVHFNKDFRQSEVKRATISLAAYFAFMVIGWPL-----IYKGTI 299

QY 295 DLAWAVSYIRPFIITYPIFYGILGALLFNIRFLESHWVVMVTQNMHIVMEIDQEAIRD 354  
D 300 -GVW-----IKWL--MPWLG-----HFWMTFTIVHTAHPIPKSKSKE 337

QY 355 W--FSSQATCNVQSPFNDFWFSQHLNFAQEHLPPTMPRNLHKLAPLVKSLCAKHGI 412  
D 338 WNAQAQLSGTVCHCVPRWIEILCHDISVHPHTISPKIPSYNLRAN---QSLNENWG- 393

QY 413 EYQKXP-----LRLALDLIRSLKSG 434  
D 394 EYLNPKSNWRLMRTIMTTCYIDKDG 420

RESULT 22  
FD3E\_TOBAC  
ID FD3E\_TOBAC  
AC P48626;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).

GN FAD3.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. SRI; TISSUE=Leaf;  
RC MEDLINE=95011532; PubMed=7926817;  
RA Hamada T., Kodama H., Nishimura M., Iba K.;  
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";  
RL Gene 147:293-294 (1994).  
CC !- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES  
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.  
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE  
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER  
CC PHOSPHOLIPIDS.  
CC !- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
CC !- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
CC !- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
CC AND/ OR BE INVOLVED IN METAL ION BINDING.  
CC !- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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EMBL; J26509; BAA05515.1; -  
PIR; J2555; JC2555.  
InterPro; IPR005804; FA desat. fam.  
pfam; PF00487; FA desaturase; 1.  
ProDom; PD001081; FA desat. fam; 2.  
Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum; Transmembrane.

FT TRANSMEM 52 72 POTENTIAL.  
FT TRANSMEM 213 233 POTENTIAL.  
FT TRANSMEM 236 256 POTENTIAL.  
FT DOMAIN 97 101 HISTIDINE BOX-1.  
FT DOMAIN 133 137 HISTIDINE BOX-2.  
FT DOMAIN 300 304 HISTIDINE BOX-3.  
SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB0251B2 CRC64;

Query Match 6.0%; Score 145.5; DB 1; Length 379;  
Best Local Similarity 21.3%; Pred. No. 0.0001;  
Matches 86; Conservative 56; Mismatches 143; Indels 119; Gaps 23;

QY 78 DLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDEFRALRKTAEADNMNLFKTNHVFLLLL 137  
D 19 EEFEDPSAPPPFLAEIRNVIP-----KHCWKYKDLRSLSYVVRDV-----IFVAILI 66

QY 138 AHIIALESIAWTFVYFGNGWIPULTITA-FVLATSOAGWLOHDIYGLSHLVYRKPKWN-- 194  
D 67 GRAIHLDLSMLFPLYWAIQG---TWFAIFVLG-----HDCGHGSPDSQLLNNV 113

QY 195 --HLVHKFVIGHLKGASANWNRHFPQHAKENIHKDPPDVNMHLVFLVGEWQP----- 246  
D 114 VGHILHSAILVPYHG-----WRISHKTHRQHNQVETDE-----SWVPMPEKLY 157

QY 247 --IEYGGKKLY-LPYNHQHEYFFLIGPPLLIPMYF----- 279  
D 158 NKVGSTKFLRYKIP-----FLLAFLMYLMKESPGKSGSHFNPSYDLFQPHR 206

QY 280 QYOIIMTMIVHKWVDLAWAVSYIRPFIITYPIFYGILGA--LLFLNFRFLSHWFWNV 337  
D 207 KYVVTSTLC---WTVMA-ALLYLCTAFGSLQMFKIYGAPYLIFV-----MWLDFV 253

QY 338 TQNMHIVMEIDQEAIR--DW--FSSQATCNVQSPFNDFWFSQHLNFAQEHLPHTMTMPR 393

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Db 254 TYLHREHYEKKLPWYRGKWSYLRGLT-TVDRDYGLENN-IHHDIGTHVIHHLFPQIPH 311
QY 394 HNLKHIAPLVKSLCAKHGEYOEK-----PL-LRALLDIIRSLKK 432
Db 312 YHLREATKAAPVLGYK---YREPKSGPIPHLVKDLTSKQ 352

RESULT 23
CYBS_CHICK STANDARD; PRT; 138 AA.
ID AC P00174;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinoptera; Cyprinodontiformes; Cyprinodontidae; Phasiinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90314412; PubMed=2369133;
RA Zhang H., Somerville C.;
RT "Soluble and membrane-bound forms of cytochrome b5 are the products
of a single gene in chicken."
RL Arch. Biochem. Biophys. 280:412-415(1990).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=88280278; PubMed=3395128;
RA Zhang H., Somerville C.;
RT "The primary structure of chicken liver cytochrome b5 deduced from
the DNA sequence of a cDNA clone."
RL Arch. Biochem. Biophys. 264:343-347(1988).
RN [3]
RN SEQUENCE OF 14-97.
RX MEDLINE=71134790; PubMed=4993957;
RA Nobrega F.G., Ozols J.;
RT "Amino acid sequences of tryptic peptides of cytochromes b5 from
microsomes of human, monkey, porcine, and chicken liver."
RL J. Biol. Chem. 246:1706-1717(1971).
RN [4]
RN SEQUENCE OF 4-16 AND 89-138.
RX MEDLINE=89323209; PubMed=2752049;
RA Ozols J.;
RT "Structure of cytochrome b5 and its topology in the microsomal
membrane."
RL Biochim. Biophys. Acta 937:121-130(1989).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; M32293; AAA48740.1; -.
DR EMBL; M18539; AAA48733.1; -.
DR PIR; A28811; LEHB.
DR HSP; P00171; LEHB.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.

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KW Electron transport; Transmembrane; Heme; Iron; Microsome.
FT DOMAIN 1 96 HEME-BINDING.
FT DOMAIN 97 138 MEMBRANE-BINDING.
FT METAL 49 73 IRON (HEME AXIAL LIGAND).
FT METAL 73 73 IRON (HEME AXIAL LIGAND).
FT CONFLICT 12 12 W -> E (IN REF. 4).
FT CONFLICT 27 29 NSQ -> ZSB (IN REF. 3).
FT CONFLICT 67 67 N -> D (IN REF. 3).
FT CONFLICT 124 124 A -> T (IN REF. 4).
FT CONFLICT 138 138 E -> EE (IN REF. 4).
SQ SEQUENCE 138 AA; 15545 MW; 168F0B87251557A8 CRC64;

Query Match 5.98; Score 144.5; DB 1; Length 138;
Best Local Similarity 26.28; Pred. No. 3.8e-05;
Matches 45; Conservative 26; Mismatches 50; Indels 51; Gaps 6;

QY 4 GNGGEGAAERYSVPTFSWBIQKHLNLTDSGLVIDRKVYNTKWSIQHPGQQRVIGHY 63
Db 3 GSSEAGCEAWRG---RYRLEEVQKHNSSQSTWIIVHHRIYDITKFLDEHPGGEVLREQ 59
QY 64 AGEDATDAFRAHPDLEFVG-----KFLPLLIIGLAEPEPSQDHGKSKITDFRALR 117
Db 60 AGGDATNF-----EDVGHSTDAALSETFIIGELHP-----DDRPKLQ 98
QY 118 KTAEDMNLFTNHFVFFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLA 169
Db 99 KPAE-----TLITTVQSNSSW-----SNWVIPAIAAIVA 129

RESULT 24
FD12 MORIS STANDARD; PRT; 400 AA.
AC P59668;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella isabellina (Umbelopsis isabellina).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Mucorales incertae sedis; Umbelopsis.
OX NCBI_TaxID=91625;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=M6-22;
RA Liu L., Li M., Xing L., Hu G.;
RT "Delta 12 fatty acid desaturase mRNA of Mortierella isabellina."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
to linoleic acid (delta9, delta12-18:2) (By similarity).
CC -1- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- DOMAIN: The histidine box domains may contain the active site
and/or be involved in metal ion binding.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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or send an email to license@isb-sib.ch).
CC EMBL; AF417245; AAU13301.1; -.
DR GO; GO:0016451; F:oxidoreductase; IDA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IDA.
DR InterPro; IPR005804; FA_Desat_fam.
DR Pfam; PF00487; FA_Desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.

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FT TRANSMEM 277 297 POTENTIAL
FT DOMAIN 112 116 HISTIDINE BOX-1.
FT DOMAIN 148 152 HISTIDINE BOX-2.
FT DOMAIN 339 343 HISTIDINE BOX-3.
SQ SEQUENCE 400 AA; 46016 MW; F5512D3F8210DBD2 CRC64;

Query Match 5.8%; Score 143.5; DB 1; Length 400;
Best Local Similarity 22.0%; Pred. No. 0.00016;
Matches 69; Conservative 42; Mismatches 95; Indels 107; Gaps 17;

Qy 177 W-LQHDYGHLSVVRKPKNHLV-----HKFVGHKGCASANWNHRRHFQHHAK 223
Db 108 WLAHECGHQSFSKSTLNNTVGMILHSMLLVPYHSWISHSK-----HHKATGHMTK 160
Qy 224 PNIF-----HKDPDVMNLHVFVLGEWQPIEYGGKKLKY 256
Db 161 DQFVFKTRSQVGLPPKESAAAAVQEDMSVHLDDEAPITLTF-----WVVIQFLGWPAY 216
Qy 257 LPYN-----HQHEFFLIGPPLIPMYFOYQIIMT-----MIVKKNWVD 295
Db 217 LIMNASQDYGRWTSHEFTY-----SPIFEPRNF-FDIIISDLGLVLAALGALYASMQLS 270
Qy 296 LAMAVSYIRFFITYIPFYGILGALLFLNIRFLSHVFWVTQMNHIVMEIDQAYRD- 354
Db 271 LLTVTKYI-----LPVNF-----WLVLTFLQHTDPLKPH--YREG 308
Qy 355 -WFSSQLTATCNVQS---PFNDWFSGHNLNFOIEHFLPTMPRNLHKAIPLVKSLCAKH 410
Db 309 AW-NFQRGALCTVDRSFGKFLDHMFHGVTHVAHLFSQMPFYHABEATYHLKLLGEY 367
Qy 411 GIEYQEKPLRLAL 423
Db 368 YV-YDPSPIVAV 379

```

## RESULT 25

```

FD12 MORAP STANDARD; PRT; 400 AA.
ID STRAIN=1S-4;
AC Q918H5; Q96TH3; Q9UVV4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_taxid=64518;
RN SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=1S-4;
RX MEDLINE=99234062; PubMed=10215899;
RA Sakuradani E., Kobayashi M., Ashikari T., Shimizu S.;
RT "Identification of delta12-fatty acid desaturase from arachidonic
RT acid-producing Mortierella fungus by heterologous expression in the
RT yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae.";
RL Eur. J. Biochem. 261:1812-1820(1999).
RN [2]
RN SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=ATCC 32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.N., Kirschner S.J., Mukerji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae.";
RL Lipids 34:649-659(1999).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 16266;
RA Liu L., Li M., Xing L., Hu G.;
RT "Delta 12 fatty acid desaturase gene of Mortierella alpina.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)

```

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to linoleic acid (delta9, delta12-18:2).
-!- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- DOMAIN: The histidine box domains may contain the active site
and/or be involved in metal ion binding.
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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EMBL; AB020033; BAA81754.1; -
DR EMBL; AF110509; AAF08684.1; -
DR EMBL; AF417244; AAL13300.1; -
DR GO; GO:001649; F:oxidoreductase; IDA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IDA.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
KW TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT DOMAIN 112 116 HISTIDINE BOX-1.
FT DOMAIN 148 152 HISTIDINE BOX-2.
FT DOMAIN 339 343 HISTIDINE BOX-3.
FT CONFLICT 17 19 STS -> TTT (IN REF. 3).
FT CONFLICT 21 23 APT -> PN (IN REF. 2).
FT CONFLICT 95 95 A -> V (IN REF. 2).
FT CONFLICT 107 107 I -> V (IN REF. 2).
FT CONFLICT 179 179 N -> S (IN REF. 3).
FT CONFLICT 180 182 AAA -> VAV (IN REF. 1).
FT CONFLICT 261 261 A -> T (IN REF. 1).
FT CONFLICT 280 280 V -> I (IN REF. 3).
FT CONFLICT 358 358 Y -> H (IN REF. 1).
FT CONFLICT 392 392 H -> Q (IN REF. 2).
SQ SEQUENCE 400 AA; 46001 MW; 40B2FCLC1E01F93F CRC64;

```

Query Match 5.8%; Score 142.5; DB 1; Length 400;  
Best Local Similarity 21.7%; Pred. No. 0.0002;  
Matches 68; Conservative 43; Mismatches 95; Indels 107; Gaps 17;

```

Qy 177 W-LQHDYGHLSVVRKPKNHLV-----HKFVGHKGCASANWNHRRHFQHHAK 223
Db 108 WLAHECGHQSFSKSTLNNTVGMILHSMLLVPYHSWISHSK-----HHKATGHMTK 160
Qy 224 PNIF-----HKDPDVMNLHVFVLGEWQPIEYGGKKLKY 256
Db 161 DQFVFKTRSQVGLPPKESAAAAVQEDMSVHLDDEAPITLTF-----WVVIQFLGWPAY 216
Qy 257 LPYN-----HQHEFFLIGPPLIPMYFOYQIIMT-----MIVKKNWVD 295
Db 217 LIMNASQDYGRWTSHEFTY-----SPIFEPRNF-FDIIISDLGLVLAALGALYASMQLS 270
Qy 296 LAMAVSYIRFFITYIPFYGILGALLFLNIRFLSHVFWVTQMNHIVMEIDQAYRD- 354
Db 271 LLTVTKYI-----LPVNF-----WLVLTFLQHTDPLKPH--YREG 308
Qy 355 -WFSSQLTATCNVQS---PFNDWFSGHNLNFOIEHFLPTMPRNLHKAIPLVKSLCAKH 410
Db 309 AW-NFQRGALCTVDRSFGKFLDHMFHGVTHVAHLFSQMPFYHABEATYHLKLLGEY 367
Qy 411 GIEYQEKPLRLAL 423
Db 368 YV-YDPSPIVAV 379

```

RESULT 26

```
CYS2_ARATH STANDARD; PRT; 134 AA.
ID CV52_ARATH STANDARD; PRT; 384 AA.
AC Q03529;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inositolphosphorylceramide-B C-26 hydroxylase (EC 1.-.-.-) (IPC-B
DE hydroxylase).
GN SCS7 OR FAH1 OR YMR272C OR YMR156.14C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jags K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RN Nature 387:90-93 (1997).
RL [2]
RP CHARACTERIZATION.
RX MEDLINE=98220296; PubMed=9559540;
RA Dunn T.M., Haak D., Monaghan E., Bealer T.J.;
RT "Synthesis of monohydroxylated inositolphosphorylceramide (IPC-C) in
RT Saccharomyces cerevisiae requires SCS7p, a protein with both a
RT cytochrome b5-like domain and a hydroxylase/desaturase domain."
RL Yeast 14:311-321 (1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98019193; PubMed=9353282;
RA Mitchell A.G., Martin C.E.;
RT "Fahp, a Saccharomyces cerevisiae cytochrome b5 fusion protein, and
RT its Arabidopsis thaliana homolog that lacks the cytochrome b5 domain
RT both function in the alpha-hydroxylation of sphingolipid-associated
RT very long chain fatty acids."
RL J. Biol. Chem. 272:28281-28283 (1997).
CC -!- FUNCTION: INVOLVED IN THE ALPHA-HYDROXYLATION OF SPHINGOLIPID-
CC ASSOCIATED VERY LONG CHAIN FATTY ACIDS. HYDROXYLATES THE C26-FATTY
CC ACID OF INOSITOLPHOSPHORYLCERAMIDE-B (IPC-B) TO FORM IPC-C.
CC -!- COFACTOR: IRON (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -----
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CC -----
DR EMBL; 249260; CAA89255.1; -
DR PIR; S54484; S54484.
DR HSSP; P04166; 1EUE.
DR SGD; S0004985; SCS7.
DR GO; GO:0005783; C: endoplasmic reticulum; IMP.
DR GO; GO:0016491; F: oxidoreductase activity; IMP.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR006087; Sterol_desat.
DR Pfam; PF04116; FA hydroxylase; 1.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRODOM; PD000612; Cyt_B5_1.
DR PROSITE; PS00191; CYTOCHROME_B5_2; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Oxidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
DR Transmembrane; Endoplasmic reticulum; Heme.
KW SCS7_YEAST

CY52_ARATH STANDARD; PRT; 134 AA.
ID CV52_ARATH STANDARD; PRT; 134 AA.
AC Q4875;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cytochrome b5 isoform 2.
GN AT2G32720 OR F24L7.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Unayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Bisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768 (1999).
CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; AC003974; AAC04491.1; -
DR PIR; T00796; T00796.
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRODOM; PD000612; Cyt_B5_1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;

Query Match 5.8%; Score 141; DB 1; Length 134;
Best Local Similarity 33.08; Pred. No. 7.2e-05;
Matches 35; Conservative 15; Mismatches 34; Indels 22; Gaps 3;

Qy 21 PSWEIQKHLRTSGVIGPRKVNITKWSIQHPGQGVVGHVAGEDATDAFRAHPDLE 80
Dy 8 FTLSVEHNGQDCWIVNGKVNITKFLSDHPGDDVLLSSTGKDADT-----DFE 60
Qy 81 FVG-----KFLKLLGLGELAP-----EEPSQDHGKNSKITE 111
Dy 61 DVGHSGSAREMNEQYVGEIDFTTIPKKVYTPPKQPHYNQDKTSE 106

RESULT 27
SCS7_YEAST
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FT DOMAIN 1 90 HEME-BINDING.
FT TRANSNM 197 217 POTENTIAL.
FT TRANSNM 223 243 POTENTIAL.
FT TRANSNM 298 318 POTENTIAL.
FT TRANSNM 353 373 POTENTIAL.
FT METAL 45 45 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 70 70 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 384 AA; 44881 MW; DF4BA5F2E0EA2218 CRC64;

Query Match 5.8%; Score 141; DB 1; Length 384;
Best Local Similarity 21.2%; Pred. No. 0.00025;
Matches 88; Conservative 59; Mismatches 139; Indels 130; Gaps 18;

QY 21 FSWEEIQKHLRTDGLVI--DRKVYITTKWSIQHPGQORVIGHAGEDATDAFR--AFHP 77
DB 12 FSKTVQEHNTANDCWYQNRKLYDTRFLSEHPGDSILDYACKDITEIMKDSVHE 71
QY 78 DLBFVGKFLK-PLILGELAPEE-----PSQDGHGKSKTDFRALRKT----- 119
DB 72 HSDSAVEILEDEVILGYLATDEEAARLLTNKHKVEVQLSADGTEFDSTTFVKELPAEEK 131
QY 120 ---AEDNMLFKTHVRFLL---LLAHITIALESIAWTFVF-----YFGNGWI 159
DB 132 LSIATDVSNDYKXKHFLLDNRPLMLQLLRSDPKDFYDQIHRPRHYGKSAPLFGNFILE 191
QY 160 PTLITAFVLATSOQAQGLQHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNRHFQ 219
DB 192 PLTKTAWWV---VPVAWLPVAVYHMGVALK--NNNQLFACFLF----- 229
QY 220 HXAPNFIHKDPDYNMLHVFVLGHWQPIEXGKKL-----KYLPLYNH--QHEVFFFLIGPP 272
DB 230 -----CVGVFV---WTLEIGHLRFHFDDWLPESNIAFATHFLHGCH 271
QY 273 LLIPMFQYQIIMTVHKWVLDLAWAVSYIRFFIYIPFYIGLALL----- 321
DB 272 HYLEFM-DKYLVMPEPL-----FVILCAPFYKLVPFALLPLYWAYAGFAG 314
QY 322 -FLAFIRLESHWV-----WYQNMHIVMEIDQAYR-----DWFSQLTAT 363
DB 315 GLFGVVCYDECHFFLHHSKLPPFRMKLKKYHLEHHYKNYQLGFGVTSWFWDEVGT 370

RESULT 28
NIA2 ARATH STANDARD; PRT; 917 AA.
AC P11035;
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
GN NIA2 OR CHL3 OR AT1G37130 OR F28122.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=88276888; PubMed=3393528;
RA Crawford N.M., Smith M., Bellissime D., Davis R.W.;
RT "Sequence and nitrate regulation of the Arabidopsis thaliana mRNA
RT encoding nitrate reductase, a metalloflavoprotein with three
RT functional domains."
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

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RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzalli A.,
RA Miltitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the Plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
RP [3]
RP SEQUENCE OF 522-917 FROM N.A.
RX MEDLINE=89091069; PubMed=2905260;
RA Cheng C., Dewdney J., Nam H., den Boer B.G.W., Goodman H.M.;
RT "A new locus (NIA 1) in Arabidopsis thaliana encoding nitrate
RT reductase."
RL EMBO J. 7:3309-3314(1988).
RP [4]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=93005711; PubMed=1840922;
RA Wilkinson J.Q., Crawford N.M.;
RT "Identification and characterization of a chlorate-resistant mutant
RT of Arabidopsis thaliana with mutations in both nitrate reductase
RT structural genes NIA1 and NIA2."
RL Mol. Gen. Genet. 239:289-297(1993).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: ROOT, LEAF, AND SHOOT.
CC -!- MISCELLANEOUS: WHEN MUTATED CONFERS RESISTANCE TO THE HERBICIDE
CC CHLORATE.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC
CC EMBL; J03240; AAA32830.1; -
CC EMBL; AC007505; AAF19225.1; -
CC EMBL; X13435; CAA31787.1;
CC EMBL; S45385; -; NOT_ANNOTATED_CDS.
CC PIR; A31821; RDMUNH.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR000572; Euk_Mb-oxred.
CC InterPro; IPR001709; FPN_Cyt_redctse.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).

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DR InterPro: IPR001221; Phe hydroxylase.
DR Pfam: PF00970; FAD binding_6; 1.
DR DR Pfam: PF00173; heme 1; 1.
DR DR Pfam: PF03404; Mo-co dimer; 1.
DR DR Pfam: PF00175; NAD binding_1; 1.
DR DR Pfam: PF00174; oxidoreductase; 1.
DR DR PRINTS: PR00406; CYT5RDFASE.
DR DR PRINTS: PR00363; CYTOCHROMES.
DR DR PRINTS: PR00407; EUMOPTERIN.
DR DR PRINTS: PR00371; PNCR.
DR DR PRINTS: PR00410; PHEVDRLASE.
DR DR PRODOM: PD000612; Cyt B5; 1.
DR DR PROSITE: PS00191; CYTOCHROME B5_1; 1.
DR DR PROSITE: PS00255; CYTOCHROME B5_2; 1.
DR DR PROSITE: PS00559; MOLYBDOPTEIN EUK; 1.
DR KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
DR Nitrate assimilation; Multigene family; Herbicide resistance.
FT METAL 191 191 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 245 245 INTERCHAIN (POTENTIAL).
FT DISULFID 433 433 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 577 577 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 600 600 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 917 AA; 102844 MW; B8909A318C04C39A CRC64;

Query Match 5.7%; Score 139.5; DB 1; Length 917;
Best Local Similarity 22.5%; Pred No. 0.00032;
Matches 59; Conservative 35; Mismatches 86; Indels 79; Gaps 11;

QY 13 EREVSV-----TFSWBIQKHNRTDGLVDRKVNITKWSIQHPGGORVIGHYAG 65
DB 530 KKSVPFNTAKMTSMSEVKHNSGADSCWIIVGHIVDCTFLMDHPGSDSILINAG 589
QY 66 EDATDAPRAHPDLEFVGKFLKLLIGELAPEPSOD-----HG----- 104
DB 590 TDCTEEFALHSK--AKKMLEDYRIGELLITGYSSDSSPNNSVGVSAVSLAPICE 647
QY 105 -----KNSKITEDPRALR--KTAEDM--NLFKTNHVFLLLLAH 139
DB 648 ATPVRNLALNPRAKVPQVLVEKTSISHDVKRFALPVEDMVLGFPVGKHFPLCATIND 707
QY 140 IIALES-----IAWFTV---FYFG-----NGWPTLITAFVLTSAQAQGWLQ 179
DB 708 KICLRATPSTVDVGFFELVWKVIYFGVHPRPNGGLMSQYLDLPGSTLEIKGPLG 767
QY 180 H-DY---GHLSVVRKPKW 193
DB 768 HVEVLGKGSFTVHGKPKF 785

RESULT 29
FD3E ARATH STANDARD; PRT; 386 AA.
AC P48623;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).
GN FAD3 OR AT2G29980 OR F23F1.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Seedling;
RX MEDLINE=94302147; PubMed=8029334;
RA Yadav N.S., Wierzbicki A., Aegeerter M., Caster C.S., Perez-Grau L.,
RA Kinney A.J., Hitz W.D., Booth J.P. Jr., Schweiger B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldmann K.A., Pierce J., Browse J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).

[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;
RA Watahiki M.C., Yamamoto K.T.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=94345020; PubMed=8066143;
RA Nishiuchi T., Nishimura M., Arondel V., Iba K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
fatty acid desaturase from Arabidopsis thaliana.";
RL Plant Physiol. 105:767-768(1994).
[4]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rinning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
[5]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
PHOSPHOLIPIDS.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -!- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
DETECTABLE IN ROOT TISSUE.
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC
CC EMBL; I22931; AAA61778.1; -
CC EMBL; D17579; BAA04505.1; -
CC EMBL; D26508; BAA0514.1; -
CC EMBL; AC004680; AAC31854.1; -
CC EMBL; AV063966; AAL36322.1; -
CC EMBL; AV096462; AAM30102.1; -
CC F1R; JQ2335; JQ2335.
CC InterPro: IPR005804; FA_desatfam.
CC Pfam: PF00487; FA_desaturase; 1.
CC ProDom: PD001081; FA_desatfam; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 101 105 HISTIDINE BOX-1.

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CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL; M33154; AAA33114.1; -.
CC PIR; A41667; A41667.
CC HSSP; P17571; 2CND.
CC DR DR
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR000572; Euk_Mb_oxrd.
CC InterPro; IPR001709; FPN_Cyt_reductase.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molvb; 1.
CC PRINTS; PR00406; CYTB5REDTASE.
CC PRINTS; PR00363; CYTOCHROMES.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FENCR.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTEIN_EUK; 1.
CC KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
CC KW Nitrate assimilation.
CC FT METAL 195 195 MOLYBDENUM-PTERIN (POTENTIAL).
CC FT METAL 249 249 MOLYBDENUM-PTERIN (POTENTIAL).
CC FT METAL 434 434 INTERCHAIN (POTENTIAL).
CC FT DISULFID 434 434 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT METAL 578 578 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT METAL 601 601 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT METAL 601 601 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SQ SEQUENCE 918 AA; 103383 MW; A2CAFDADAIEA1B2D1 CRC64;
CC -----
CC Query Match 5.6%; Score 137.5; DB 1; Length 918;
CC Best Local Similarity 31.08; Pred. No. 0.0013;
CC Matches 39; Conservative 15; Mismatches 47; Indels 25; Gaps 3
CC -----
CC QY 5 GNOGGEAARE-----VSP-----TFSWEETQKNLRDTSGLVIDR 41
CC Db 507 GNOGSGWMDRERHLEISTEGNQLTKKSVTFPMWTASNTYTLSEVKGNHSPQSAIIIVHG 566
CC QY 42 KYVNTIKWSIQHPGQQRVIGHAGEDATDAFRAHPDLEFVGKFLKPLIGSLAPEEPSQ 101
CC Db 567 HYPDCTRLKDPHGGSDSILNAGTCTEEFDAIHSDK--AKKQLEDYRIGSLITTVAS 624
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CC QY 102 DEGKNS 107
CC Db 625 DSSNS 630
CC -----
CC RESULT 31
CC PD6C_ARATH STANDARD; PRT; 448 AA.
CC ID PD6C_ARATH STANDARD; PRT; 448 AA.
CC AC P46312; Q9M094;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DT Onega-6 fatty acid desaturase, chloroplast precursor (BC I.14.19.-).
CC GN DE O6R FADC OR AT4G30950 OR F6118.140.
CC GN Arabidopsis thaliana (Mouse-ear cress).
CC OC Arabidopsis; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Eukaryota;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 CC NCBI\_taxID=3702;  
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 CC SEQUENCE OF 1-418 FROM N.A.  
 CC STRAIN=cv. Columbia;  
 CC RX MEDLINE=20083488; PubMed=10617198;  
 CC RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
 CC RA Pohl T., Duesterhoef A., Stiekema W., Entian K.-D., Terry N.,  
 CC RA Harris B., Ansoorge W., Brand P., Grivell L., Rieger M.,  
 CC RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,  
 CC RA Kreis M., Delany M., Puigdomenech P., Watson M., Schmidheini T.,  
 CC RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
 CC RA Vos P., Heiseisel J., Zimmermann W., Wedler H., Ridley P.,  
 CC RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 CC RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,  
 CC RA Braeken M., Weljens J., Voet M., Bastiaens I., Aert R., Defoor E.,  
 CC RA Weitzenegger T., Boche G., Ransperger U., Hilbert H., Braun M.,  
 CC RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,  
 CC RA Mooljhan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,  
 CC RA Berner S., Hempel S., Feldpausch M., Lambrecht S., Van den Baele H.,  
 CC RA De Keyser A., Buyschaert C., Gielens J., Villarroel R., De Clercq R.,  
 CC RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,  
 CC RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,  
 CC RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,  
 CC RA Borkova D., Bloeker H., Schaefer M., Grimm M., Lehnert T.H.,  
 CC RA Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,  
 CC RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,  
 CC RA Neumann S., Argiriou A., Vitale D., Ligouri R., Piravandi E.,  
 CC RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
 CC RA Schnabl S., Hiller R., Glabaud G., Lecharny A., Aubourg S.,  
 CC RA Chedford T., Cooke R., Berger C., Monfort A., Casacuberta E.,  
 CC RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,  
 CC RA Perez-Perez A., Funnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 CC RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,  
 CC RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 CC RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,  
 CC RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
 CC RA Senkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 CC RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 CC RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
 CC RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 CC RA Kraner J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,  
 CC RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,  
 CC RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
 CC RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 CC RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,  
 CC RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,  
 CC RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,  
 CC RA Chen E., Marra M., Martienssen R., McCombie W.R.,  
 CC RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 CC RT thaliana."  
 CC RL Nature 402:769-777(1999).  
 CC (3)  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=cv. Columbia;  
 CC RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 CC RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
 CC RT SSP consortium (Salk/stanford/SGEC)."  
 CC RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC CC -!- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES  
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT  
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.  
 CC CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
 CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.  
 CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
 CC AND/OR BE INVOLVED IN METAL ION BINDING.  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 CC

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CC EMBL; U09503; AAA92800.1; -  
 CC EMBL; AL022198; CAA18198.1; -  
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 CC EMBL; AY045621; AAK73979.1; -  
 CC EMBL; AY058078; AAL24186.1; -  
 CC EMBL; AY058852; AAL24240.1; -  
 CC FIRM; D85362; D85362.  
 CC FIRM; IPR005804; FA\_desat\_fam.  
 CC FIRM; PF00487; FA\_desaturase; 1.  
 CC FIRM; PD01081; FA\_desat\_fam; 2.  
 CC KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
 CC TRANSIT peptide.  
 CC FT CHAIN 1 69 CHLOROPLAST (BY SIMILARITY).  
 CC FT DOMAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.  
 CC FT DOMAIN 171 175 HISTIDINE BOX-1.  
 CC FT DOMAIN 207 211 HISTIDINE BOX-2.  
 CC FT DOMAIN 367 371 HISTIDINE BOX-3.  
 CC SQ SEQUENCE 448 AA; 51225 NW; C3AC72FB28FE287 CRC64;  
 CC

Query Match 5.6%; Score 137; DB 1; Length 448;  
 Best Local Similarity 21.8%; Pred. No. 0.00064;  
 Matches 67; Conservative 50; Mismatches 122; Indels 58; Gaps 16;  
 QY 111 EDPRALRTAEDMNLKTNHVFLLLA-----HIATAESIATVTFYFGNGWIFLIAP 166  
 DB 122 DLKALKSVL-----ISVTSYTLGLFWIAKSPWYLLPL-----AW-----AWTGTATGF 166  
 QY 167 VLATSOAQAGWLOHDYGHLSVVRKPNHNLVHKFVGHKLGASANN-----WNHRHFQHA 222  
 DB 167 FV-----IGHCAHKSFSK-----NKLVED-IVGLAFLLPLVYFEPWFKKDRHA 212  
 QY 223 KENIFHKDPDVMNLHVFLGEMQPI---EYKKKLKLFLYNHQHEFFLIGP--PLL--- 274  
 DB 213 KTNMLVHDT-----AMQVPPEFESSPW-----RKALIFGYGIRPWLSTA 255  
 QY 275 --IPMYFQOIINTWLVKQWDLAWASYIRFITTYIPFYGILGALLFLNFIRFLESH 332  
 DB 256 HWYNWHFNLKPRASEVNRVKISLACVAFMAVGMPILVYKVGILGWKFW-LMPWLGYH 314  
 QY 333 -FVWVTOMNHVMEIDQAYRDW--FSSQLTATCNVEGFFNDWFSGLHNFQIEHHLFP 389  
 DB 315 FWMSTITWVHTAPHFPKPADEWNAQAQLNGTVHCDYPSYIEILCHDINVHIPHISP 374  
 QY 390 TMRPHNL 396  
 DB 375 RIPSYNL 381  
 RESULT 32  
 CYS1\_SCHPO STANDARD; PRT; 124 AA.  
 ID CYS1\_SCHPO  
 AC O94351;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable cytochrome b5 1.  
 GN SPEC9A10.16C.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Guillermo R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leathers S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,  
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
RA "The genome sequence of Schizosaccharomycetes pombe";  
RT Nature 415:871-880(2002).  
CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron  
CC carrier for several membrane bound oxygenases (By similarity).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE  
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
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CC  
CC EMBL; AL034463; CAA22444.1; -;  
CC F1R; T40071; T40071.  
CC HSP; P04166; 1EUE.  
CC GeneDB:SPombe; SPBC29A10.16G; -;  
CC InterPro; IPR001199; Cyt B5.  
CC Pfam; PF00173; heme\_1; 1-  
CC PRINTS; PR00363; CYTOCHROMES.  
CC ProDom; PD000612; Cyt\_B5; 1.  
CC PROSITE; PS0255; CYTOCHROME\_B5\_2; 1.  
CC Electron transport; Transmembrane; Heme; Iron; Microsome.  
KW TRANSMEM 100 120 POTENTIAL.  
FT METAL 38 38 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
FT METAL 62 62 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 124 AA; 13910 MW; 299D12CB693831D4 CRC64;  
Query Match 5.6%; Score 136.5; DB 1; Length 124;  
Best local Similarity 31.8%; Pred. No. 0.00016;  
Matches 42; Conservative 24; Mismatches 49; Indels 17; Gaps 4;  
QY 16 VSVPTSWIEIOKHLRTSGLVDRKYNITKWSIQHPGQGVICHYAGEDATDAFRAF 75  
DB 1 MSVKYEPPEIVEHNNSKQWYINGKVDVSNFADHFGGLDMLDYAQDTRAYQDI 60  
QY 76 HPDLFVGKPLKLLIGELAPEPSQDHQKNSKITEFDRLAKRTAEDMNLFTNHFVILL 135  
DB 61 GHSIA-ADELLEEMYGDLKP-----GTEERLKE-----LKKPRS-----FDNTPPLP 103

QY 136 LLAHIIIALESIA 147  
DB 104 LLAIVIVPAIA 115

RESULT 33  
FD3D ARATH STANDARD; PRT; 435 AA.  
ID FD3D ARATH STANDARD; PRT; 435 AA.  
AC P48622;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast  
DE Precursor IEC 1.14.19.-.  
GN FAD8 OR ATSG0580 OR MOP10.12.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Aerial parts;  
RX MEDLINE=95148742; PubMed=7846164;  
RA Gibson S., Aronoff V., Iba K., Somerville C.R.;  
RT "Cloning of a temperature-regulated gene encoding a chloroplast  
RT omega-3 desaturase from Arabidopsis thaliana";  
RL Plant Physiol. 106:1615-1621(1994).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;  
RA Watanabe M.C., Yamamoto K.T.;  
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=97471969; PubMed=9330910;  
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
RA Miyajima N., Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
RT features of the 1.6 Mb regions covered by twenty physically assigned  
RT clones";  
RL DNA Res. 4:215-230(1997).  
CC -!- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES  
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY  
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT  
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
CC ESTERIFIED TO GALACTOLIPIDS. SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.  
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
CC -!- INDUCTION: BY LOW TEMPERATURE.  
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
CC AND/ OR BE INVOLVED IN METAL ION BINDING.  
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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CC  
CC EMBL; L27158; AAA65621.1; -;  
CC EMBL; U08216; AAB60302.1; -;  
CC EMBL; D17578; BAA04504.1; -;  
CC EMBL; AB005241; BAB11547.1; -;  
CC InterPro; IPR005804; FA desat fam.  
CC Pfam; PF00487; FA desaturase; 1.  
CC ProDom; PD001081; FA desat fam; 2.  
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
KW Transit peptide.



RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Glasser K.,  
RA Fuster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.C., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Moutkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,  
RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Renington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Scapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.,  
RA "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review".  
RA Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RL MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Battencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.,  
RA "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review".  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
CC OXYGENASES (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE  
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
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CC -----  
CC EMBL; AB003840; AAF59233.3; -  
CC HSSP; P00171; 1WDB.  
CC FlyBase; FBgn0031189; Cyt-b5.  
CC InterPro; IPR001199; Cyt B5.  
CC Pfam; PF00173; heme\_1; 1.  
CC PRINTS; PR00363; CYTOCHROME B5.  
CC ProDom; PD000612; Cyt\_b5; 1.  
CC PROSITE; PS00191; CYTOCHROME B5\_2; 1.  
CC PROSITE; PS02055; CYTOCHROME B5\_2; 1.  
CC Electron transport; Transmembrane; Heme; Iron; Microsome.  
CC TRANSMEM 111 131 POTENTIAL.  
CC FT METAL 41 41 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC -----

SQ SEQUENCE 134 AA; 15206 MW; 11D1FB03EFAB40DC CRC64;  
Query Match 5.5%; Score 133.5; DB 1; Length 134;  
Best Local Similarity 36.5%; Pred. No. 0.0003; Mismatches 27; Indels 13; Gaps 2;  
Matches 31; Conservative 14;  
QY 20 TFSWEIQTQKHNRTDSGLVIDKVNITKWSIQHFGQGVVGHYAGEDATAFRAHPDL 79  
DB 8 TTFRAEVAKENTKDTWLLJHNNIVDTAFLEHFGGEEVLIEQAGKDATENF----- 60  
QY 80 EFVG-----KFLKPLLIIGELAPER 98  
DB 61 EDVGHNSNDARDMMKXYKIGELVESE 85  
RESULT 36  
FD3E PHAAU STANDARD; PRT; 380 AA.  
ID \_FD3E PHAAU  
AC P32291;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)  
DE (Indole-3-acetic acid induced protein ARG1).  
GN ARG1.  
OS Phaseolus aureus (Mung bean) (Vigna radiata).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
OX NCBI\_TaxID=3916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hypocotyl;  
RA Yamamoto K.T., Mori H., Inaseki H.;  
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of  
RL elongating hypocotyls of mung bean (Vigna radiata).";  
PL Plant Cell Physiol. 33:113-20(1992).  
CC -!- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES  
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,  
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE  
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER  
CC PHOSPHOLIPIDS.  
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
CC -!- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.  
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
CC AND/ OR BE INVOLVED IN METAL ION BINDING.  
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; D14410; BAA03306.1; -  
CC PIR; T10898; T10898.  
CC InterPro; IPR005804; FA desat fam.  
CC Pfam; PF00487; FA desaturase; 1.  
CC ProDom; PD001081; FA desat fam; 2.  
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;  
CC Transmembrane.  
CC TRANSMEM 59 78 POTENTIAL.  
CC TRANSMEM 208 231 POTENTIAL.  
CC TRANSMEM 238 256 POTENTIAL.  
CC DOMAIN 97 101 HISTIDINE BOX-1.  
CC DOMAIN 133 137 HISTIDINE BOX-2.  
CC DOMAIN 300 304 HISTIDINE BOX-3.  
CC FT SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;  
SQ SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;



CC N-TERMINAL DOMAIN.  
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.  
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE  
CC C-TERMINAL DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: D38219; BAA07394.1; --  
CC PIR: T08105; T08105.  
CC HSP: P17571; 2CND.  
CC InterPro: IPR001199; Cyt\_B5.  
CC InterPro: IPR001834; Cyt\_B5\_reductase.  
CC InterPro: IPR000572; Euk\_Mb\_oxred.  
CC InterPro: IPR001709; Euk\_Cyt\_redctase.  
CC InterPro: IPR005066; Mo-Co\_dimer.  
CC InterPro: IPR001433; Oxred\_FAD/NAD(P).  
CC InterPro: IPR001221; Phe\_hydroxylase.  
CC Pfam: PF00970; FAD\_binding\_6; 1.  
CC Pfam: PF00173; heme\_1; 1.  
CC Pfam: PF03404; Mo-co\_dimer; 1.  
CC Pfam: PF00175; NAD\_binding\_1; 1.  
CC Pfam: PF00174; oxidized\_molyb; 1.  
CC PRINTS: PR00406; CYTB5REDTASE.  
CC PRINTS: PR00363; CYTOCHROMEBS.  
CC PRINTS: PR00407; EUMOPTERIN.  
CC PRINTS: PR00371; EUMOPTERIN.  
CC PRINTS: PR00410; PHEHYDRLXASE.  
CC ProDom: PD000612; Cyt\_B5; 1.  
CC PROSITE: PS00191; CYTOCHROME\_B5\_1; 1.  
CC PROSITE: PS00255; CYTOCHROME\_B5\_2; 1.  
CC PROSITE: PS00559; MOLYBDOTERIN\_EUK; 1.  
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;  
CC Nitrate assimilation; Multigene family.  
CC METAL 191 191 MOLYBDENUM-PTERIN (POTENTIAL).  
CC METAL 245 245 MOLYBDENUM-PTERIN (POTENTIAL).  
CC FT METAL 430 430 INTERCHAIN (POTENTIAL).  
CC FT METAL 574 574 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC FT METAL 597 597 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC FT METAL 597 597 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC SEQUENCE 911 AA; 102252 MW; BBA4E19635E03D8C CRC64;  
  
CC Query Match 5.4%; Score 131.5; DB 1; Length 911;  
CC Best Local Similarity 27.6%; Pred. No. 0.0042;  
CC Matches 42; Conservative 20; Mismatches 61; Indels 29; Gaps 5;  
  
CC 5 GNQGG--AAREV-----SVPT-----FSWEEIOKHLRTDSGLVIDR 41  
CC 503 GNQGGWMAKERQIEKSESHTLKSVSTFFWNTASKYMSGEVRKHSABSAWIIHG 562  
  
CC 42 KVNITKWSIQHPGQGVIGHYAGEDATDAFRAFPDLEFVGKFLKPLIGELA-----PE 97  
CC 563 HIYDCTFLKHDPGGSILINAGTCTEETFAHSDK--AKLLEDYRIGELITTTGYDS 620  
  
CC 98 EPSQDHGKSKITDFPALAKTAEDMNLFTN 129  
CC 621 SPNVSVHGGSVMSLLAPIRQLAPTQNLWN 652  
  
CC RESULT 39  
CC CY55\_TOBAC  
CC ID -CY55\_TOBAC STANDARD; PRT; 135 AA.  
CC AC P45099;  
CC DT 01-FEB-1996 (Rel. 33, Created)  
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)  
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
CC DE Cytochrome b5, seed isoform.  
CC OS Nicotiana tabacum (Common tobacco).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
  
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
CC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.  
CC NCBI\_TaxID=40997;  
CC [1]  
CC SEQUENCE FROM N.A.  
CC STRAIN=cv. Samsun; TISSUE=Seed;  
CC MEDLINE=9609039; PubMed=7580860;  
CC Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;  
CC "Isolation of a cDNA encoding a cytochrome b5 specifically expressed  
CC in developing tobacco seeds.";  
CC Planta 197:200-202(1995).  
CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH  
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND  
CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY  
CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN  
CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE  
CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE  
CC LIPIDS.  
CC -!- SUBCELLULAR LOCATION: MICROSMAL MEMBRANE. BOUND TO THE  
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).  
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEEDS.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.  
CC -----  
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CC -----  
CC EMBL: X80008; CAA56318.1; --  
CC PIR: S49200; S49200.  
CC HSP: P00171; LCYO.  
CC InterPro: IPR001199; Cyt\_B5.  
CC Pfam: PF00173; heme\_1; 1.  
CC ProDom: PD000612; Cyt\_B5; 1.  
CC PROSITE: PS00191; CYTOCHROME\_B5\_1; 1.  
CC PROSITE: PS00255; CYTOCHROME\_B5\_2; 1.  
CC Electron transport; transmembrane; Heme; Iron; Microsome;  
CC Multigene family.  
CC TRANSMEM 107 127 POTENTIAL.  
CC FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC SEQUENCE 135 AA; 14869 MW; A36CCA081A72ECBC CRC64;  
  
CC Query Match 5.4%; Score 131; DB 1; Length 135;  
CC Best Local Similarity 35.0%; Pred. No. 0.00049;  
CC Matches 35; Conservative 11; Mismatches 44; Indels 10; Gaps 2;  
  
CC 21 FSWEEIOKHLRTDSGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATDAF----- 72  
CC 8 FTLAEVSHNNNAKDCWLIISKVYNTKFLDHPGGGVLLSATGKATDDFDIGHSSS 67  
  
CC 73 -RAFPDLEFVGKFLKPLIGELAPEPSQDHGKNSKITE 111  
CC 68 ARAM-LDEYVYVDIDSSITPTKVKYTPPKQPHYNQDKTTE 106  
  
CC RESULT 40  
CC NIA\_CICIN  
CC ID NIA\_CICIN STANDARD; PRT; 920 AA.  
CC AC P43101;  
CC DT 01-NOV-1995 (Rel. 32, Created)  
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
CC DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).  
CC NIA.  
CC GN Cichorium intybus (Chicory).  
CC OS Cichorium intybus (Chicory).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
CC Asteridae; campanulids; Asterales; Asteraceae; Cichorioideae;  
CC Cichorieae; Cichorium.

OX NCBI\_TaxID=13427;  
RN [1]\_SEQUENCE FROM N.A.  
RP STRAIN=cv. Witloof; TISSUE=Leaf, and Root;  
RC MEDLINE=97141273; PubMed=8987617;  
RA Palms B.; Goupil P.; de Almeida Engler J.; Van der Straeten D.;  
RX Van Montagu M.; Rambour S.;  
RA "Evidence for the nitrate-dependent spatial regulation of the nitrate  
RT reductase gene in chicory roots.";  
RL Planta 200;20-27(1996).  
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first  
CC step of nitrate assimilation in plants, fungi and bacteria.  
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.  
CC -!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,  
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME  
CC GROUP IS CALLED CYTOCHROME B-557.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- TISSUE SPECIFICITY: In cortical cells of roots grown at low  
CC nitrate concentrations, in vascular tissues of roots at high  
CC nitrate concentrations and in root apex under both conditions.  
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE  
CC N-TERMINAL DOMAIN.  
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.  
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE  
CC C-TERMINAL DOMAIN.  
CC -----  
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CC -----  
CC EMBL; X84103; CAA58909.1; -;  
CC EMBL; X84102; CAA58908.1; -;  
CC PIR; S52301; S52301.  
CC HSP; P17571; 2CND.  
DR InterPro; IPR001199; Cyt\_B5.  
DR InterPro; IPR001834; Cyt\_B5\_reductase.  
DR InterPro; IPR000572; Euk\_Mb\_Oxred.  
DR InterPro; IPR001709; FPN\_cyt\_reductase.  
DR InterPro; IPR005066; Mo-Co\_dimer.  
DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam; PF00970; FAD\_binding\_6; 1.  
DR Pfam; PF00173; heme\_1; 1.  
DR Pfam; PF03404; Mo-Co\_dimer; 1.  
DR Pfam; PF00175; NAD\_binding\_1; 1.  
DR Pfam; PF00174; oxidored\_molyb; 1.  
DR PRINTS; PR00406; CYTB5RD7ASE.  
DR PRINTS; PR00363; CYTOCHROMEBS.  
DR PRINTS; PR00407; EUMOPTERIN.  
DR PRINTS; PR00371; FPNCR.  
DR PRODOM; PD000612; Cyt\_B5; 1.  
DR PROSITE; PS00191; CYTOCHROME\_B5\_1; 1.  
DR PROSITE; PS0255; CYTOCHROME\_B5\_2; 1.  
DR PROSITE; PS00559; MOLYBDOPTERIN\_EUK; 1.  
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;  
KW Nitrate assimilation.  
FT METAL 185 185 MOLYBDENUM-PTERIN (POTENTIAL).  
FT METAL 239 239 MOLYBDENUM-PTERIN (POTENTIAL).  
FT DISULFID 424 424 INTERCHAIN (POTENTIAL).  
FT METAL 569 569 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
FT METAL 592 592 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 920 AA; 103519 MW; FE1E332CC9A4D58 CRC64;  
  
Query Match 5.4%; Score 131; DB 1; Length 920;  
Best Local Similarity 29.3%; Pred. No. 0.0047;  
Matches 41; Conservative 15; Mismatches 48; Indels 36; Gaps 5;  
  
OY 5 GNQGGAAERE-----VSP-----TFSWEEIQGNLRTDGLVID 40  
DB 497 GNQGGWAKREKHLIEISSELAHPTLKSVSPFPMNTLSLTFTTSEVKGNHNSADSAMIVVH 556

OY 41 RKVYNITKMSIOHPGGORVIGHYAGEDATDAPRAHPDLEFVGKFKPLLLIGEL----- 94  
DB 557 GHIDCTSFVKDHPGSDSILLNAGTDCTEEDAIHSDK--AKGLLEEVYVGLITMGYS 614  
OY 95 ---APEEPSQD-HGKNSKIT 110  
DB 615 SDSAASSPNNNSVHGATNYLT 634

Search completed: December 9, 2003, 10:18:08  
Job time : 19 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 10:16:46 ; Search time 21 seconds  
(without alignments)  
2033.281 Million cell updates/sec

Title: US-09-719-601-5

Perfect score: 2438

Sequence: 1 MGKGGNQGGAAREVSVPT.....DIIRSLKSKGLWLDAYLHK 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID     | Description              |
|------------|-------|---------------|--------|--------|--------------------------|
| 1          | 2425  | 99.5          | 444    | T13155 | linoleoyl-CoA desaturase |
| 2          | 2190  | 99.8          | 444    | J00180 | Delta6 fatty acid        |
| 3          | 453.5 | 18.6          | 458    | S68358 | Delta8 sphingolip        |
| 4          | 431.5 | 17.7          | 449    | A84900 | hypothetical prote       |
| 5          | 426.5 | 17.5          | 449    | T47950 | delta-8 sphingolip       |
| 6          | 422.5 | 17.3          | 449    | T50555 | delta-8 sphingolip       |
| 7          | 371.5 | 15.2          | 473    | T26280 | linoleoyl-CoA desaturase |
| 8          | 366.5 | 15.0          | 447    | T43319 | Delta5 fatty acid        |
| 9          | 356   | 14.6          | 454    | H88791 | protein fl32.1 [1        |
| 10         | 347.5 | 14.3          | 523    | UC7556 | linoleoyl-CoA desaturase |
| 11         | 277.5 | 11.4          | 345    | T36617 | probable Delta6 fa       |
| 12         | 245.5 | 8.6           | 368    | S54809 | linoleoyl-CoA desaturase |
| 13         | 210   | 8.6           | 359    | S35157 | Delta6 fatty acid        |
| 14         | 173   | 7.1           | 134    | CB05   | cytochrome b5, mic       |
| 15         | 172   | 7.1           | 134    | CBP5   | cytochrome b5, mic       |
| 16         | 170   | 7.0           | 370    | B33034 | conserved hypothe        |
| 17         | 169.5 | 7.0           | 134    | CBR5   | cytochrome b5, mic       |
| 18         | 164   | 6.7           | 133    | CBH5   | cytochrome b5, mic       |
| 19         | 160   | 6.6           | 134    | CBRT5  | cytochrome b5, mic       |
| 20         | 159   | 6.5           | 134    | CBH5   | cytochrome b5, mic       |
| 21         | 158.5 | 6.5           | 98     | JN0316 | cytochrome b5, ery       |
| 22         | 158   | 6.5           | 573    | S06600 | L-lactate dehydrog       |
| 23         | 157.5 | 6.5           | 98     | J05783 | cytochrome b5, ery       |
| 24         | 156   | 6.4           | 427    | G70590 | probable desA3 pro       |
| 25         | 155.5 | 6.4           | 351    | S54259 | Delta12 fatty acid       |
| 26         | 154.5 | 6.3           | 98     | CBH5   | cytochrome b5, ery       |
| 27         | 154.5 | 6.3           | 359    | AQ2005 | omega-3 fatty acid       |
| 28         | 153.5 | 6.3           | 881    | S25445 | nitrate reductase        |
| 29         | 150.5 | 6.2           | 87     | S07959 | cytochrome b5, mic       |

ALIGNMENTS

RESULT 1

T13155  
linoleoyl-CoA desaturase (EC 1.14.19.3) [validated] - human  
N;Alternate names: Delta6 fatty acid desaturase; protein DRFZp586C201.1  
C;Species: Homo sapiens (man)  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 03-Jun-2002  
C;Accession: T13155; T08765  
R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D.  
J. Biol. Chem. 274, 471-477, 1999  
A;Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase  
A;Reference number: Z17612; M0ID:99085046; PMID:9967867  
A;Accession: T13155  
A;Status: preliminary; translated from GB/EMBL/DBSJ  
A;Molecule type: mRNA  
A;Residues: 1-444 <CHO>  
A;Cross-references: EMBL:AF126799; NID:G4406527; PID:G4406528; PIDN:RAD20018.1  
R;Nambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, March 1999  
A;Reference number: Z16471  
A;Accession: T08765  
A;Molecule type: mRNA  
A;Residues: 'RTG', 138-428, 'D', 430, 'M', 432-444 <WAM>  
A;Cross-references: EMBL:AL050118  
A;Experimental source: adult uterus; clone DRFZp586C201  
C;Genetics:  
A;Gene: GDB: FADSD6  
A;Cross-references: GDB: 9956652  
A;Note: DRFZp586C201.1  
C;Superfamily: cytochrome b5 core homology  
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid; binding site: heme iron (His) (axial ligands) #status predicted  
F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted  
  
Query Match 99.5%; Score 2425; DB 2; Length 444;  
Best Local Similarity 99.5%; Pred. No. 2.3e-197;  
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MGKGGNQGGAAREVSVPTSWERIQXHNLTDSGLVIDRKVYNTKWSIQHPGQQRVI 60  
DB 1 MGKGGNQGGAAREVSVPTSWERIQXHNLTDSGLVIDRKVYNTKWSIQHPGQQRVI 60  
  
QY 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLIGELAPEPSQDHGKNSKITEDFRALRKTA 120  
DB 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLIGELAPEPSQDHGKNSKITEDFRALRKTA 120  
  
QY 121 EDNMLFKTNHVFLLLAHIALESIAFTVYFGNGHPIPLITAFVLATSOAQAGNLQH 180  
DB 121 EDNMLFKTNHVFLLLAHIALESIAFTVYFGNGHPIPLITAFVLATSOAQAGNLQH 180  
  
QY 181 DYGHLSVVRKPKWNHNVKHFVIGHLKGASANNWNRHFRQHHAKPNIHKDPDNNMLHFV 240  
DB 181 DYGHLSVVRKPKWNHNVKHFVIGHLKGASANNWNRHFRQHHAKPNIHKDPDNNMLHFV 240

QY 241 LGWQPIEYGGKKLKYLPNNHSHYEFLLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
 Db 241 LGWQPIEYGGKKLKYLPNNHSHYEFLLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
 QY 301 SYIRFFIYIPFYGILGALLFLNFRFLESFHWFWVVTQNMHI VMEIDQAYRDWFSQ 360  
 Db 301 SYIRFFIYIPFYGILGALLFLNFRFLESFHWFWVVTQNMHI VMEIDQAYRDWFSQ 360  
 QY 361 TATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKS LCAKGGIEYQEKPL 420  
 Db 361 TATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKS LCAKGGIEYQEKPL 420  
 QY 421 RALLDIIRSLKSGKLMDAYLHK 444  
 Db 421 RALLDIIRSLKSGKLMDAYLHK 444

RESULT 2  
 JG0180  
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 21-Jul-2000  
 C:Accession: JG0180  
 R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.  
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999  
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase  
 A:Reference number: JG0180; MUID:99160394; PMID:10049752  
 A:Accession: JG0180  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-444 <AKI>  
 A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAA75496.1; PID:g4514722  
 C:Superfamily: cytochrome b5 core homology  
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthesis  
 F:16-94/Domain: cytochrome b5 core homology <CB5>  
 F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 89.8%; Score 2190; DB 2; Length 444;  
 Best Local Similarity 87.8%; Pred. No. 1.8e-177;  
 Matches 390; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGKGGNGEAGAAEVSVPFSEIEQKHLRTDGLVIDRKYNITKWSIQHPGQORVI 60  
 Db 1 MGKGGNGEAGSTLQAPMPTFRNEEQKHLRTDRLVIDRKYNITKWSIQHPGHRVI 60  
 QY 61 GHYAGEDATDAFRAHPDLEFVGKFLKPLIGELAPEEPSQDHGKNSKITEDFRALR 120  
 Db 61 GHYSGEDATDAFRAHLDLDFVGKFLKPLIGELAPEEPSLDRGKSSQITEDFRALK 120  
 QY 121 EDNMLFNTNHFVFLILAHIIALESIAFWFVFGNGWPTLTITAFVLTSAQAAGWLQ 180  
 Db 121 EDNMLFNTNHFVFLILSHIIVESIAFWFVFGNGWPTLTITAFVLTSAQAAGWLQ 180  
 QY 181 DYGLSVYRKPKNNHLVHKFVIGHLKGASANNWNRHFFQHAKPNIFHKDPDVMMLHVF 240  
 Db 181 DYGLSVYKKSINWNIHVKEFVIGHLKGASANNWNRHFFQHAKPNIFHKDPDVKSLHVF 240  
 QY 241 LGWQPIEYGGKKLKYLPNNHSHYEFLLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
 Db 241 LGWQPIEYGGKKLKYLPNNHSHYEFLLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAV 300  
 QY 301 SYIRFFIYIPFYGILGALLFLNFRFLESFHWFWVVTQNMHI VMEIDQAYRDWFSQ 360  
 Db 301 SYIARFFIYIPFYGILGALLFLNFRFLESFHWFWVVTQNMHI VMEIDLDHVRDWFSSQ 360  
 QY 361 TATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKS LCAKGGIEYQEKPL 420  
 Db 361 AATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLVKS LCAKGGIEYQEKPL 420  
 QY 421 RALLDIIRSLKSGKLMDAYLHK 444  
 Db 421 RALLDIIVSLKSGKLMDAYLHK 444

## RESULT 3

S68358  
 Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower  
 C:Species: Helianthus annuus (common sunflower)  
 C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jul-2000  
 C:Accession: S68358  
 R:Sperling, P.; Schmidt, H.; Heinz, E.  
 Eur. J. Biochem. 232, 798-805, 1995  
 A:Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desaturase  
 A:Reference number: S68358; MUID:96028121; PMID:7588718  
 A:Accession: S68358  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-458 <SPE>  
 A:Cross-references: EMBL:X87143; NID:G1040728; PIDN:CAA60621.1; PID:G1040729  
 C:Superfamily: cytochrome b5 core homology  
 C:Keywords: heme; iron; metalloprotein; oxidoreductase  
 F:16-90/Domain: cytochrome b5 core homology <CB5>  
 F:51,74/Binding site: heme iron (His) (axial ligands) #status predicted

## Query Match

Best Local Similarity 18.6%; Score 453.5; DB 2; Length 458;  
 Matches 124; Conservative 68; Mismatches 179; Indels 77; Gaps 12;

QY 24 BEIQKHLRTDGLVIDRKYNITKWSIQHPGQORVIGHYAGEDATDAFRAHP----- 77

Db 22 KELKKNPNNDLMTSILGKYNVTEWAKHPGGDAPLINLAGQDVTDAFIAHPGTAWKH 81

QY 78 -DLFVGVKFLKPLIGELAPEEPSQDHGKNSKITEDFRALRKTAEOMNLFKTNHVFLL 136

Db 82 LDKLFTGYHLKDVQV-----SDISRYRKLASEFAKAGFEKKGHGVYS 126

QY 137 LAHTIALESIAFWFVFGNGWPTLTITAFVLTSAQAAGWLQDVGHLGVYRKPKNNHL 196

Db 127 LCFVSLLSACVGVLYSGSFWI-HMLSGAILGLAWMQIAYLGDHAGHYQMATRGWKF 185

QY 197 VHKFVIGHLKGASANNWNRHFFQHAKPNIFHKDPDVMMLHVF-----VLGEWQPIEY 251

Db 186 AGIFGNCITGISTAWKWTNNAHNAACNSLDYDPLQHLPLMLAVSKLNSITSFYG- 244

QY 252 KKLKYL-----VNHQHEYFLLIGPPLIPMYFOYQIIMTMIVHKWVDLAWAVSYIRF 306

Db 245 RQLFDFELARFVSYQHYLYVPMCVARNLYL--QTILLISKRK----- 288

QY 307 FITVFPYG--IICALLFLNFIREFSHWFV-----VTQNMHI VMEIDQ--- 349

Db 289 ----IPDRGNILGTLIFWTWFLVSRLENPNWPERVAVLVSCVTGIQIQTINHFSG 344

QY 350 EAY-----RDWSSQLTATCNVQSFNDWFSGHNLFOIEHLLFPTMPRHNLKIAPLV 403

Db 345 DVVYVPPKGDWFEKQTRGTIDTACSSMDWFFGGLQFQLEHLLFPLRPLRSLRISPIC 404

QY 404 KSLCAKGGIEYQEKPLRALLDIIRSLK 431

Db 405 RELCKKNLPYVSLVSFDVANDVTLKTLR 432

## RESULT 4

A84900  
 Hypothetical protein At2g46210 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: A84900

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

meus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84900

A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-449 <STO>  
A:Cross-references: GB:AE002093; NID:g3702328; PIDN:AA62885.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g46210  
A:Map position: 2

Query Match 17.7%; Score 431.5; DB 2; Length 449;  
Best Local Similarity 28.0%; Pred. No. 1.1e-28;  
Matches 124; Conservative 72; Mismatches 184; Indels 63; Gaps 15;

QY 24 BEIQKHNRTDGLVIDRKVNITKWSIOHPGQORVIGHYAGEDATDAFRPHPLDFVFG 83  
DB 13 EDLKKNKPGDLWISIQGVYDVSQVAKSHPGGEAAILNLAQDQVDTDAFIAYHFGTAW-- 70  
QY 84 KFLKPLLIGELAPEEPSQDHGKSNKITEDFRALRKTAEADNLF-KTNHVFVFLLLAHIA 142  
DB 71 HLEKLNHYHV-----RDH-HVSDVSDYRRLAAEFKRGGLFDKKGHTVLTTCVGVM 124  
QY 143 LESIAWTFVFGNGWITPLITAFVLATSOAQAGLQHDYGHLSYRKPKNHLVHKFVI 202  
DB 125 LAANL-YGVLAQTSIW-AHLISAVLLGLLWISAVYGHDSGHYTVTSTKPCNKLIQLLSG 182  
QY 203 GHLKASANNWNRHFQHKAKENIFHKDPDYNMLHVFVL-----GEWQPIEYGGKKLYL 257  
DB 183 NCLTGISIAWKNWNAHIAACNSLDHDPDQHIPIFAVSTKFNMTSRFYG-RKLTFD 241  
QY 258 P-----YNHOHEYFFLIGPPLIPMYFOYQIIM-----TMIVHKNNVDL-- 296  
DB 242 PLARELISYQHWTFYPMVCGVGRINLFITQTELLFSKRVHVPDRALNIAGILVFWTFPLLV 301  
QY 297 AWAVSYIRFFITYIPFYGILGALLFLNFIREFLESWFVWQNMHIVMEIDQAY----- 352  
DB 302 SFLPNQERFIYVVSF-----AVTAIOHQVFC-----LNHFAADV-----YTGPP 342  
QY 353 --RDVSSQLTATCNVEOSFFNDFSGHLNFIQIEHLEFPTPRNHLKIAPIVLKSLCAKH 410  
DB 343 NGNDWFEXQTAGTLDISCRSFMDFGGLQFQLEHHLFPLRCHLRTVSPVVKELCKKH 402  
QY 411 GIEYQEKPLLRALLDIIRSLKKS 433  
DB 403 NLPYRSLSWNEANVTIRTKNA 425

RESULT 5  
T47950  
delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana  
N:Alternate names: protein F2A19.180  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Sep-2000  
C:Accession: T47950; T51848  
R:De Haan, M.; Maatse, A.C.; Grivelli, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.P.X.; Quer  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: 224480  
A:Accession: T47950  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-449 <DEH>  
A:Cross-references: EMBL:AL132962; PIDN:CAE71088.1  
A:Experimental source: cultivar Columbia; BAC clone F2A19  
R:Spelling, P.; Zaehring, U.; Heinz, E.  
J. Biol. Chem. 273, 28590-28596, 1998  
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome  
A:Reference number: 222986; MUID:99003197; PMID:9786850  
A:Accession: T51848  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-449 <SPE>  
A:Cross-references: EMBL:AJ224161; PIDN:CAA11858.1  
A:Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots  
C:Genetics:  
A:Gene: slid  
A:Map position: 3

A>Note: F2A19.180  
C:Function:  
A:Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, MUID:9900319  
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 17.5%; Score 426.5; DB 2; Length 449;  
Best Local Similarity 25.8%; Pred. No. 3e-28;  
Matches 118; Conservative 70; Mismatches 174; Indels 95; Gaps 14;

QY 24 BEIQKHNRTDGLVIDRKVNITKWSIOHPGQORVIGHYAGEDATDAFRPHPLDFVFG 77  
DB 13 EDLKKNKPGDLWISIQGVYDVSQVAKSHPGGEAAILNLAQDQVDTDAFIAYHFGTAWH 72  
QY 78 -DLIEVGFELKPLLIGELAPEEPSQDHGKSNKITEDFRALRKTAEADNLF-KTNHVFVFLLLAHIA 131  
DB 73 LDHLFTGYHIDPQV-----SEVSRDYRMAAEFRKGLGFENKGHVTLTY 117  
QY 132 -----FFLLLAHIIAIESIAWTFVFGNGWITPLITAFVLATSOAQAGLQHDYGH 185  
DB 118 LAFVAAMFLGVYGLVLAQTSV-----FAHQIAAALLGLLWISAVYGHDSGHY 165  
QY 186 SVYRKPKNHLVHKFVIGHLKASANNWNRHFQHKAKENIFHKDPDYNMLHVFVLG-- 242  
DB 166 VINSKSYNRFPAQLLSGNCITGISIAWKNWNAHIAACNSLDYDPLQHIPIFAVSTK 225  
QY 243 -EQPIEYGGKKLYL-----YNHOHEYFFLIGPPL-----IPMYFOYQIIM----- 285  
DB 226 FSSLTSRFYDRKLTDFVARFLVSYQHFTYY-----PVMCFGRINLFITQTELLFSKREVP 281  
QY 286 -----TMIVHKNNVDL--AWAVSYIRFFITYIPFYGILGALLFLNFIREFLESWFVW 336  
DB 282 DRALNFAGILVFWTFPLLVSCLPNWPFFVFFTSF-----TVTALQHIQF----- 328  
QY 337 VTQNMHIVME-IDQAYRDWFSQTLATCNVEOSFFNDFSGHLNFIQIEHLEFPTPRNHL 394  
DB 329 --TLNFAADVYVGPPTGSDWFEKQAGTIDISCRSFMDFGGLQFQLEHHLFPLRPRC 386  
QY 395 NLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLK 431  
DB 387 HLKRVSVQELCKKNLPIRSMSEFANVLINTLK 423

RESULT 6  
T50555  
delta-8 sphingolipid desaturase [imported] - rape  
C:Species: Brassica napus (rape)  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 15-Sep-2000  
C:Accession: T50555  
R:Spelling, P.; Zaehring, U.; Heinz, E.  
J. Biol. Chem. 273, 28590-28596, 1998  
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome  
A:Reference number: 222986; MUID:99003197; PMID:9786850  
A:Accession: T50555  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-449 <SPE>  
A:Cross-references: EMBL:AJ224160; PIDN:CAA11857.1  
A:Experimental source: cultivar Drakkar  
C:Genetics:  
A:Gene: slid

Query Match 17.3%; Score 422.5; DB 2; Length 449;  
Best Local Similarity 28.2%; Pred. No. 6.6e-28;  
Matches 125; Conservative 73; Mismatches 182; Indels 63; Gaps 15;

QY 24 BEIQKHNRTDGLVIDRKVNITKWSIOHPGQORVIGHYAGEDATDAFRPHPLDFVFG 83  
DB 13 EDLKKNKPGDLWISIQGVYDVSQVAKSHPGGEAAILNLAQDQVDTDAFIAYHFGTAW-- 70  
QY 84 KFLKPLLIGELAPEEPSQDHGKSNKITEDFRALRKTAEADNLF-KTNHVFVFLLLAHIA 142  
DB 71 RHLENLHNGYHV-----KDH-HVSDVSDYRRLAAEFKRGGLFDKKGHV-TLYTLTCVAA 123



```
Db 254 HVHTWMLPFLRLSWLLQSIIFVSQMPHTHYDYRNTAIVEQVGLSHWMSLGQLYFLP 313
QY 306 FFITYIPFY---GILGALLFLNFIRELESHFWVWVQMMHVM---IDQAYRWDFSSQ 359
Db 314 DWSTRIMFLVSLVGG-----FLLSH---VTFNFHVSVEKFAUSSNMSYACLQ 361
QY 360 LTATCNVEQSFNDWFSGHNFQIEHLLPPTPRHNLHKLIAPLVSKLCAKHGIEY 414
Db 362 IMTRNRWPGRFIDMLWGLNGLYQIEHLLPPTPRHNLNVTMPLVKEFAAANGLPY 416

RESULT 9
H88791
A:Title: T13F2.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88791
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:G3879828; GSPDB:GN00022; CESP:T13F2.
C:Genetics:
A:Map position: 4
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match 14.6%; Score 356; DB 2; Length 454;
Best Local Similarity 26.3%; Pred. No. 2.8e-22;
Matches 111; Conservative 67; Mismatches 156; Indels 88; Gaps 16;

QY 53 HPGQGVGHYAGEDATDAFRPHDLEFVGKFLKLLIGELAPEPSOD-----102
Db 30 HPGGS-AITTKNMADTTVFHTGSKRAYQWLT-----ELKSCPTQEPPIDKDDP 83
QY 103 -----HGKSKITDPRLRKTAEADNMFKTNHVFLLLAHIALESIA 147
Db 84 IKGIDVNMGTFNISEKSAQINKSFIDLRMVRAEGLMDGSPFVIRKI-----LETI- 137
QY 148 WPTV---FY---FGNGWIPILITAFVLTATSOAGWLOHDYGHLSVYRKPKWHLVHKFY- 201
Db 138 -FTLFAFYLOVHTYLP---SAILMGVAMQQLGLWLIHEFAHQFKNRYNDLASFYVG 193
QY 202 ---IGHL--KGASANNWHRHFOHAKPNIHKDPDVMNLHVFLGEMQPIEYKXKLLK 255
Db 194 NFIQVSHIFNNGPSSGKWEQHNVAATNVVGRDGLDLPFYATVAEHLNYSQDSWV 253
QY 256 YLPYNQHEYFFLIGPLIIPMYFQIIM-----TWLVHKNWVDLAWVS- 301
Db 254 MTLFRQWVHTMFLPFLRLSMLLSQIIFVSQMPHTHYDYRNTAIVEQVGLSFWMSL 313
QY 302 ---YIRFFITYIPFY---GILGALLFLNFIRELESHFWVWVQMMHVM---IDQAY 352
Db 314 GQLYFPDSTRIMFLVSLVGG-----FLLSH---VTFNFHVSVEKFAUSSNIM 361
QY 353 RWFSSQLTATCNVEQSFNDWFSGHNFQIEHLLPPTPRHNLHKLIAPLVSKLCAKHG 412
Db 362 SNVACLQIMTRNWRPGRFIDMLWGLNGLYQIEHLLPPTPRHNLNVTMPLVKEFAAANG 421
QY 413 EY 414
Db 422 PY 423
```

RESULT 10  
JC7556

```
linoleoyl-CoA desaturase (EC 1.14.19.3) - Mucor rouxii
N:Alternate names: delta6-desaturase
C:Species: Mucor rouxii
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
C:Accession: JC7556
R:Lacteng, K.; Manontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desatur
A:Reference number: JC7556; MUID: 20563795; PMID:11112411
A:Accession: JC7556
A:Molecule type: DNA
A:Residues: 1-523 <LAC>
A:Cross-references: GB:AF290983
A:Experimental source: strain ATCC 24905
C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformat
C:Keywords: oxidoreductase; transformation

Query Match 14.3%; Score 347.5; DB 2; Length 523;
Best Local Similarity 23.4%; Pred. No. 1.8e-21;
Matches 112; Conservative 76; Mismatches 178; Indels 113; Gaps 17;

QY 24 BEIQKHLRTDGLVIDRKVNITKMSIQHPGQGVGHYAGEDATDAFRPHDLEFVG 83
Db 25 EKFDLTKQSDSVFIYQKYRVNNFMFKHPGGEALRSALGRDVTDEIRTMHP- QVYE 83
QY 84 KFLKPLLIGELAPE-----EPSQD-----HGK 105
Db 84 KLINLYCIGDYPDVIKPSMKQOHTFKPKEDKPVLTATWEGFTVQAYDDAIQDLHKH 143
QY 106 NS-----KITEPRALRKTAEADNMFLKTNH-----VFLLLL 137
Db 144 HSHDLIKDAVLQKDLNGDQIRNAYKLEALYKGLFKCNKYKAREGCRYTLLIFLSL- 202
QY 138 AHIALESIAWFTV-----FYFGNGWIPILITAFVLTATSOAGWLOHDYGHLSVYRKPK 192
Db 203 -----WFLTKGTETWYTAG-----AAFMAFWHQVLFVTAHADAGHNEITKSE 245
QY 193 WNLVHKFVILGKASANNWHRHFOHAKPNIHKDPDVMNLHV---FVLGEMQPIEY 249
Db 246 IDHVGIVIANFICGLSLGWNKNHNVHIVTHPEHDPDIO--HVDFMAITTKFFNNIY 303
QY 250 GKXKLYLPYN-----HQEYFFLI---GPPLIPMYFQIYIMTMVHKNWVDLAW 298
Db 304 STYKRVLPDPAASRPFVRHQVLYLILSGFNLHRLSFAY-LTCKNVRTTLELVG 362
QY 299 AVSYVIRF--FITVPIFYGILGALLFLNFIRELESHFWVWVQMMHVMDEIDQAYEDWF 356
Db 363 ITFFVWFGSLSLTLPWNIRIATVWSYMLTTPPLH--VOIT-LSHFGMSTEDRGPDEPF 419
QY 357 -SSQLTATCNVEQSFNDWFSGHNFQIEHLLPPTPRHNLHKLIAPLVSKLCAKHGIEY 414
Db 420 PAKMLRTMDVDCPEWHDWFHGGIYQAVHHLFPLRPHNLRCQVPLVKKFCDEVLHY 478

RESULT 11
T36617
A:Title: Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomy
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T36617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: T36617
A:Accession: T36617
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <OLI>
A:Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB: SCH35.42c
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
```

[illegible]

C:Species: Bos primigenius taurus (cattle)  
 C>Date: 12-Aug-1981 #sequence\_revision 05-May-1995 #text\_change 15-Sep-2000  
 A:Accession: A47215; S03428; F24211; S07963; A90383; A92053; B93774; A92231; A00170  
 R:Cristiano, R.J.; Giordano, S.J.; Steggle, A.W.  
 Genomics 17, 348-354, 1993  
 A>Title: The isolation and characterization of the bovine cytochrome b5 gene, and a transcribed sequence  
 A:Reference number: A47215; MUID:94010328; PMID:8406485  
 A:Accession: A47215  
 A:Molecule type: DNA  
 A:Residues: 1-134 <CR1>  
 A:Cross-references: GB:M63226; GB:M63227; GB:M63228; GB:M63329; GB:L22966; NID:G987590  
 A:Note: Sequence extracted from NCBI backbone and corrected to correspond with the public release  
 A:Note: The authors conclude that the erythrocyte form is generated by posttranslational modification  
 R:Cristiano, R.J.; Steggle, A.W.  
 Nucleic Acids Res. 17, 799, 1989  
 A>Title: The complete nucleotide sequence of bovine liver cytochrome b(5) mRNA.  
 A:Reference number: S03428; MUID:89128451; PMID:2915932  
 A:Accession: S03428  
 A:Molecule type: mRNA  
 A:Residues: 1-134 <CR2>  
 A:Cross-references: EMBL:X13617; NID:G297; PIDN:CAA31949.1; PID:G298  
 R:Abe, K.; Kimura, S.; Kizawa, R.; Anan, P.K.; Sugita, Y.  
 J. Biochem. 97, 1659-1668, 1985  
 A>Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythrocytes  
 A:Reference number: A91992; MUID:85289161; PMID:4030743  
 A:Accession: F24211  
 A:Molecule type: protein  
 A:Residues: 2, '2', '4'-98 <ABE>  
 A:Experimental source: erythrocyte  
 A:Note: residues 2-3 were positioned by homology with the bovine liver sequence  
 R:Ozols, J.  
 Biochim. Biophys. Acta 997, 121-130, 1989  
 A>Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.  
 A:Reference number: S04976; MUID:89323209; PMID:2752049  
 A:Accession: S07963  
 A:Molecule type: protein  
 A:Residues: 2-6,15-18 <OZ01>  
 R:Ozols, J.  
 Biochemistry 13, 426-434, 1974  
 A>Title: Cytochrome beta-5 from microsomal membranes of equine, bovine, and porcine liver  
 A:Reference number: A90383; MUID:74080219; PMID:4810060  
 A:Accession: A90383  
 A:Molecule type: protein  
 A:Residues: '2B', '2', '2Z', '5-11', '131-133', 'D' <OZ02>  
 R:Ozols, J.; Strittmatter, P.  
 J. Biol. Chem. 244, 6617-6618, 1969  
 A>Title: Correction of the amino acid sequence of calf liver microsomal cytochrome b5.  
 A:Reference number: A92053; MUID:70067001; PMID:5391285  
 A:Accession: A92053  
 A:Molecule type: protein  
 A:Residues: 6-15, 'QBI', '19-61', 'D', '63-97' <OZ03>  
 A:Experimental source: liver  
 R:Tsugita, A.; Kobayashi, M.; Tani, S.; Kyo, S.; Rashid, M.A.; Yoshida, Y.; Kajihara, T.  
 Proc. Natl. Acad. Sci. U.S.A. 67, 442-447, 1970  
 A>Title: Comparative study of the primary structures of cytochrome b-5 from four species  
 A:Reference number: A93774; MUID:70289989; PMID:5272324  
 A:Accession: B93774  
 A:Molecule type: protein  
 A:Residues: 6-17, 'E', '19-61', 'D', '63-96' <TSU>  
 R:Fleming, P.J.; Dailey, H.A.; Corcoran, D.; Strittmatter, P.  
 J. Biol. Chem. 253, 5369-5372, 1978  
 A>Title: The primary structure of the nonpolar segment of bovine cytochrome b5.  
 A:Reference number: A92231; MUID:78218214; PMID:670203  
 A:Accession: A92231  
 A:Molecule type: protein  
 A:Residues: 92-134 <FLR>  
 R:Muskett, F.W.; Kelly, G.P.; Whitford, D.  
 submitted to the Brookhaven Protein Data Bank, February 1996  
 A:Reference number: A66921; PDB:1WDB  
 A:Contents: annotation; conformation by (1)H-, (15)N-NMR, residues 6-89  
 R:Muskett, F.W.; Kelly, G.P.; Whitford, D.  
 J. Mol. Biol. 258, 172-189, 1996  
 A>Title: The solution structure of bovine ferricytochrome b5 determined using heteronuclear NMR

A:Reference number: A58628; MUID:96200988; PMID:8613986  
 A:Contents: annotation; conformation by (1)H-, (15)N-NMR  
 R:Durley, R.C.E.; Mathews, F.S.  
 submitted to the Brookhaven Protein Data Bank, August 1994  
 A:Reference number: A52769; PDB:1CYO  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 6-93  
 R:Mathews, F.S.; Durley, R.C.E.  
 submitted to the Brookhaven Protein Data Bank, January 1990  
 A:Reference number: A50568; PDB:3B5C  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms, 8-92  
 R:Mathews, F.S.; Argos, P.; Levine, M.  
 Cold Spring Harb. Symp. Quant. Biol. 37, 387-395, 1971  
 A>Title: The structure of cytochrome b-5 at 2.0 angstrom resolution.  
 A:Reference number: A90922  
 A:Contents: annotation; oxidized form, X-ray crystallography, 2.0 angstroms; revision 1  
 R:Argos, P.; Mathews, F.S.  
 J. Biol. Chem. 250, 747-751, 1975  
 A>Title: The structure of ferrocyclochrome b5 at 2.8 A resolution.  
 A:Reference number: A92186; MUID:7509526; PMID:1167544  
 A:Contents: annotation; reduced form, X-ray crystallography, 2.8 angstroms  
 A:Note: the structure of the reduced form was found to be the same as that of the oxidized form of the heme crevice  
 C:Comment: This protein contains two domains: a hydrophilic, catalytic, amino-terminal domain and a hydrophobic, catalytic, amino-terminal domain  
 the cytochrome to biological membranes.  
 C:Genetics:  
 A:Gene: CYB5  
 A:Introns: 43/3; 86/3; 96/3; 108/2  
 C:Function: <MIC>  
 A:Description: acts as an electron carrier for membrane bound oxygenases; with cytochrome b5  
 A:Note: microsomal form  
 C:Function: <ERY>  
 A:Description: acts to reduce methemoglobin to functional hemoglobin; the oxidized form of cytochrome b5; cytochrome b5 core homology  
 C:Superfamily: cytochrome b5; cytochrome b5 core homology  
 C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; membrane  
 E:2-134/Product: cytochrome b5, microsomal form #status experimental <MAT>  
 F:2-98/Product: cytochrome b5, erythrocyte form #status experimental <MA2>  
 F:9-84/Domains: cytochrome b5 core homology <CB5>  
 F:105-127/Domains: membrane-bound #status predicted <MEM>  
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
 F:4,68/Binding site: heme iron (His) (axial ligands) #status experimental  
 Query Match 7.1%; Score 173; DB 1; Length 134;  
 Best Local Similarity 32.0%; Pred. No. 1.9e-07;  
 Matches 47; Conservative 26; Mismatches 48; Indels 26; Gaps 4;  
 Qy 11 AARESVPTFSVEEIQKLNRLTDSGLVIDRKYNITKWSIQHPGQGVIGHYAGEDATD 70  
 Db 2 AEESSKAVKYTLEIEIQKNNKSTWLLHYKYDITKPLEHPGGEVLRQAGGDATE 61  
 Qy 71 ARAFHDPDFVG-----KFLKPLLIGELAPEPSQDHKSKITDFALRKTAEDVN 124  
 Db 62 NF-----EDVGHSTDAEELSTFFIGELHPDD-----RSKITPSESITTTDSNP 107  
 Qy 125 LFTKN-----HVFLLLLAHIALES 145  
 Db 108 SWTNWMLIPALISALFVALIVHLYTSEN 134  
 RESULT 15  
 CBPGS  
 cytochrome b5, microsomal splice form [validated] - pig  
 N:Alternate names: hepatic cytochrome b5; membrane-bound cytochrome b5  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 29-Jul-1981 #sequence\_revision 20-Apr-2000 #text\_change 05-May-2000  
 C:Accession: JC5782; C24211; S07962; B90383; B92077; A93813; A00171  
 R:VanDerMark, P.K.; Steggle, A.W.  
 Biochem. Biophys. Res. Commun. 240, 80-83, 1997  
 A>Title: The isolation and characterization of the soluble and membrane-bound porcine cytochrome b5  
 A:Reference number: JC5782; MUID:98042520; PMID:9367886  
 A:Accession: JC5782  
 A:Molecule type: mRNA  
 A:Residues: 1-134 <VAN>



A;Cross-references: GB:AF016389; NID:G2642485; PIDN:AAC48779.1; PID:G5642486  
A;Experimental source: testis  
P;Abe, K.; Kimura, S.; Kizawa, R.; Anan, F.K.; Sugita, Y.  
J. Biochem. 97, 1659-1668, 1985  
A;Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythrocyte  
A;Reference number: A91992; MUID:85289161; PMID:4030743  
A;Contents: sequence revisions  
A;Accession: C24211  
A;Molecule type: protein  
A;Residues: 2-134 <O201>  
P;Ozols, J.  
Biochim. Biophys. Acta 997, 121-130, 1989  
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.  
A;Reference number: S04976; MUID:89323209; PMID:2752049  
A;Accession: S07962  
A;Molecule type: protein  
A;Residues: 2-134 <O201>  
P;Ozols, J.  
Biochemistry 13, 426-434, 1974  
A;Title: Cytochrome beta-5 from microsomal membranes of equine, bovine, and porcine liver  
A;Reference number: A90383; MUID:74080219; PMID:4810060  
A;Accession: B90383  
A;Molecule type: protein  
A;Residues: 'ZZDA5', 7 <O202>  
P;Nobrega, F.G.; Ozols, J.  
J. Biol. Chem. 246, 1706-1717, 1971  
A;Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes of  
A;Reference number: A92077; MUID:71134790; PMID:4993957  
A;Accession: B92077  
A;Molecule type: protein  
A;Residues: 8-14, 'ZZ', 17, 'Z', 19-89 <NOB>  
P;Ozols, J.; Gerard, C.  
Proc. Natl. Acad. Sci. U.S.A. 74, 3725-3729, 1977  
A;Title: Primary structure of the membranous segment of cytochrome b-5.  
A;Reference number: A93813; MUID:78012290; PMID:269425  
A;Accession: A93813  
A;Molecule type: protein  
A;Residues: 15-16, 'D', 90-134 <O203>  
A;Note: the residue 62 was identified as Asp  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfer  
F;9-84/Domain: cytochrome b5 core homology <CB5>  
F;109-130/Domain: transmembrane #status predicted <TRM>  
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F;44, 68/Binding site: heme iron (His) (axial ligands) #status predicted  
Query Match 7.1%; Score 172; DB 1; Length 134;  
Best Local Similarity 31.3%; Pred. No. 2.48-07;  
Matches 47; Conservative 28; Mismatches 47; Indels 28; Gaps 4;  
QY 11 AAEREVSPTFSWBEIQKHLNRLDGLVDRKYNITKWSIQHPGQGVICHVAGEDATD 70  
Db 2 AEQSDKAVKYITLBEIQKNNKSTWLLIHHKVVYDLTKFLEHPGGEVLREQAGDATE 61  
QY 71 AFRAFPHDLEFVG-----KFLKLLIGELAPEPSQDHGKNKSKITDFRALRKTAE DMN 124  
Db 62 NF-----EDVGHSTDAEELSKTFTIGELHPD-----RSKIAPSETLITVESN 107  
QY 125 LFKTNHVFELLLAHIIALEGIAWFTVTFYF 154  
Db 108 SWTNWV-----IPALSIVSLVMYHF 129  
RESULT 16  
B83034  
conserved hypothetical protein PA4888 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: B83034  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: B83034  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-370 <STO>  
A;Cross-references: GB:AE004902; GB:AE004091; NID:G9951162; PIDN:AAG08273.1; GSPDB:GN01  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA4888

Query Match 7.0%; Score 170; DB 2; Length 370;  
Best Local Similarity 21.7%; Pred. No. 1.28-06;  
Matches 70; Conservative 51; Mismatches 129; Indels 72; Gaps 15;

QY 157 GWIPT--LITAFVLTSAQAQAGW--LQHD--YGHLSVVRKPKWNHVLHVKFVIGHLKGASAN 211  
Db 67 GMLPTWLLGSLLLGLKILENMELGHNVMHGQYDWNDEPAGRAYEWDI---AGPSD 122  
QY 212 WNNRHFQ-HHAKNIFHKDDPV--NMLHVFVLGEWQPIEGYKKLKYLPYNNHCHYEYFL 268  
Db 123 FWRHTHNHHHTYTNVLGKDDVGCVVRLPPEQRWKP-----YRWQ----- 165  
QY 269 IGPPJ---LIPWYFOYQIIMTM-----VHKWVDLA-----WAVSYIIR 305  
Db 166 ---PLWVTLQALLFQYAVAIQHLRLDKYAKGRDLKALMPLRLRLAKLGHQWTKDYLL- 221  
QY 306 FFITVIPPYIGLALLFNFI-REFSHWFVVMQMHVME-----IDQAYRDWF 356  
Db 222 -PFLGLFAGGFGAVFVGNLLANVLRNLWTFVFCGHFTEKAVVFPSPVLEGETRGHWY 280  
QY 357 SSQLTATCNVRSFDFNSGHLNEFOIEHLFPMPRHLNHLKIAPLVKSCLKAGIEYQE 416  
Db 281 LRQLAGSNLGGFLPHLTGNLHSHQIEHLJYPLPARRYAALSREVRREIARRVGTQVNS 340  
QY 417 KPLLRALLDIIRSLKSKGLWL 438  
Db 341 GRLGROFLTVLR-----RIWV 356

## RESULT 17

CBEB5  
cytochrome b5, microsomal splice form [validated] - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 29-Jul-1981 #sequence\_revision 31-Dec-1993 #text\_change 20-Apr-2000  
C;Accession: S03373; S07961; A91920; A93774; A92068; A91953; A92269; A61482; A00168; A  
R;Darius, N.; Fisher, C.W.; Steggles, A.W.  
Protein Seq. Data Anal. 1, 351-353, 1988  
A;Title: The nucleotide sequence of rabbit liver cytochrome b(5) mRNA.  
A;Reference number: S03373; MUID:89128816; PMID:3222252  
A;Accession: S03373  
A;Molecule type: mRNA  
A;Residues: 1-134 <DAR>  
A;Cross-references: GB:M24844; NID:G1431635; PIDN:AAB03878.1; PID:G164785  
A;Note: the authors translated the codon GAC for residues 6 and 8 as Asn, AAC for resi  
R;Ozols, J.  
Biochim. Biophys. Acta 997, 121-130, 1989  
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.  
A;Reference number: S04976; MUID:89323209; PMID:2752049  
A;Accession: S07961  
A;Molecule type: protein  
A;Residues: 2-4 <O20>  
R;Sugita, A.; Kobayashi, M.; Kajihara, T.; Hagiwara, B.  
J. Biochem. 64, 727-730, 1968  
A;Title: Primary structure of rabbit liver cytochrome b5.  
A;Reference number: A91920; MUID:69108767; PMID:5709273  
A;Accession: A91920  
A;Molecule type: protein  
A;Residues: 3-46, 40-61, 'D', 63-91 <TS1>  
R;Sugita, A.; Kobayashi, M.; Tani, S.; Kyo, S.; Rashid, M.A.; Yoshida, Y.; Kajihara,  
Proc. Natl. Acad. Sci. U.S.A. 67, 442-447, 1970  
A;Title: Comparative study of the primary structures of cytochrome b-5 from four speci  
A;Reference number: A93774; MUID:70289989; PMID:5272324

A;Accession: A93774  
A;Molecule type: protein  
A;Residues: 7-8,47-49 <TS2>  
R;Ozols, J.  
J. Biol. Chem. 245, 4863-4874, 1970  
A;Title: Amino acid sequence of rabbit liver microsomal cytochrome b-5.  
A;Reference number: A92068; MUID:71001482; PMID:5506260  
A;Accession: A92068  
A;Molecule type: protein  
A;Residues: 5-15,'O',17-98 <O22>  
A;Note: the two minor components have either 11-Phe and 14-Clu or 96-Thr and an addition  
R;Kondo, K.; Tajima, S.; Sato, R.; Narita, K.  
J. Biochem. 86, 1119-1128, 1979  
A;Title: Primary structure of the membrane-binding segment of rabbit cytochrome b-5.  
A;Reference number: A91953; MUID:80049603; PMID:500581  
A;Accession: A91953  
A;Molecule type: protein  
A;Residues: 92-103,'N',105-134 <ON>  
A;Note: this segment corresponds to the membrane-binding carboxyl end of the molecule  
R;Takagaki, Y.; Gerber, G.E.; Nihei, K.; Khorana, H.G.  
J. Biol. Chem. 255, 1536-1541, 1980  
A;Title: Amino acid sequence of the membranous segment of rabbit liver cytochrome b-5.  
A;Reference number: A92269; MUID:80115672; PMID:7354043  
A;Accession: A92269  
A;Molecule type: protein  
A;Residues: 99-134 <TAK>  
R;Gibson, B.W.; Fallick, A.M.; Lipka, J.J.; Waskell, L.A.  
J. Protein Chem. 9, 695-703, 1990  
A;Title: Mass spectrometric analysis of rabbit and bovine trypsin-solubilized cytochrome  
A;Reference number: A61482; MUID:91158806; PMID:2073321  
A;Accession: A61482  
A;Molecule type: protein  
A;Residues: 2-3,'E',5-16 <GB>  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; heme; iron; metal  
F;2-134/Product: cytochrome b5 #status experimental <MAT>  
F;9-84/Domain: cytochrome b5 core homology <CB5>  
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F;44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 7.0%; Score 169.5; DB 1; Length 134;  
Best Local Similarity 33.1%; Pred. No. 3.8e-07;  
Matches 46; Conservative 27; Mismatches 45; Indels 21; Gaps 4;

QY 11 AAREVSVPTFSEIEIOKHLRTDGLVIDRKYNITKMSIOHPGSGORVIGHVAGEDATD 70  
DB 2 AASDKDKVYTYTLEIEIKKHNSKSTWLIHKKVYDLTKFLEHPGSGEVLRQAGGDAT 61  
QY 71 AFRAFHDPLEFVG-----KFLKPLLIGELAPSEPSQDHGKNSKITEDFRALRKTAEDMN 124  
DB 62 NF-----EDVGHSTDAEELSKTFIIGELHPDD-----RSKLSKPMETLITTVDSNS 107  
QY 125 LFKTNHVFFLLLAHIAL 143  
DB 108 SWTNVW-IPASALIVAL 125

RESULT 18  
CBH05  
cytochrome b5, microsomal form [validated] - horse  
N;Alternate names: hepatic cytochrome b5; membrane-bound cytochrome b5  
C;Species: Equus caballus (domestic horse)  
C;Date: 29-Jul-1981 #sequence revision 20-Apr-2000 #text\_change 05-May-2000  
C;Accession: S07964; A92196; A92218; A00169  
R;Ozols, J.  
Biochim. Biophys. Acta 997, 121-130, 1989  
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.  
A;Reference number: S04976; MUID:89323209; PMID:2752049  
A;Accession: S07964  
A;Molecule type: protein  
A;Residues: 1-133 <OZO1>  
R;Ozols, J.; Gerard, C.; Nobrega, F.G.  
J. Biol. Chem. 251, 6767-6774, 1976

A;Title: Proteolytic cleavage of horse liver cytochrome b5.  
A;Reference number: A92196; MUID:77028943; PMID:977596  
A;Accession: A92196  
A;Molecule type: protein  
A;Residues: 'Z',2,'DAS',6-41,'D',43-98 <OZO2>  
A;Note: the amino terminal is shown to be blocked by acetylation and not pyroglutamic  
R;Ozols, J.; Gerard, C.  
J. Biol. Chem. 252, 8549-8553, 1977  
A;Title: Covalent structure of the membranous segment of horse cytochrome b-5. Chemical  
A;Reference number: A92218; MUID:78045981; PMID:562879  
A;Accession: A92218  
A;Molecule type: protein  
A;Residues: 89-133 <OZO3>  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfer  
F;8-83/Domain: cytochrome b5 core homology <CB5>  
F;108-129/Domain: transmembrane #status predicted <TRM>  
F;1/Modified site: acetylated amino end (Ala) #status experimental  
F;43,67/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.7%; Score 164; DB 1; Length 133;  
Best Local Similarity 27.3%; Pred. No. 1.1e-06;  
Matches 45; Conservative 29; Mismatches 43; Indels 48; Gaps 5;

QY 11 AAREVSVPTFSEIEIOKHLRTDGLVIDRKYNITKMSIOHPGSGORVIGHVAGEDATD 70  
DB 1 AEQSDKAVKYTYTLEIEIKKHNSKSTWLIHKKVYDLTKFLEHPGSGEVLRQAGGDAT 60  
QY 71 AFRAFHDPLEFVG-----KFLKPLLIGELAPSEPSQDHGKNSKITEDFRALRKTAEDMN 124  
DB 61 NF-----EDIGHSTDAEELSKTFIIGELHPDD-----RSKIAKFPVETLITTVD--- 103  
QY 125 LFKTNHVFFLLLAHIAL 143  
DB 104 -----SNSSWMT-----NNVIPASAVVVA 123

RESULT 19  
CBH15  
cytochrome b5, microsomal splice form [validated] - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 15-Oct-1982 #sequence revision 31-Dec-1992 #text\_change 16-Jun-2000  
C;Accession: S28404; A00172; A23338; JC5597; JS0745; S07960  
R;Mitoma, J.; Ito, A.  
EMBO J. 11, 4157-4203, 1992  
A;Title: The carboxy-terminal 10 amino acid residues of cytochrome b(5) are necessary  
A;Reference number: S28404; MUID:93011015; PMID:1396600  
A;Accession: S28404  
A;Molecule type: mRNA  
A;Residues: 1-134 <MIT>  
A;Cross-references: EMBL:D13205; NID:g220729; PIDN:BAA02492.1; PID:g220730  
R;Ozols, J.; Heinsmann, F.S.  
Biochim. Biophys. Acta 704, 163-173, 1982  
A;Title: Chemical structure of rat liver cytochrome b-5. Isolation of peptides by high-  
A;Reference number: A00172; MUID:82232110; PMID:7093287  
A;Accession: A00172  
A;Molecule type: protein  
A;Residues: 2-134 <OZO>  
R;Lederer, F.; Ghir, R.; Guillard, B.; Cortial, S.; Ito, A.  
Eur. J. Biochem. 132, 95-102, 1983  
A;Title: Two homologous cytochromes b-5 in a single cell.  
A;Reference number: A91128; MUID:83182449; PMID:6840088  
A;Accession: A23338  
A;Molecule type: protein  
A;Residues: 7,'B',9-17,'E',19-89 <LED>  
R;Yoo, M.  
Biochem. Biophys. Res. Commun. 235, 641-642, 1997  
A;Title: Identification of two homologous cytochrome b5s in rat brain.  
A;Reference number: JC5596; MUID:97396150; PMID:9245704  
A;Accession: JC5597  
A;Molecule type: mRNA  
A;Residues: 1-134 <YOO>  
A;Cross-references: DDBJ:AF007108; NID:g2257956; PIDN:AAB67610.1; PID:g2257957

A;Experimental source: brain  
C;Comment: This protein is a small heme-containing protein which supplies electrons for 1.  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfer  
F;2-134/Product: cytochrome b5 #status experimental <MAT>  
F;9-84/Domain: cytochrome b5 core homology <CB5>  
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F;44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.6%; Score 160; DB 1; Length 134;  
Best Local Similarity 27.9%; Pred. No. 2.4e-06;  
Matches 46; Conservative 26; Mismatches 45; Indels 48; Gaps 5;

QY 11 AAEREVSVPTSWIEIOKHNLRDTSGLVDRKVNITKWSIQHPGGORVIGHVAGEDATD 70  
DB 2 AEQSDKVYVYLEBIOKHDKSKTWTLLHKHYDITKFLBEPGGEVLRQAGGDATE 61

QY 71 AFRAHPDLEFVG-----KFLKPLLIGELAPESPQDHGKNKSKITDFPALRKTAE DMN 124  
DB 62 NF-----EDVGHSTDAEELSKYIIGELHPDD-----RSKIAPSETLITVE--- 104

QY 125 LFKTNHVFLLLAHIALESIATFTVFGNGWIPTLITAFVLA 169  
DB 105 -----SNSSWT-----NWIPIAISALVA 124

RESULT 20  
CBHUS  
Cytochrome b5, microsomal splice form [validated] - human  
C;Species: Homo sapiens (man)  
C;Date: 29-Jul-1991 #sequence revision 05-Apr-1995 #text change 20-Apr-2000  
C;Accession: A28936; S04976; A00167; A24211; A32912  
R;Yoo, M.; Steggle, A.W.  
Biochem. Biophys. Res. Commun. 156, 576-580, 1988  
A;Title: The complete nucleotide sequence of human liver cytochrome b5 mRNA.  
A;Reference number: A28936; MUID:89025904; PMID:3178851  
A;Accession: A28936  
A;Molecule type: mRNA  
A;Residues: 1-134 <YOO>  
A;Cross-references: GB:M22865; NID:G181226; PIDN:AAA35729.1; PID:G181227  
A;Experimental source: liver  
R;Ozols, J.  
Biochim. Biophys. Acta 997, 121-130, 1989  
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.  
A;Reference number: S04976; MUID:89323209; PMID:2752049  
A;Accession: S04976  
A;Molecule type: protein  
A;Residues: 2-3,'E','5-36;84-121,'V',123-134 <OZO>  
A;Experimental source: liver  
R;Rashid, M.A.; Hagihara, B.; Kobayashi, M.; Tani, S.; Tsugita, A.  
J. Biochem. 74, 985-1002, 1973  
A;Title: Structural studies of cytochrome b-5. III. Sequential studies on human liver cy  
A;Reference number: A91933; MUID:74074962; PMID:4770377  
A;Accession: A91933  
A;Molecule type: protein  
A;Residues: 'QZA','5-14','Q','16-17','E','19-21,23-61,'D','63-88,'K','90,'R' <RAS>  
A;Experimental source: liver  
A;Note: blocked amino-terminal peptide attributed to pyrrolidone carboxylic acid  
R;Nobrega, F.G.; Ozols, J.  
J. Biol. Chem. 246, 1706-1717, 1971  
A;Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes of  
A;Reference number: A32077; MUID:71134790; PMID:4993957  
A;Accession: A00167  
A;Molecule type: protein  
A;Residues: 5-14,'Q','16-17','E','19-61,'D','63-88,'K','90,'R' <NOB>  
A;Experimental source: liver  
R;Yoo, M.; Steggle, A.W.  
Biochem. Biophys. Res. Commun. 163, 18-24, 1989  
A;Title: The characterization of three types of partially processed mRNA and two pseud  
A;Reference number: A32912; MUID:89374222; PMID:2775258  
A;Contents: annotation; introns  
R;Abe, K.; Kimura, S.; Kizawa, R.; Anan, F.K.; Sugita, Y.

J. Biochem. 97, 1659-1668, 1985  
A;Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythro  
A;Reference number: A91922; MUID:85289163; PMID:4030743  
A;Contents: annotation; amino-terminal acetylation  
R;Ozols, J.  
J. Biol. Chem. 247, 2242-2245, 1972  
A;Title: Cytochrome b-5 from a normal human liver. Isolation and the partial amino acid  
A;Reference number: A92103; MUID:72154531; PMID:5062820  
A;Contents: annotation  
C;Comment: Cytochrome b5 exists in at least two alternative splice forms. This longer  
m (see PIR:CBHUS) is found in erythrocytes.  
C;Genetics:  
A;Gene: GDB:CYB5  
A;Cross-references: GDB:125236; OMIM:250790  
A;Map position: 18q22.3-18q23  
A;Introns: 86/3  
A;Note: the list of introns may be incomplete  
C;Function:  
A;Description: acts as an electron carrier for membrane bound oxygenases; with cytochrome  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfr  
F;2-134/Product: cytochrome b5, microsomal splice form #status experimental <MAT>  
F;9-84/Domain: cytochrome b5 core homology <CB5>  
F;119-131/Domain: transmembrane #status predicted <TRM>  
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F;44,68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.5%; Score 159; DB 1; Length 134;  
Best Local Similarity 30.8%; Pred. No. 3e-06;  
Matches 44; Conservative 27; Mismatches 44; Indels 28; Gaps 4;

QY 11 AAEREVSVPTSWIEIOKHNLRDTSGLVDRKVNITKWSIQHPGGORVIGHVAGEDATD 70  
DB 2 AEQSDKVYVYLEBIOKHDKSKTWTLLHKHYDITKFLBEPGGEVLRQAGGDATE 61

QY 71 AFRAHPDLEFVG-----KFLKPLLIGELAPESPQDHGKNKSKITDFRALRKTAE DMN 124  
DB 62 NF-----EDVGHSTDAEELSKYIIGELHPDD-----RPLNKPPETLITIDSS 107

QY 125 LFKTNHVFLLLAHIALESIATFTVFGNGWIPTLITAFVLA 147  
DB 108 SWMTNW-----IPAISAVA 122

RESULT 21  
JN0316  
cytochrome b5, erythrocyte splice form [validated] - rabbit  
N;Alternate names: soluble cytochrome b5  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 16-Jun-2000  
C;Accession: JN0316; S29841  
R;Takematsu, H.; Kozutsumi, Y.; Suzuki, A.; Kawasaki, T.  
Biochem. Biophys. Res. Commun. 185, 845-851, 1992  
A;Title: Molecular cloning of rabbit cytochrome b5 genes; evidence for the occurrence  
A;Reference number: JN0316; MUID:92328788; PMID:1627141  
A;Accession: JN0316  
A;Molecule type: mRNA  
A;Residues: 1-98 <RAK>  
A;Cross-references: GB:D10901; NID:G471149; PIDN:BA01712.1; PID:G471150  
A;Note: Thr-96 was also found  
R;Giordano, S.J.; Steggle, A.W.  
Biochim. Biophys. Acta 1172, 95-100, 1993  
A;Title: Differential expression of the mRNAs for the soluble and membrane-bound forms  
A;Reference number: S29841; MUID:93176833; PMID:8439576  
A;Accession: S29841  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-98 <GIO>  
A;Cross-references: EMBL:Z14091; NID:G1542  
A;Note: this translation is not annotated in GenBank entry OCCVTB5, release 113.0  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron transfr  
F;9-84/Domain: cytochrome b5 core homology <CB5>





A;Cross-references: GB:BA000019; PIDN:BAB77963.1; PID:g17135417; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all1597  
C;Superfamily: omega-3 fatty acid desaturase

Query Match 6.3%; Score 154.5; DB 2; Length 359;  
Best Local Similarity 20.6%; Pred. No. 2.4e-05;  
Matches 80; Conservative 54; Mismatches 131; Indels 123; Gaps 20;

QY 96 PEEPSQDHGKSKTEDPRALKTAEDM-----NLFTKNHVF-----LLL 136  
DB 7 PSDNSPQSGENT-----TLPTQLDALKAPACQPNVSKSLFFPFDVLIVGLIYA 62  
QY 137 LAHIALESIAWTFVFGNGMIPLITA-FVLATSOAQAGWLQHDYCHLSVVRKPKW-- 193  
DB 63 VAHY--LDSWYFIFWLIQO---TMEWALFVVG-----HDCGHQS-FSKKWLN 106  
QY 194 ---NHLVHKFVIGHLKGSANWNRHFOHKAENIFHKOPDYNMLHVFVLGWEQPIEG 250  
DB 107 DLIGHLTHFTFLVPHYG-----WRISHRTHKNTGNINDB-----SWYPTQS 150  
QY 251 KKXLYLPYNNHQHYFFLIGPL-----LTPMYFOYQIIMTIVHK 291  
DB 151 QYKEMPLGQKIGRYVFLAYPVVLFKESPNKESGSHLPSSLFKPKSEKNDVITSLWS 210  
QY 292 NWVL-----ANAVSYIREFITYIPFYGLGALLFLNFIRLESHWFVWYQMN 341  
DB 211 CMVGLLGELTYQGMWMLLKYYAAPYIVF-----IWLDLVTFLEH 250  
QY 342 HIVMEIDQAYR--DWFSQLTATCNVQSPFNDFWFGHLNFQI-----EHLPTMPRHN 395  
DB 251 H--TEADLPWRGEDW-TFLKGLASSIDRNY---GLVNHIIHDIGTHVAHIFLNPYHN 304  
QY 396 LHKIAPLVKSLCAKHGYEQKPLRAL 423  
DB 305 LKATEAIKPMVGEY-YRKSEPIWKS 331

## RESULT 28

S25445  
nitrate reductase (NADH) (EC 1.7.1.1) 1 - kidney bean  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 22-Nov-1993 #sequence\_revision 08-Sep-1995 #text\_change 03-Jun-2002  
C;Accession: S25445  
R;Hoff, T.; Stummann, B.M.; Henningsen, K.W.  
Physiol. Plantarum 82, 197-204, 1991  
A;Title: Cloning and expression of a gene encoding a root specific nitrate reductase in  
A;Reference number: S25445  
A;Accession: S25445  
A;Molecule type: DNA  
A;Residues: 1-881 <HOF>  
A;Cross-references: EMBL:X53603; NID:g21018; PIDN:CAA37672.1; PID:g21019  
A;Experimental source: cv. Saxonia  
C;Genetics:  
A;Introns: 322/1; 369/1; 446/3  
C;Complex: homodimer  
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu  
C;Keywords: electron transfer; FAD; flavoprotein; heme; homodimer; iron; metalloprotein;  
F:63-455/Domain: molybdopterin-binding domain homology <PCO>  
F:515-589/Domain: cytochrome b5 core homology <CB5>  
F:632-881/Domain: cytochrome-b5 reductase homology <CBR>  
F:167/Binding site: molybdopterin (Cys) (covalent) #status predicted  
F:550,573/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.3%; Score 153.5; DB 2; Length 881;  
Best Local Similarity 25.2%; Pred. No. 8.7e-05;  
Matches 69; Conservative 40; Mismatches 78; Indels 87; Gaps 14;

QY 5 GNQCGGAARE-----VSVP-----TFSWBIQKHNRDTSGLVIDR 41  
DB 479 GNQCGGWAREKQLEKSESNPILKKSVPFMTATKSYSLSEVRHNRDSAWIIVG 538

QY 42 KYVNIITKWSIQHGGQGVIGHYAGEDATDAFRAHFDLFVKGFLKPLLLIGELAPEESQ 101  
DB 539 HYVDCRFLKDHPPGGEDSILLNAGTDCTEFEFAIHSK--AKKMLEDYRIGELMTDTYS 596  
QY 102 D-----HGKN-----SKITDFRALR--KTRED--M 123  
DB 597 DSSSSNNSVHGNSETTHLAPIREVALNPREKIPCKLLSKTISHDVRLRLPALPAEDQM 656  
QY 124 NLFTKNHVF-----LILLAH--IIALESIAWF-----TVFY-----FGNGMIPTL-I 163  
DB 657 GLPVGNHVFLCATVDEKLCMRAYTSSVDVGFDFLVVYFKGVHFNFGNGIMSQHL 716  
QY 164 TAFVLATSOAQAGWLQHDY---GHLVSVVRKPKW 193  
DB 717 DSLPIGVSVDVVRKPLGHIETGGRGNFLVHGKPRF 750

## RESULT 29

S07959  
cytochrome b5, microsomal splice form [validated] - brown howler monkey (fragment)  
N;Alternate names: hepatic cytochrome b5  
C;Species: Alouatta fusca (brown howler monkey)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-May-2000  
C;Accession: S07959; A92077; A00167  
R;Ozols, J.  
Biochim. Biophys. Acta 997, 121-130, 1989  
A;Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.  
A;Reference number: S04976; MUID:89323209; PMID:2752049  
A;Accession: S07959  
A;Molecule type: protein  
A;Residues: 1-87 <OZO>  
R;Nobrega, F.G.; Ozols, J.  
J. Biol. Chem. 246, 1706-1717, 1971  
A;Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes of  
A;Reference number: A92077; MUID:71134790; PMID:4993957  
A;Accession: A92077  
A;Molecule type: protein  
A;Residues: 1-10, 'Q', 12-13, 'E', 15-57, 'D', 59-74, 'Y', 76-84, 'K', 86, 'R' <NOB>  
C;Superfamily: cytochrome b5; cytochrome b5 core homology  
C;Keywords: electron transfer; heme; iron; liver; metalloprotein  
F:5-80/Domain: cytochrome b5 core homology <CB5>  
F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.2%; Score 150.5; DB 2; Length 87;  
Best Local Similarity 38.6%; Pred. No. 9.2e-06;  
Matches 34; Conservative 17; Mismatches 24; Indels 13; Gaps 2;

QY 17 SVPTFSWBIQKHNRDTSGLVIDRKYVNIKWSIQHGGQGVIGHYAGEDATDAFRAH 76  
DB 4 AVKYITLSEIQKHNSKSTWLILHKVYDLTKFLEHFGGBEVLREQAGDATENF---- 59

QY 77 PDLEFVG-----KFLKPLIGELAPEE 98  
DB 60 ---EDVGHSTDARELSKTFIIGELHPDD 84

## RESULT 30

JQ2337  
omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 [similarity] - rape  
C;Species: Brassica napus (rape)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C;Accession: JQ2337  
R;Radav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.;  
J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browne, J.  
Plant Physiol. 103, 467-476, 1993  
A;Title: Cloning of higher plant omega-3 fatty acid desaturases.  
A;Reference number: JQ2335; MUID:94302147; PMID:8029334  
A;Contents: cDNA:BN3  
A;Accession: JQ2337  
A;Molecule type: mRNA  
A;Residues: 1-377 <YAD>  
A;Cross-references: GB:L22962; NID:g408491; PIDN:AAA61775.1; PID:g408492  
C;Comment: This enzyme introduces the third double bond in the biosynthesis of 18:2 and

C:Superfamily: omega-3 fatty acid desaturase  
C:Keywords: oxidoreductase

Query Match 6.1%; Score 148.5; DB 1; Length 377;  
Best Local Similarity 23.6%; Pred. No. 8.1e-05;  
Matches 91; Conservative 58; Mismatches 137; Indels 99; Gaps 25;  
QY 88 PLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFKTNHVFLLALLAHIALESIA 147  
Db 24 PFKIGDIRAAIP-----KHCWKSPLRSMYSVARD-----IFAVVALLA-VAAYVYFDS 69  
QY 148 WF--TVFPGNWIPTLITA-FVLATSOAQAGWLOHDYCHLSVYRKPKWN-----HLVHKF 200  
Db 70 WFFWFLYAAQAG--TLFWAIFVLG-----HDCGHSFSDIPLLNTAVGHILRSP 116  
QY 201 VTCHLKGASANNWNRHFFOHAKPNI FHKDPDNNMLHVFVLGEMOPIEYGGKKLKLIPYN 260  
Db 117 ILVPYHG-----WRISHRTHH--QNHGHNDES-----WVPLP--EKLYKNLSHS 158  
QY 261 HQHEVFFLIGPPLIPMFQYQIIMTVHKH-----WDLAWAY 300  
Db 159 TMLRYTVLEPLMLAYPLXLYWSPGKSGSHYNYPSLFPAPGERKLIATSTTCW-SIMLAT 217  
QY 301 SVYIRFP---ITVIPPYGLGALLFLNPIRFLFESHWFVMTOMNHVMEIDQAYR--DW 355  
Db 218 LVYLSFLVCPVTLKYGV---PYIIFWMLDA-----VTYLHHGHDDKLPWYRGKEW 268  
QY 356 --FSSQLTATCNVEOSFFNDFSGHNLFOIEHHLPTWPRNLHKLAPLVKSLCAKH--G 411  
Db 269 SVYRGGLT-TIDRDYGIFFNN-IHHDIGTHVHHLFPQIPHYHL---VDATEKS--AKHVLG 321  
QY 412 IEYOEKPLRAL-LDIIRSLKSGK 435  
Db 322 RYREPKTSGAIPHILVESLVSIAK 346

## RESULT 31

A44227  
omega-3 fatty acid desaturase (EC 1.14.99.-) [similarity] - rape  
N:Alternate names: omega-3 linoleate desaturase  
C:Species: Brassica napus (rape)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: A44227  
R:Arondel, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.  
Science 258, 1353-1355, 1992  
A:Title: Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arab  
A:Reference number: A44227; MUID:93088059; PMID:1455229  
A:Accession: A44227  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-383 <ARO>  
A:Cross-references: GB:I01418; NID:G167147; PIDN:AAA32994.1; PID:G167148  
A:Experimental source: developing seed  
A:Note: sequence extracted from NCBI backbone (NCBIP:119842)  
C:Superfamily: omega-3 fatty acid desaturase  
C:Keywords: oxidoreductase

Query Match 6.1%; Score 148.5; DB 1; Length 383;  
Best Local Similarity 22.5%; Pred. No. 8.3e-05;  
Matches 92; Conservative 62; Mismatches 149; Indels 105; Gaps 25;  
QY 65 GEDATDAFAFHFDLEFVGKFLPLIGELAPEPSQDHGKNSKITEDFRALRKTAEADN 124  
Db 13 GDSGARKEBGFDSAQ-----PPFKIGDIRAIP-----KHCWKSPLRSMYS----- 54  
QY 125 LFTKNHVFLLALLAHIALESIAWF--TVFYFGNGWIPITLITA-FVLATSOAQAGWLOHD 181  
Db 55 -YVTRDIFAVALA-NAAYVYFDSWFLWPLYWVAQ--TLFWAIFVLG-----HD 99  
QY 182 YGHLVYRKPKWN-----HLVHKFVIGHLKASANNWNRHFFOHAKPNI FHKDPDNNMLH 237  
Db 100 CGHGSFSDIPLLNSVVGHLHSLFVLYHG-----WRISHRTHH--QNHGHNDES--- 149

## RESULT 32

S43771  
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)  
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misidenti  
C:Species: Synecococcus sp.  
A:Variety: PCC 7002  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S43771  
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.  
Plant Mol. Biol. 24, 643-650, 1994  
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacter  
A:Reference number: S43770; MUID:94207189; PMID:8155883  
A:Accession: S43771  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-347 <SAK>  
A:Cross-references: GB:D13779; NID:G488510; PIDN:BAA02922.1; PID:G488511  
C:Superfamily: omega-3 fatty acid desaturase  
C:Keywords: oxidoreductase

Query Match 6.1%; Score 148; DB 2; Length 347;  
Best Local Similarity 22.5%; Pred. No. 8.1e-05;  
Matches 75; Conservative 58; Mismatches 120; Indels 80; Gaps 18;

QY 106 NSKITEDFRALRKTAEADNLFKT-NHVFLLALLAHII---ALESIA-WFTVF--YFGNGW 158  
Db 19 NLRLRIDLTLPKSVTEINPLKASRV--LLSVAVVGCVALLAIAFVWLLPWLGTG- 75  
QY 159 IPTLITAFVLATSOAQAGWLOHDYCHLSVYRKPKWNHVLKFKVIGHLKASANNW----WN 214  
Db 76 --ITLTGFPV-----IGHDCGHSFSPSRKWNWNLV-----GHAFPLPLIYPFHSWR 119  
QY 215 HRHFQHHAKENIFHKDPDNNMLHVFVLGEMOPIEYGGKKLKLIP--YNNHQHEVFFLIGPP 272  
Db 120 ILNHHHRYTNNMDED-----NAWAP-----FTELYDDSPAFIKAVYRA 159  
QY 273 LLIPMFQYQIIMTVHKWN-----VDLAWAVSYIIRFFITYIPFYG 315  
Db 160 IRGKLWLASVHQLKLFHNFNFAFEGKQREQVRSALFVIAAGAIAPVPMFYT-----LG 214  
QY 316 ILGALLFLNPIRFLFESH-WFVWVMTOMNHVMEIDQAYRDNFS---SOLTATCNVEQSFF 371  
Db 215 WGVYKFW-LMPWLGWYHFMNSTFTLVHHTVPEI-PFSYRDKWNEA-AQLSGTVHCDYPKW 272  
QY 372 NDFPSGHLNFOIEHHLPTWPRNLHKLAPLVK 404  
Db 273 VEVLCHDINVHVPHLLSTGIPSYNLKAYASIK 305

## RESULT 33

T10063  
Omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - castor bean  
N:Alternate names: linoleoyl desaturase  
C:Species: Ricinus communis (castor bean)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: T10063





Db 194 MFLIYEPWRPKDQHTKTWMLREDTAWLPIMKEDTSSPGLRKALIIYAVGLRTWMS 253  
Qy 247 IEYGGKKLKYLPYNHGEY-----FFLIGPPLLIPMYFOYQIIMTIVHKWV 294  
Db 254 IAHWLKVHFNKDFQSEVKRATISLAFAFPMVIGWPL-----IYKTGI 299  
Qy 295 DIAMAVSYIRFFIYIPFYIGLALLFLNFIREFLESHFWVVTQMNHIVMEIDQEAIRD 354  
Db 300 -VGW-----IKFWL--MPWLG-----HFMSTFTIVHTAPHIPKSSKE 337  
Qy 355 W--FSSQATATCNVCQSFNDWFSHLNFOEHLFPMPDRHNLKIAPIVKSICAKHGI 412  
Db 338 WMAAQALSGVCHDPRMIEIICHDISVHIPHISPKIPSYNLRAN---OSLNENWG- 393  
Qy 413 EYQEXP-----LLRALDIIRSLKSG 434  
Db 394 EYLNPKSNWRLMRTIMTCHYIDKG 420

## RESULT 36

JC5596  
cytochrome b5, brain splice form - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 05-May-2000  
C:Accession: JC5596  
R:Yoo, M.  
Biochem. Biophys. Res. Commun. 236, 641-642, 1997  
A:Title: Identification of two homologous cytochrome b5s in rat brain.  
A:Reference number: JC5596, MUID:97396150; PMID:9245704  
A:Accession: JC5596  
A:Molecule type: mRNA  
A:Residues: 1-100 <FOO>  
A:Cross-references: DDBJ:AF007107; NID:92257954; PIDN:AAB67609.1; PID:92257955  
C:Experimental source: brain  
C:Superfamily: cytochrome b5; cytochrome b5 core homology  
C:Keywords: alternative splicing; heme; iron; metalloprotein  
F:9-84/Domain: cytochrome b5 core homology <CB5>  
F:44/68/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.0%; Score 145.5; DB 2; Length 100;  
Best Local Similarity 35.1%; Pred. No. 2.9e-05;  
Matches 34; Conservative 20; Mismatches 30; Indels 13; Gaps 2;  
Qy 11 AAREVSVTFEWEIEQKHLRTDGLVIDRKYVNTKWSIQHGGQGVIGHYAGEDATD 70  
Db 2 AEGSDKVKYILEIQKDKSKSTWILHHKVYDLTKLEHPSGGEVLRQAGGDATE 61  
Qy 71 AFRAPHPLDFVG-----KFLKPLLIGELAPEPSQ 101  
Db 62 NF-----EDVGHSTDAEELSKVTYIGELHPDRSK 91

## RESULT 37

T19614  
probable cytochrome b5 C31E10.7 [similarity] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T19614  
R:Swihurne, J.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z19151  
A:Accession: T19614  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-138 <WIL>  
A:Cross-references: EMBL:Z78539; PIDN:CAB01732.1; GSPDB:GN00028; CESP:C31E10.7  
C:Experimental source: clone C31E10  
C:Genetics:  
A:Gene: CESP:C31E10.7  
A:Map position: X  
A:Introns: 42/3; 85/3; 111/2  
C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: heme; iron; metalloprotein  
F:43/67/Binding site: heme iron (His) (axial ligands) #status predicted  
Query Match 6.0%; Score 145.5; DB 2; Length 138;  
Best Local Similarity 30.9%; Pred. No. 4.3e-05;  
Matches 46; Conservative 26; Mismatches 50; Indels 27; Gaps 6;  
Qy 14 REVSVTFEWEIEQKHLRTDGLVIDRKYVNTKWSIQHGGQGVIGHYAGEDATDAPR 73  
Db 4 RMADLQKITLKEIAEHTNKSAWLIGNKVFDFLDEHPGCGCEVLLQAGSDGTEAFE 63  
Qy 74 -----AHPDLEFVGKFLKPLLIGE-LAPEPSODHGKNS-KITEDFRAUKRTAEDNN 124  
Db 64 DVGHSTDAHKMDEY-----LGEVVASERKYISYDKKWKSTTEQDNKQRGESM- 114  
Qy 125 LFKTNHVFLLLAHIIALESIAWFTVFY 153  
Db 115 -QTDNIVVFALLAIVAL-----VYY 134

## RESULT 38

JC2555  
omega-3 fatty acid desaturase - common tobacco (cv. SR1)  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 20-Jun-2000  
C:Accession: JC2555  
R:Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.  
Gene 147, 293-294, 1994  
A:Title: Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.  
A:Reference number: JC2555; MUID:95011632; PMID:7926817  
A:Accession: JC2555  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-379 <HAM>  
A:Cross-references: DDBJ:D26509; NID:91311480; PIDN:BA05515.1; PID:9599592  
C:Superfamily: omega-3 fatty acid desaturase

Query Match 6.0%; Score 145.5; DB 2; Length 379;  
Best Local Similarity 21.3%; Pred. No. 0.00015;  
Matches 86; Conservative 56; Mismatches 143; Indels 119; Gaps 23;  
Qy 78 DLEFVGKFLKPLLIGELAPEPSODHGKNSKITEDFRAUKRTAEDNNLKTNNHVFLLLL 137  
Db 19 EFEFDPSAPPPFLAIRNIP-----KHCWKDPURLSVYVRDV-----IFVATLI 66  
Qy 138 AHIIALESIAWFTVFYFGNGWIPTLITA-FVLATSOAQAGWLQHDYGHLSVYRKPKWN-- 194  
Db 67 GIAIHLDNLFFLYWAIQG---TWFAIFVLG-----HDCGHGSPSDSOLLNV 113  
Qy 195 --HLVHKFVIGHLKGASANNWHRHFOHAKPNIHKDPDVMMLHVFVLGEWQP----- 246  
Db 114 VGHILSAAILVPYHG-----WRISHKTHHQNGVETDE-----SWVPMPEKLY 157  
Qy 247 --IEYGGKKLKY-LPYNHQHEYFFLIGPPLLIPMYF----- 279  
Db 158 NKGYSTKFLRYKIPP-----PFLAYPMYLMKSPGKSGSHENFYSDLPQFHER 206  
Qy 280 QYQIIMTIVHKWDLAWAVSYIRFFIYIPFYIGLGA--LLFLNFIREFLESHFWV 337  
Db 207 KYVVTSLC---WTVMA-ALLYLCTAFGSLQMFKIYGAPYLIFV-----MWLDVF 253  
Qy 338 TOMNHIWMEIDQEAIR--DW--FSSQATATCNVCQSFNDWFSHLNFOEHLHFTMPR 393  
Db 254 TYLHHGYEKKLPYRGKESWYLRGGLT-JVDYDYGFLFN- IHHDIGTHVHILFPQIPH 311  
Qy 394 HNLKIAPIVKSICAKHGEIYQEK----PL-LRALDIIRSLK 432  
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## RESULT 39

CECH5  
cytochrome b5 precursor - chicken





http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DD007CE05NP1.

## FEATURES

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source
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      /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      261 a  345 c  240 t  19 others
ORIGIN
Query Match      34.9%; Score 1110.6; DB 9; Length 1201;
Best Local Similarity 97.3%; Pred. No. 1.1e-221;
Matches 1109; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 97 CCGGCTGGGAGGACGCGTCTGTGACGACGACCGCGCGGGAGCGCGCAGTGACG 156
DB 61 CCGGCTGGGAGGACGCGTCTGTGACGACGACCGCGCGGGAGCGCGCAGTGACG 120

QY 157 GGGCGTCACAGTCGCGACGAGCATGGGAGGAGGAGGACCGAGGCGGCGCGCG 216
DB 121 GGGCGTCACAGTCGCGACGAGCATGGGAGGAGGAGGAGGAGGAGGCGGCGCG 180

QY 217 AGCGCGAGGTGTGCGTGCACCTTCCAGCTGGGAGGAGATTCAGAACATTAACCTGGCA 276
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QY 277 CGGACAGTGGCGTGTGATTCACCGCAGGTTTACACATCACCACATGCTCCATCCAGC 336
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QY 337 ACCCGGGGGCCAGCGGGTCTATCGGGCACTACGCTGGAGAGATGCAACGAGTCCCTCC 396
DB 301 ACCCGGGGGCCAGCGGGTCTATCGGGCACTACGCTGGAGAGATGCAACGAGTCCCTCC 360

QY 397 GGGCTTCCACCTGACCTGATTCGTTGGCAGATTTCTTCAACCCCTGCTGATTCGGTG 456
DB 361 GGGCTTCCACCTGACCTGATTCGTTGGCAGATTTCTTCAACCCCTGCTGATTCGGTG 420

QY 457 AACTGGCCCGGAGAGCCAGCCAGGACCCAGGACCAAGAACTCAAGATCACTGAGGACT 516
DB 421 AACTGGCCCGGAGAGCCAGCCAGGACCCAGGACCAAGAACTCAAGATCACTGAGGACT 480

QY 517 TCCGGCCCTGAGGAGAGCGGTGAGGACATGAACCTGTTCAAGACCAACCAAGTGTCT 576
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QY 577 TCTCTCTCTCTGCGCCACATCATCGCCCTGGAGAGCATTCGATGTTCACTGCTTCT 636
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QY 637 ACTTTGGCAATGGCTGATTCCTACCTCATACCGGCTTTGCTCTGCTACCTCTCAGG 696
DB 601 ACTTTGGCAATGGCTGATTCCTACCTCATACCGGCTTTGCTCTGCTACCTCTCAGG 660

QY 697 CCCAGCTGGAGTGGTCAACATGATTATGGCCACTGCTGCTTACAGAAACCCCAAGT 756
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QY 757 GGAACCACTTGTCCACAAATTTGTCATTGGCCACTTAAGGGTGCTCTGCGCAACTGGT 816
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QY 817 GGAATCATGCCACTTCCAGCAGCCAGCCAGCCTTAACATCTTCCACAGGATCCCGATG 876
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QY 877 TGAACATGCTGCACGCTGTTTGTCTGGCGAATGGCGACCCATCGAGTACGGCAAGAGA 936
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QY 937 AGCTGGAATACCTCGCTTACAAATCACCAGACAGCAATATCTTCTCTCATTTGGCGCGCGC 996
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QY 997 TGCTCATCCCCCATGTAATTCAGTACAGATCATCATGATCATGCTGCTCATAGAACT 1056
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QY 1057 GGTGGACCTGCGCTGGCGCGTCACTACATCCCGTCTTCTCATCACCTCATACCTCTT 1116
DB 1021 GGTGGACCTGCGCTGGCGCGTCACTACATCCCGTCTTCTCATCACCTCATACCTCTT 1080

QY 1117 TCTACGGCATCCTGGAGCCCTCTTTTCTCAATCTCATCAGTTCTCTGGAGAGCACT 1176
DB 1081 TCTACGGCATCCTGGAGCCCTCTTTTCTCAATCTCATCAGTTCTCTGGAGAGCACT 1140

QY 1177 GGTGTTGCTGGTCAACAGATGAATCATCGTCATGGAGATTCAGCAGGAGCCTTACC 1236
DB 1141 GGTGTTGCTGGTGAACAAAWRAAWMAWCGTCATGAGATGAAACAGAGGCGCHCCB 1200

RESULT 2
ALS30345      1201 bp      mRNA      linear      EST 23-MAY-2003
LOCUS      ALS30345 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION      CDNA clone CS0DD007YJ09 3-PRIME, mRNA sequence.
ACCESSION      ALS30345
VERSION        ALS30345.2 GI:31068178
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1. (bases 1 to 1201)
AUTHORS        Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
COMMENT        On Feb 13, 2001 this sequence version replaced gi:12793838.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6148.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CE05NP1&cluster=6148.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CE05NP1.
FEATURES
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    /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      235 a  375 c  344 g  200 t  47 others
ORIGIN
Query Match      32.9%; Score 1049; DB 9; Length 1201;
Best Local Similarity 93.0%; Pred. No. 8.1e-209;
Matches 1096; Conservative 38; Mismatches 38; Indels 6; Gaps 4;

```



AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2862)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-3216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers

FEATURES

source 1..2862

organism="Mus musculus"

mol\_type="mRNA"

strain="C57BL/6J"

db\_xref="FANTOM\_DB.C630034B17"

db\_xref="taxon:10090"

clone="C630034B17"

sex="male"

tissue\_type="hippocampus"

clone\_lib="RIKEN full-length enriched mouse cDNA library"

dev\_stage="adult"

misc\_feature 115..1376

note="fatty acid desaturase 2 (MGD|MGI:1930079, GI:19699, evidence: BLASTN, 100%, match=1266)

polyA\_signal 2845..2850

note="putative"

polyA\_site 2862

note="putative"

BASE COUNT 637 a 779 c 758 g 688 t

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Query Match 32.2%; Score 1023.8; DB 11; Length 2862;

Best Local Similarity 78.5%; Pred. No. 1.6e-203;

Matches 1310; Conservative 0; Mismatches 282; Indels 77; Gaps 4;

QY 68 GAAGCGAAGGCGCGGCTGCACACACCGGCTGGAG-GCAGCGCTGTGTGAGCGA 126

Db 2 GAAGCGAGGAGGCGCGGACCGCACACTCGCGCCAGGAGGAGCGGTGGTGGCA 61

QY 127 GCAGCGCGCGGAGGCGCGAGTCACGCGGGCGTCACAGTCGGGAGGAGCATGGGGA 186

Db 62 GCAGCGCGCGCGGAGGCGGTAGCGACACGCGGCATCCGGGTAGACTGGCAGCATGGGA 121

QY 187 AGGAGGAGACCGGCGAGGGGCGCCCGAGCGAGGTGTGCGTGCACCTTCAGCT 246

Db 122 AGGAGGAGTACCGGAGGAGGGAGGACCGAGCGCCAGGCGCGGATGCCACCTCCGTT 181

QY 247 GGGAGGAGATTTCAGAGCATAACTGTGCGCACCGACAGTGGGCTGGTCAATTGACCGCAAG 306

Db 182 GGGAGGAGATTTCAGAGCATAACTGTGCGCACCGACAGTGGGCTGGTCAATTGACCGCAAG 212

QY 307 TTTTCAACATCA CAAATGTTCATCCAGCACCCGGGGGCGCAGCGGTCATCGGSCACT 366

Db 213 -----CGTGTTCATCGGCACT 228

QY 367 ACCTGGAGAGATGCAACCGATGCCTTCGGCGCTTCCACCCCTGACCTGGATTCGTGG 426

Db 229 ATTGCGGAGAGATGCTACCGATGCCCTTCGTCCTCTCCATCTGACCTGGATTCGTGG 288

QY 427 GCAAGTTCTTTAAACCCCTCTGATTGGTGAATGCGCCCGGAGGAGCCAGCAGGACC 486

Db 289 GCAAGTTCTTTAAAGCCCTCTGATTGGTGAATGCGCCCGGAGGAGCCAGCAGGACC 348

QY 487 ACGCCAAGAACTCAAGATCACTGAGACTTCGGCGCCCTGAGGAAGAGCGCTGAGACA 546

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QY 547 TGAACCTGTTTCAAGACCAACCAAGTGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 606

Db 409 TGAACCTCTTCAAAACCAACCAAGTGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 468

QY 607 TGGAGAGATTGATGATGCTTCACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 666

Db 469 TGGAAAGCTTGTGCTGCTGCTTCACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 528

QY 667 TCAGCGCTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 726

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Db 709 AGCCCAACATCTTCCACAGAGATCCCGACATAAAGAGCCCTGCAATGTGTGTGTGTGGCG 768

QY 907 AATGGCGACCATCGAGTACGCAAGAAAGTGAATACCTGCCCTTCAATCAACACGACG 966

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QY 967 ACGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1026

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QY 1027 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCTGGCGCTCAGCTACT 1086

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QY 1147 TCACCTTCATCAGGTTCTTCTGGAGGCCACTGTGTGTGGTGCACACAGATGAATCA 1206

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QY 1327 TTGAGCACCACTCTTCTCCCACTATGCCCGGCGCAACTTACACAGATCGCCCGCTGG 1386



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Db 1189 TTGAGCACACCTCTTCCACATATGCAACCTGCAACAGATTGCCCACTGG 1248
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Qy 1567 AGA-GGAATGATGGCTTTTGTCTGAGGGGTGCGAGAGGCTGTGATGACACTGCTC 1625
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clone CSOD1040YK05 3-PRIME, mRNA sequence.
ACCESSION BX397627
VERSION BX397627.1 GI:30629236
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 1127)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1040AF03NP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1040AF03NP1.
FEATURES
Location/Qualifiers
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 218 a 345 c 324 g 222 t 18 others
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Query Match 31.1%; Score 990.8; DB 13; Length 1127;
Best Local Similarity 97.4%; Pred. No. 1.2e-196;
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Qy 2173 ATCACTAGAGTGTCTGACCTCGGCTTTCAGCGGCGCCATTCACGCGCTCCG-CAACT 2231
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Qy 2292 AGTGGCCACCTTCAGGAGGGCGCGGCTGGAGGCTCAGCCACCTTCAGCTTTT 2351
Db 873 AGTGGCCACCTTCAGGAGGGCGCGGCTGGAGGCTCAGCCACCTTCAGCTTTT 814
Qy 2352 CCTCAGGGGTGCTGAGGTCCAAAGATTCTGAGCAATCTGAGCCCTTCTTCAAAGGCTCTG 2411
Db 813 CCTCAGGGGTGCTGAGGTCCAAAGATTCTGAGCAATCTGAGCCCTTCTTCAAAGGCTCTG 754
Qy 2412 TTATCAGCTGGGCGAGTCCAGCCCAATCCTCGGCAATTTGGCCGCCAGGGGAGAGTGGGCC 2471
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Qy 2472 TGCAGGCTGCAGGAGGGGCACTGGAGTGGGAGGCTCGTCCAGCCCTCCCATCTCGGG 2531
Db 694 TGCAGGCTGCAGGAGGGGCACTGGAGTGGGAGGCTCGTCCAGCCCTCCCATCTCGGG 635
Qy 2532 GCTGTGTGTGAGGCGGCTGCTCAGCACTCTCTGTCTGAACTGCGCTTACTGTGT 2591
Db 634 GCTGTGTGTGAGGCGGCTGCTCAGCACTCTCTGTCTGAACTGCGCTTACTGTGT 575
Qy 2592 TTAACCTGTTCTCCAGGATGCATCTGATAGGAGGGGCGGAGGCTGGGCTTGTGA 2651
Db 574 TTAACCTGTTCTCCAGGATGCATCTGATAGGAGGGGCGGAGGCTGGGCTTGTGA 515
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Db 514 CAATCTGCTTTTCAACCATGCGCTTGTCTCGTGGGCGCTTACTGTTCAGGAGGCGCAGG 455
Qy 2712 GAGCGAGAGCGGAGGGAGTCTCAGGAGGAGGCTGCGCTGAGGGGCTGGGAGGGGTAC 2771
Db 454 GAGCGAGAGCGGAGGGAGTCTCAGGAGGAGGCTGCGCTGAGGGGCTGGGAGGGGTAC 395
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Qy 3132 CTTCCCGACCCCTACATTTTGTAAATAATAAATAA 3165
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ACCESSION BX355607
VERSION BX355607.1 GI:30375985
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1001DD06QPI&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1001DD06QPI.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 217 a 361 c 353 g 251 t 19 others
ORIGIN
Query Match 30.8%; Score 979.8; DB 13; Length 1201;
Best Local Similarity 98.1%; Pred. No. 2.4e-194;
Matches 1017; Conservative 5; Mismatches 12; Indels 3; Gaps 3;

QY 1693 CCCTCCCTCATTGGGACCTGCTCCCTCCTCAGCCCTCAGCCATCAGCCATGCCCTCCAG 1752
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QY 1753 TGCTCCCTAGCCCTTCTTCAAGAGAGAGAGAGGTGGCCACCGGGGGTGGCTCTGCT 1812
DB 121 TGCTCCCTAGCCCTTCTTCAAGAGAGAGAGAGGTGGCCACCGGGGGTGGCTCTGCT 180
QY 1813 ACCTCCACTCTGCCCCCTAAAGATGGAGAGAGAGAGCGGTCCATGGCTGGCCCTGTG 1872
DB 181 ACCTCCACTCTGCCCCCTAAAGATGGAGAGAGAGAGCGGTCCATGGCTGGCCCTGTG 240
QY 1873 AGCTCCCTCTGACGCTGGTCACTAGGATCACCCTCCCTTGGTCTTCAGATGCTCT 1932
DB 241 AGCTCCCTCTGACGCTGGTCACTAGGATCACCCTCCCTTGGTCTTCAGATGCTCT 300
QY 1933 TGGGGTTCATAGGGGACGCTCTAGTCCGGGAGGCGCCCTGACCTCCGGCCCTGGCTTC 1992
DB 301 TGGGGTTCATAGGGGACGCTCTAGTCCGGGAGGCGCCCTGACCTCCGGCCCTGGCTTC 360
QY 1993 ACTCTCCCTGAGCGGTGCATGGTCCACCTTTTCATAGAGAGCGCTCTTGTACAAA 2052
DB 361 ACTCTCCCTGAGCGGTGCATGGTCCACCTTTTCATAGAGAGCGCTCTTGTACAAA 420

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QY 2053 GCTCGGCTCTCCCTCCTGCGAGCTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTCCAGG 2112
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QY 2113 GCCCAGGCGCGCGGACAGCCAGCCAGCCAAACCTTTGGGCGCTGGAAGAGTCTTCACACCC 2172
DB 481 GCCCAGGCGCGCGGACAGCCAGCCAGCCAAACCTTTGGGCGCTGGAAGAGTCTTCACACCC 540
QY 2173 ATCACTAGAGTCTCTGACCTGCGCTTTTCAAGGCGCCCAATTCACCGCTTCCCAACTT 2232
DB 541 ATCACTAGAGTCTCTGACCTGCGCTTTTCAAGGCGCCCAATTCACCGCTTCCCAACTT 600
QY 2233 GAGCTGTGACCTTTGGGACCAAAAGGAGTCCCTCTCTCTTCTGCTACTCAGCAGAGGCA 2292
DB 601 GAGCTGTGACCTTTGGGACCAAAAGGAGTCCCTCTCTCTTCTGCTACTCAGCAGAGGCA 660
QY 2293 GTGCCACGTTTCAAGGAGGCGCGCTGGCTGGAGGCTCAGCCACCTTCAGCTTTTC 2352
DB 661 GTGCCACGTTTCAAGGAGGCGCGCTGGCTGGAGGCTCAGCCACCTTCAGCTTTTC 720
QY 2353 CTCAGGCTCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTG 2412
DB 721 CTCAGGCTCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTG 780
QY 2413 TATCAGCTGGGCGAGTGCAGCCAAATCCCTGCGCAATTTGGCCAGGCGGACGTGGGCGCT 2472
DB 781 TATCAGCTGGGCGAGTGCAGCCAAATCCCTGCGCAATTTGGCCAGGCGGACGTGGGCGCT 839
QY 2473 GCAGCTCAGAGGAGGCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTG 2532
DB 840 GCAGCTCAGAGGAGGCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTGAGGTCCTG 898
QY 2533 CTGCTGTGTGGACGCGCTGCTCAGGCACTCTCTCTGCTGAACTGCTGCTTACTGTGT 2592
DB 899 CTGCTGTGTGGACGCGCTGCTCAGGCACTCTCTCTGCTGAACTGCTGCTTACTGTGT 957
QY 2593 TAACCTGTGTCTCAGGATGATCTGATAGAGGCGGCGGCGGCTGGGCTTGTGAC 2652
DB 958 TAACCTGTGTCTCAGGATGATCTGATAGAGGCGGCGGCGGCTGGGCTTGTGAC 1017
QY 2653 AATCTGCTCTTCCACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2712
DB 1018 AATCTGCTCTTCCACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077
QY 2713 AGCGAGCGGAGGGA 2729
DB 1078 AAGCARAAGCGGAGGAA 1094

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RESULT 6
AL520270
LOCUS
DEFINITION AL520270 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
cDNA clone CSODB006YM17 5-PRIME, mRNA sequence.
ACCESSION AL520270
VERSION AL520270.2 GI:31038611
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12783763.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see

```

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DB006AG09QPl&cluster=6148.f>. Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DB006AG09QPl.

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DB006YM17"  
/tissue type="NEUROBLASTOMA COT 10-NORMALIZED"  
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/note="1st strand cDNA was primed, with a NotI-oligo(GT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." BASE COUNT 222 a 334 c 373 g 243 t 29 others  
ORIGIN  
Query Match 30.4%; Score 967.2; DB 9; Length 1201;  
Best Local Similarity 97.9%; Pred. No. 1e-191;  
Matches 1022; Conservative 9; Mismatches 7; Indels 6; Gaps 5;  
QY 1966 GGCCTCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTTGCTCCACCTT 2025  
Db 63 GGGATCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTTGCTCCACCTT 122  
QY 2026 TCATAGAGAGCGCTGCTTTGTTACAAAGCTCGGTCTCCCTCTGAGAGCTCGGTAAAGTA 2085  
Db 123 TCATAGAGAGCGCTGCTTTGTTACAAAGCTCGGTCTCCCTCTGAGAGCTCGGTAAAGTA 182  
QY 2086 CCCGAGGCGCTCTTTAAGATGTCAGGGCCCGGCGGCGGACAGCCAGCCCAACC 2145  
Db 193 CCCGAGGCGCTCTTTAAGATGTCAGGGCCCGGCGGCGGACAGCCAGCCCAACC 242  
QY 2146 TTGGCCCTGGAAGAGTCTCCACCCCATCTAGAGTCTCTGACCTGGCTTTCAAG 2205  
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Db 303 GGCCTCATCCAGCGCTCCCAACTTGAGCTGTGACCTTGAGCCCAAGAGGGGAGTCC 362  
QY 2266 CTGCTCTTTGACTCAGCAGAGAGCAGTGCACCTGTCAGGGAGGGCGCGCTGGCTG 2325  
Db 363 CTGCTCTTTGACTCAGCAGAGAGCAGTGCACCTGTCAGGGAGGGCGCGCTGGCTG 422  
QY 2326 GAGGCTCAGCCACCTCCACCTTTCTCAGGCTGTCTGAGTCCCAAGATTTGAGC 2385  
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QY 2386 AATCTGACCTTCTCCAAAGCTCTGTTATCAGCTGGGCGAGTGCAGCCCAATCCCTGGCC 2445  
Db 483 AATCTGACCTTCTCCAAAGCTCTGTTATCAGCTGGGCGAGTGCAGCCCAATCCCTGGCC 542  
QY 2446 ATTTGGCCAGGGGAGCTGGGCGCTGCAGCTGCAGAGGGCAGTGGAGCTGGAGGT 2505  
Db 543 ATTTGGCCAGGGGAGCTGGGCGCTGCAGCTGCAGAGGGCAGTGGAGCTGGAGGT 601  
QY 2506 CTGCTCCAGCGCTCCCATCTCGGGGCTGTGTGTGAGAGGGCGCTGCCTCAGCACTCT 2565  
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QY 2566 CTGCTGAACTGCGCTTACTGTGTTAACTGTTGCTCAGGATGATCTGATAGGA 2625  
Db 662 CTGCTGAACTGCGCTTACTGTGTTAACTGTTGCTCAGGATGATCTGATAGGA 721  
QY 2626 GGGGCGGCGAGGCTGGGCTTTGACAACTGCTTTTACCAATGCTTCCATGCTTCCCTGCT 2685  
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QY 2686 GGCCTTGACTCTCAGGGAGGGCCAGGGAGGCGAGAGGGAGTCTCAGGAGGAGCT 2745

Db 782 GGCCTTGACTGTGAGGAGGGCCAGGAGGAGAGAGCGGAGGAGCTCTCAGGAGGAGCT 841  
QY 2746 GCCTCTGAGGGCTGGGAGGGGCTACCTCATGAGGAGCAGAGGAGTGGAGTGAAGAGGAG 2805  
Db 842 GCCTCTGAGGGCTGGGAGGGGCTA-CTCATGAGGAGCAGGGTGGAGCTGAGAGGAGG 900  
QY 2806 GAGGTGGGGCTGGAGGTGCTGCTGAGTGGAGGGGCGGCAAGTGAAGGGGAGGAGG 2865  
Db 901 GAGGTGGGGCTGGAGGTGCTGCTGAGTGGAGGGGCGGCAAGTGAAGGGGAGGAGG 960  
QY 2866 AAGTCTGGGAGGATCTTGAGCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2925  
Db 961 AAGTCTGGGAGGAT-CTGAGCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1019  
QY 2926 CAGGGGAGGGGAGGAGCACCACCACTCAGAACTGAGGAGGGGCTTTTCGGGAGGGCGCTAGTCC 2985  
Db 1020 CAGGGGAGGGG-AGGSAMCAACAACAACAACAACAACAACAACAACAACAACAACA 1076  
QY 2986 CCCCAGCTCTAAGCAGCCAGGAGG 3009  
Db 1077 CCCCAGCTCTAAGCAGCCAGGAGG 1100

## RESULT 7

BX417399 1201 bp mRNA linear EST 13-MAY-2003  
LOCUS BX417399 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009FE07  
DEFINITION 5-PRIME, mRNA sequence.  
ACCESSION BX417399  
VERSION BX417399.1 GI:30658393  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bonyfish; Eutheraia; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6148.f For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE009AC04QPl&cluster=6148.f>. Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DE009AC04QPl.

## FEATURES

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/clone="CS0DE009FE07"  
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/clone lib="Homo sapiens PLACENTA"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." BASE COUNT 282 a 321 c 306 g 237 t 55 others  
ORIGIN

Query Match 29.9%; Score 953.4; DB 13; Length 1201;  
Best Local Similarity 95.0%; Pred. No. 8e-189;  
Matches 997; Conservative 25; Mismatches 22; Indels 6; Gaps 4;  
QY 106 AGGCGAGCCCTGCTGTGACGAGGAGCGGCGGAGGAGCGGCGGAGTGTGACGAGGAGGCT 165



|    |      |     |   |      |
|----|------|-----|---|------|
| QY | 2559 | GC  | ACTCTCTCTGCTGGAACCTGCGCCCTTACTGTGTTTAACTGTGCTCCAGGATGCATCTCT  | 2618 |
| Db | 600  | GC  | ACTCTCTCTGCTGGAACCTGCGCCCTTACTGTGTTTAACTGTGCTCCAGGATGCATCTCT  | 541  |
| QY | 2619 | GAT | AGAGGGGGGGCGGACGGGCTGGCCCTTCTGTGACATCTGCCCTTACCAACATGGCCTTG   | 2678 |
| Db | 540  | GAT | AGAGGGGGGGCGGACGGGCTGGCCCTTCTGTGACATCTGCCCTTACCAACATGGCCTTG   | 481  |
| QY | 2679 | CT  | TCGGTGGCCCTGACTGTTCAGGAGGGCCAGGAGGCGACAGGGGAGGAGTCTCAGGA      | 2738 |
| Db | 480  | CT  | TCGGTGGCCCTGACTGTTCAGGAGGGCCAGGAGGCGACAGGGGAGGAGTCTCAGGA      | 421  |
| QY | 2739 | GA  | AGGCTGCCCTCAGGGGCTGGGAGGGGCTACTCATGAGGACACAGGCTGGAGCTGAGA     | 2798 |
| Db | 420  | GA  | AGGCTGCCCTCAGGGGCTGGGAGGGGTACTCATGAGGACACAGGCTGGAGCTGAGA      | 361  |
| QY | 2799 | AG  | AGGAGGAGGTGGGGCTCGAGGCTGTGTAGCTGAGGGGACGGCCAACTGAGAGGGGA      | 2858 |
| Db | 360  | AG  | AGGAGGAGGTGGGGCTCGAGGCTGTGTAGCTGAGGGGACGGCCAACTGAGAGGGGA      | 301  |
| QY | 2859 | GG  | AGGGAGTCTCTGGGAGGATCCTGAGCTGCTGTTCAGTCTAAACCACTAATCAGTTC      | 2918 |
| Db | 300  | GG  | AGGGAGTCTCTGGGAGGATCCTGAGCTGCTGTTCAGTCTAAACCACTAATCAGTTC      | 241  |
| QY | 2919 | TT  | AGATTTCAGGGAAAGGCGAGGCACCAACAACCTCAGAATGGGGGCTTTCCGGGAGAGCGCG | 2978 |
| Db | 240  | TT  | AGATTTCAGGGAAAGGCGAGGCACCAACAACCTCAGAATGGGGGCTTTCCGGGAGAGCGCG | 181  |
| QY | 2979 | CT  | AGTCCCCCAGCTTAAGCAGCGAGGAGGACCTGCATCTAAGCATCTGGGTTGCCAT       | 3038 |
| Db | 180  | CT  | AGTCCCCCAGCTTAAGCAGCGAGGAGGACCTGCATCTAAGCATCTGGGTTGCCAT       | 121  |
| QY | 3039 | GG  | CAATTGGCATGCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGGCAGAAATGAAC      | 3098 |
| Db | 120  | GG  | CAATTGGCATGCCCCAGCTACTGTATGCCCCCGACCCCGCAGAGGCAGAAATGAAC      | 61   |
| QY | 3099 | CAT | AGGAGCTGATCGPAATGTTTATCANGTACTTCCCCACCCCTACATTTTTT            | 3153 |
| Db | 60   | CAT | AGGAGCKGATCGTAANNTTATCC--TNTTCTTCCCAACCCCTTANNBNKTK           | 8    |

| BASE COUNT  |     | 276 a 318 c 330 g 201 t 76 others                             |     |
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| ORIGIN  |     |   |     |
| <p>Query Match 27.1%; Score 861.4; DB 13; Length 1201;<br/>           Best Local Similarity 95.6%; Pred. No. 1.4e-169;<br/>           Matches 871; Conservative 21; Mismatches 18; Indels 1; Gaps 1</p> |     |   |     |
| Qy  | 1   | CTCCCGACGCGAGCGGAGAGGGCTGGGGGAGGGGGCGCGTGGGAGAGTAGGAGAGAGAC   | 600 |
| Db  | 83  | CTCCCGAGCGAGCGGAGAGAGGCTGGGGGAGGGGGCGCGTGGGAGAGTAGGAGAGAGAC   | 142 |
| Qy  | 61  | AAAAGCCGAAGCAAGAGGGCCGGCTGCACACACCGGCTGGGAGGAGCGGCTCTGTG      | 120 |
| Db  | 143 | AAAAGCCGAAGCGAGAGGGCCGGCTGCACACACCGGCTGGGAGGAGCGGCTCTGTG      | 202 |
| Qy  | 121 | CAGCAGACAGCGCGGGGAGGCGCAGTGTGACGGGGGCTCACAGTGGGAGGAGCAGA      | 180 |
| Db  | 203 | CAGCAGACAGCGCGGGGAGGCGCAGTGTGACGGGGGCTCACAGTGGGAGGAGCAGA      | 262 |
| Qy  | 181 | TGGGGAAAGGAGAGGAAACAGGCGAGGGGGCGCGCGAGCGAGGTGTGGTGCACCACCT    | 240 |
| Db  | 263 | TGGGGAAAGGAGGAGAACAGGCGAGGGGGCGCGCGAGCGAGGTGTGGTGCACCACCT     | 322 |
| Qy  | 241 | TGAGCTGGGAGAGATTGAGAGCATTAACCTGGGACCGACAGTGGGCTGGTTCATTGACC   | 300 |
| Db  | 323 | TGAGCTGGGAGAGATTGAGAGCATTAACCTGGGACCGACAG-GTGGTGGTTCATTGACC   | 381 |
| Qy  | 301 | GCAAGGTTTACAAATCACCAAAATGGTTCATCCAGCACCGGGGGGCCAGCGGGTCATCG   | 360 |
| Db  | 382 | GCWAGGTTTACAAATCACCAAAATGGTTCATCCAGCACCGGGGGGCCAGCGGGTCATCG   | 441 |
| Qy  | 361 | GGCATTAGCTGGAGAGATGACAGCATGCGCTTCGGCGCTTCCACCTGACCTGGGAT      | 420 |
| Db  | 442 | GGCATTAGCTGGAGAGATGACAGCATGCGCTTCGGCGCTTCCACCTGACCTGGGAT      | 501 |
| Qy  | 421 | TGCTGGGCAAGTTCTTGAAACCCCTGCTGATTGGTGAATGGGCCCGGAGGAGCCAGCC    | 480 |
| Db  | 502 | TGCTGGGCAAGTTCTTGAAACCCCTGCTGATTGGTGAATGGGCCCGGAGGAGCCAGCC    | 561 |
| Qy  | 481 | AGGACCGGCAGAGACTCAAGATCACTGAGCACTTCGGGCGCTTGAGGAGAGCGGCTG     | 540 |
| Db  | 562 | AGGACCGGCAGAGACTCAAGATCACTGAGCACTTCGGGCGCTTGAGGAGAGCGGCTG     | 621 |
| Qy  | 541 | AGGACATGAACCTGTTCAAGACCAACACCGTGTTCCTCTCTCTCTCTGGGCCCATCA     | 600 |
| Db  | 622 | AGGACATGAACCTGTTCAARACCAACACCGTGTTCCTCTCTCTCTCTGGGCCCATCA     | 681 |
| Qy  | 601 | TGCGCTGGAGAGCATTCGATGTTCTACTGTTCTTACTTTGGCATGCTGGATTCTTA      | 660 |
| Db  | 682 | TGCGCTGGAGAGCATTCGATGTTCTACTGTTCTTACTTTGGCATGCTGGATTCTTA      | 741 |
| Qy  | 661 | CCCTCATCAGCGCCCTTCTCTCTCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATG   | 720 |
| Db  | 742 | CCCTCATCAGCGCCCTTCTCTCTCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATG   | 801 |
| Qy  | 721 | ATTATGGCCACTGTCTGTCTACAGAAACCCAGTGGACACCACTTGTCCCAATTCG       | 780 |
| Db  | 802 | ATTATGGCCACTGTCTGTCTACAGAAAMCCAGTGGACCACTTGTCCCAATTCG         | 861 |
| Qy  | 781 | TCATTGGCCACTTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCAC | 840 |
| Db  | 862 | TCATTGGCCACTTAAAGGGTGCCCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAAAC  | 921 |

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Qy 841 ACCGAGCCTACATCTTCCCAAGGATCCCGATGCGATGTAACATGCTGACGCTGTTGTC 900
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Qy 901 TGGCGGAATGG 911
Db 982 TRRRCATAGS 992

RESULT 10
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AGENCOURT 8726156 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340921
5', mRNA sequence.
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VERSION BQ881930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 884)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2538 row: c column: 02
High quality sequence stop: 689.
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 201 a 271 c 199 g 211 t 2 others
ORIGIN
Query Match 26.9%; Score 857.4; DB 13; Length 884;
Best Local Similarity 99.5%; Pred. No. 9.5e-169;
Matches 869; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Qy 683 TGCTACCTCTCAGGCCCAAGCTGATGCTGCTCAACATGATTATGGCCACCTGCTGTCTA 742
Db 61 TGCTACCTCTCAGGCCCAAGCTGATGCTGCTCAACATGATTATGGCCACCTGCTGTCTA 120
Qy 743 CAGAAACCCCAAGTGGACCAACCTTTGTCCACAAATTCGTATTGGCCCACTAAAGGTGC 802
Db 121 CAGAAACCCCAAGTGGACCAACCTTTGTCCACAAATTCGTATTGGCCCACTAAAGGTGC 180

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Qy 803 CTCTGCCAACTGTGTGAATCATCGCCACTTCCAGCACCCAGCCCAAGCTAAACATCTTCCA 862
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Qy 1403 CAAGCATGGCATTAATACAGGAGAGCGCTACTGAGGCGCTGCTGGACATCATCAG 1462
Db 781 CAAGCATGGCATTAATACAGGAGAGCGCTACTGAGGCGCTGCTGGACATCATCAG 840

Qy 1463 GTCCCTGAAGAAGTCT-GGGAAGCTGTGGCTGG 1494
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DEFINITION cDNA clone CS0DC005YH18 5-PRIME, mRNA sequence.
ACCESSION AL525170
VERSION AL525170.2 GI:31043425
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 929)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12788663.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For

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more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DC005DD09QPI&cluster=6148.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DC005DD09QPI.

FEATURES  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR-V  
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 168 a 302 c 250 g 208 t 1 others  
ORIGIN

Query Match 26.9%; Score 855.8; DB 9; Length 929;  
Best Local Similarity 98.9%; Pred. No. 2.1e-168;  
Matches 871; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 1373 GATCGCCCGCTGCTGAGTCTCTATGTCACAGCATGGCATTCAATACAGAGAGACC 1432  
DB |||||  
50 GAATCCCGGATGGAAGTCTCTATGTCACAGCATGGCATTCAATACAGAGAGACC 109  
QY 1433 GCTACTGAGGCGCTGCTGAGCATCATCAGTCTCCTGAAGAAGTCTGGAGAGCTGTGGCT 1492  
DB |||||  
110 GCTACTGAGGCGCTGCTGAGCATCATCAGTCTCCTGAAGAAGTCTGGAGAGCTGTGGCT 169  
QY 1493 GGAGCCTTACCTTCAATGAAGCAGACGCGCGGACACCTGTGGAGAGGCTGCAG 1552  
DB |||||  
170 GGAGCCTTACCTTCAATGAAGCAGACGCGCGGACACCTGTGGAGAGGCTGCAG 229  
QY 1553 GTGGGCTGATGCCAGAGAAATGATGGCTTTTGTCTGAGGGGTGTCCAGAGAGCTGGT 1612  
DB |||||  
230 GTGGGCTGATGCCAGAGAAATGATGGCTTTTGTCTGAGGGGTGTCCAGAGAGCTGGT 289  
QY 1613 GTATGCTGCTCAGGACCCGATGTTGATCTTCTCCCTTTCTCTCTCTCTCTCTCTCT 1672  
DB |||||  
290 GTATGCTGCTCAGGACCCGATGTTGATCTTCTCCCTTTCTCTCTCTCTCTCTCTCTCT 349  
QY 1673 TTCATATCTCCCCATAGCACCTGCTCTATGGAGCTGCTCCCTCCCTCAGCGCTCAGCC 1732  
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350 TTCATATCTCCCCATAGCACCTGCTCTATGGAGCTGCTCCCTCCCTCAGCGCTCAGCC 409  
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410 ATCAGCATGCGCTCCAGTGCCTCTAGCCCTTTTCAAGAGCAGAGAGGTGCC 469  
QY 1793 ACCGGGGTGGCTGTGCTACTCTCTGCTCCCTAAAGATGGAGAGAGACGAGC 1852  
DB |||||  
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DB |||||  
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DB |||||  
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QY 1973 GACCTTCCCGGCTGCTGCTTCACTCTCCCTGACGGTGCATTTGGTCCACCTTTTCATAGA 2032  
DB |||||  
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DB |||||  
710 GAGGCTGCTTTGTTACAAARCTCGGCTCTCCCTCTCTGAGCTCGGTTAAGTACCCGAGG 769

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770 CCTCTCTTAAGATGTCCAGGCCCCCAGG-CGGCGGCGACAGCCAGCCAAACCTTTGGGCC 828  
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DB |||||  
829 CTGGAGAGTCTCTCCACCCCATCACTAGAGTCTCTGACCTTGGGCTTTTCAGGGCCCCCA 888  
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DB |||||  
889 TTCCACCGCTCTCCCAACTTGAAGCTGTGACCTTTGGGACCA 929

RESULT 12  
BX441083  
LOCUS  
DEFINITION  
CS0DF014YML1 5-PRIME, mRNA sequence.  
ACCESSION  
BX441083  
VERSION  
BX441083.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 952)  
AUTHORS  
Li W.B., Gruber C., Jessee J. and Polayes D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6148.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DF014AG06QPI&cluster=6148.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DF014AG06QPI.

FEATURES  
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/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: Brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
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enriched, double-strand cDNA was digested with Not I and  
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vector. Library was not normalized."

BASE COUNT 237 a 280 c 236 g 168 t 31 others  
ORIGIN

Query Match 26.7%; Score 851.2; DB 13; Length 952;  
Best Local Similarity 95.0%; Pred. No. 1.9e-167;  
Matches 861; Conservative 23; Mismatches 21; Indels 1; Gaps 1;

QY 81 GCCCGGGCTGCACACACCGGCTGGAGGCGAGCGCTGTGTGACGAGCGCGGCGCGG 140  
DB |||||  
48 GCCCGGACAGCAGACACCGGCTGGAGGCGAGCGCTGTGTGACGAGCGCGGCGG 107  
QY 141 GAGCGCGCAGTGCACCGGGGCGTCACAGTCGGCAGGCGATGGGAAGGAGGACAC 200  
DB |||||  
108 GAGCGCGCAGTGCACCGGGGCGTCACAGTCGGCAGGCGATGGGAAGGAGGACAC 167  
QY 201 GGGCAGGGGCGCGCAGGCGGAGGTGTGGTGGCCACCTTCAGCTGGGAGGATTCAG 260  
DB |||||  
168 GGCRAAGGGGCGCGCGACGAAAGTGTGGTACCCACCTTCARCTGGGAGGATWCAA 227



|    |     |  |     |
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| QY | 261 | AAGCATAACTCGGCACCGACAGTGGGGTGCTCATTTGACCGCAAGGTTTACAACTCACC    | 320 |
| DB | 228 | AAGCATAACTCGGCACCGACA-AGKGTGGTCATTGAMCGCAAGGTTWACAACATCA       | 286 |
| QY | 321 | AAATGGTCCATCCAGCAACCGGGGGCCAGCGGGTCATCGGGCACTACGCTGGAGAGAT     | 380 |
| DB | 287 | AAAWGGTCCAWCGACACCGGGGGCCAGCGGTCTATCGGGCACTACGCTGGAGAGAT       | 346 |
| QY | 381 | GCAAACGGATGCCTTCGCGGCCTTCACCCCTGACCTGGAAATTCGTGGCGAAGTTCCTGAA  | 440 |
| DB | 347 | GCMAACGGATGCCTTCCAAACAAACCAACCTGACATGCGATWCGTGGCGAATTCCTGAA    | 406 |
| QY | 441 | CCCTGCTGANTGGTGAATCGCCCGGAGAGCCCAAGCAGGACCAACGCGAAGAACTCA      | 500 |
| DB | 407 | CCCTGCTGANTGGTGAATCGCCCGGAGAGAGCCCAAGCAGGACCAACGCGAAGAACTCA    | 466 |
| QY | 501 | AAGATCACTGAGGACTTCGGGCCCTGAGGAAGACGCTGAGGACATGAACCTGTTCAAG     | 560 |
| DB | 467 | AAAPWCACTGARGACTTCGGGCCCTGAGGAARAGGCTGARGACATGAACCTGTTCAAA     | 526 |
| QY | 561 | ACCAACACAGTGTTCTTCCTCTCTCTGCGCCACACATCATCGCCCTGGAGAGCAATTGCA   | 620 |
| DB | 527 | ACCAACACAGTGTTCTTCCTCTCTCTGCGCCACACATCATCGCCCTGGAGAGCAATTGCA   | 586 |
| QY | 621 | TGTTCACTGTCTTCTACTTTTGGCAATGGCTGGATTCCTACCTCATCACGGCCTTTGTC    | 680 |
| DB | 587 | TGTTTCACTGTCTTTTACTTTTGGCAATGGCTGGATTCCTACCTCATCACGGCCTTTGTC   | 646 |
| QY | 681 | CTTGCTACCTCTCAGGCCCAAGCTGGATGGGTGGCAACATGATTATGGCCAACCTGTCTGTC | 740 |
| DB | 647 | CTTGCTACCTCTCAGGCCCAAGCTGGATGGGTGGCAACATGATTATAGCCACCTGTCTGTC  | 706 |
| QY | 741 | TACAGAAAACCCAAAGTGGAAACCACTTGTGCACAAATTCGTATGGCCACTTAAAGGTT    | 800 |
| DB | 707 | TACAGAAAACCCAAAGTGGAAACCACTTGTGCACAAATTCGTATGGCCACTTAAAGGTT    | 766 |
| QY | 801 | GCCTCTGCCAACTGGTGGAAATCATCGCACCTTCAGACACACGCGCAAGCCTAACATCTTC  | 860 |
| DB | 767 | GCCTCTGCCAACTGGTGGAAATCATCGCACCTTCAGACACACGCGCAAGCCTAACATCTTC  | 826 |
| QY | 861 | CACAAGGATCCCGATGTGAACATGCTGCACTGTGTTTGTCTGGGCGAATGGCGGCCATC    | 920 |
| DB | 827 | CACAAGGATCCCGATGTGAACATGCTGCACTGTGTTTGTCTGGGCGAATGGCGGCCATC    | 886 |
| QY | 921 | GAGTACGGCAAGAGAGCTGGAATACCTCGCCCTACATCACCAGCAGAATACCTCTTC      | 980 |
| DB | 887 | GAGTACGGCAAGAGAGCTGGAATACCTCGCCCTACATCACCAGCAGAATACCTCTTC      | 946 |
| QY | 981 | CTGATT   | 986 |
| DB | 947 | CTGATT   | 952 |

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|------------|---|-----------------|
| RESULT 13  | linear  | EST 02-MAY-2003 |
| EX341258   | 933 bp  |                 |
| LOCUS      | mrna  |                 |
| DEFINITION | EX341258 Homo sapiens T   |                 |
|            | CELLS (JURKAT CELL LINE) COT 10-NORMALIZED                        |                 |
|            | Homo sapiens cDNA clone CS0DU014YC21 5-PRIME, mRNA sequence.      |                 |
| ACCESSION  | EX341258  |                 |
| VERSION    | EX341258.1  |                 |
| KEYWORDS   | GI:30343944   |                 |
| SOURCE     | EST.  |                 |
| ORGANISM   | Homo sapiens (human)  |                 |
|            | Homo sapiens  |                 |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                 |
|            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |                 |
| REFERENCE  | 1 (bases 1 to 933)  |                 |
| AUTHORS    | Li, W.B., Gruber, C., Jesses, J., and Polayes, D.                 |                 |
| TITLE      | Full-length cDNA libraries and normalization                      |                 |
| JOURNAL    | Unpublished   |                 |
| COMMENT    | Contact: Genoscope  |                 |
|            | Genoscope - Centre National de Sequencage                         |                 |
|            | BP 191 91006 EVRY cedex - France                                  |                 |

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6148.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DJ014AB11Q1P1cluster=6148.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0DJ014AB11Q1P1.  
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/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT  
10-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
231 a 258 c 204 g 194 t 46 others

| Query Match           | 26.6% | Score 845.6  | DB 13        | Length 933 |
|-----------------------|-------|--|--------------|------------|
| Best Local Similarity | 94.1% | Pred. No. 2.8e-166   |              |            |
| Matches               | 824   | Conservative 44  | Mismatches 8 | Indels 0   |
| Qy                    | 642   | GGCAATGGCTGGATTCCTACCCCTCATCAGCGCCCTTGTCTCTGTACCTCTCAGGCCCCAA      | 701          |            |
| Db                    | 58    | GGGATTGGCTGGATTCTTAMCCTCATCAGGCCCTTGTCTCTGTACCTCTCAGGCCCAA         | 117          |            |
| Qy                    | 702   | GCTGGATGGCTGCAACATGATTATGGCCACTCTCTGTCTTACAGAAAAACCAAGTGGAAAC      | 761          |            |
| Db                    | 118   | GCTGGAAAGGCTGCAACAWGATTATGGCCAMCTGTCTGTCTAMAAAAAACCAAGTGGAAAC      | 177          |            |
| Qy                    | 762   | CACCTCTGCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCACAACTGGTGGAAAT      | 821          |            |
| Db                    | 178   | CAMCTTGTCCAAAAAAWCGTCAMTGGCCACTTAAARGGTGCCTCTGCCAACTGGTGGAAW       | 237          |            |
| Qy                    | 822   | CATCGCACTTCCAGCACCCAGCCGCAATCATCTTCCACAAGGATCCCGATGTGGAAC          | 881          |            |
| Db                    | 238   | CAWCGCACCTCCAGCACCCAGCCGCAAGCCCTTAAWAVCTTCCAAAAAGATCCCGATGTGAAM    | 297          |            |
| Qy                    | 882   | ATGCTGCACGTTGTTCTGTGGCGAATGCAGCCCATCGAGTACGCAAGAAAGAAAGCTG         | 941          |            |
| Db                    | 298   | AWGCTGCACGTTGTTCTGTGGCGAATGGCAGCCCATCGCCCATCGARTAMGCAAAAAARNAAGCTG | 357          |            |
| Qy                    | 942   | AAATACCTGGCCCTACAAATCACACGACGAATATCTTCTCTGATTTGGCGCGCGCTGCTC       | 1001         |            |
| Db                    | 358   | AAAAAMCTGCCCTAMAAAAACAMCARMACGAAWACTTCTTCTCTGATTTGGCGCGCGCTGCTC    | 417          |            |
| Qy                    | 1002  | ATCCCATGTATTTTCCAGTACCCAGATCATCATGACCATGATCGTCCCAATAAGAACTGGGTG    | 1061         |            |
| Db                    | 418   | ATCCCATGTATTTTCCAGTACCAAWCATCAWGAACCAWAGWCGTCCATATARAACATGGGTG     | 477          |            |
| Qy                    | 1062  | GACCTGGCGCTGGCGCGTCAGCTACTACATCCGGTCTTTCATCACTACATCCCTTTCTAC       | 1121         |            |
| Db                    | 478   | GACCTGGCGCTGGCGCGTCAGCTATAMATCCGGTCTTTCATCAWCACTTAMAWCCCTTTCTAC    | 537          |            |
| Qy                    | 1122  | GGCATCTGGAGCGCTCTTTTCTCTCAACTTATCATAGGTTCTCTGGAGGCCACTGGTTT        | 1181         |            |
| Db                    | 538   | GGCATCTCTGGAGCGCTCTTTTCTCTCAACTTATCATAGGTTCTCTGGAGGCCACTGGTTT      | 597          |            |
| Qy                    | 1182  | GTGTGGGTCCACACAGATGAATCACAATCGTCATGGAGATTGACCAAGGAGGCGCTACCGTGAC   | 1241         |            |
| Db                    | 598   | GTGTGGGTCCACACAGATGAATCACAATCGTCATGGAGATTGACCAAGGAGGCGCTACCGTGAC   | 657          |            |
| Qy                    | 1242  | TGGTTTCATGACGCTGACAGCCACTGMAACCTGGAGCGAGTCTCTTCTTCAACGACTGG        | 1301         |            |
| Db                    | 658   | TGGTTTCATGACGCTGACAGCCACTGMAACCTGGAGCGAGTCTCTTCTTCAACGACTGG        | 717          |            |

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QY 1302 TTCAGTGACACCTTAACTTCAGATTGAGCACCACTCTTCCACCATGCCCGGCAC 1361
Db 718 TTCAGTGACACCTTAACTTCAGATTGAGCACCACTCTTCCACCATGCCCGGCAC 777
QY 1362 AACTTACACAGATCGCCCGTGTGTGAAGTCTCTATGTGCAGATGGCAATGAATAC 1421
Db 778 AACTTACAAATATCGCCCGTGTGTGAAGTCTCTATGTGCAGATGGCAATGAATAC 837
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Db 838 CAGGAGAGCCGCTACTGAGGCGCTGTGTGACATCAWAGGTCCCTGAAAGTCTGGG 897
QY 1482 AGCTGTGTGTGAGCGCTACTCTTCAAAAAGAAGC 1517
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DEFINITION mRNA sequence.
ACCESSION BG696762
VERSION BG696762.1 GI:13962248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 912)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM10698 row: k column: 01
High quality sequence start: 3
High quality sequence stop: 876.
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/note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI.
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 148 a 305 c 258 g 200 t
ORIGIN
Query Match 26.5%; Score 845; DB 10; Length 912;
Best Local Similarity 96.7%; Pred. No. 3.7e-166;
Matches 884; Conservative 0; Mismatches 26; Indels 4; Gaps 2;

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QY 1491 CTGGAGCGCTACTTTCACAAATGAAGCCACAGCCCCCGGACACCGTGGGAAGGGGTGC 1550
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QY 1791 CCACCGGGGGTGGCTCTGTCTTACCTTCCACTCTCTGCCCCCTAAAGATGGAGGAGACAG 1850
Db 361 CCACCGGGGGTGGCTCTGTCTTACCTTCCACTCTCTGCCCCCTAAAGATGGAGGAGACAG 420
QY 1851 CGGTCCATGGGTCTGGCCCTGTGAGTCTCCCTTGCAGCCCTGCTCACTAGGCAATCACCCC 1910
Db 421 CGGTCCATGGGTCTGGCCCTGTGAGTCTCCCTTGCAGCCCTGCTCACTAGGCAATCACCCC 480
QY 1911 GCTTTGGTTCTTCAGATGCTCTTGGGGTTCATAGGGGCAAGTCTCTAGTCCGGCAGGGCCC 1970
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Db 541 CTGACCCCTCCCGGCTGGCTTCACTCTCCCTGACGGTCCCATTTGGTCCACCCCTTTTCA 600
QY 2031 GAGAGCGCTGCTTTGTACAAAGCTCGGGTCTCCCTCTGACAGTCCGGTTAAGTACCCGA 2090
Db 601 GAGAGCGCTGCTTTGTACAAAGCTCGGGTCTCCCTCTGACAGTCCGGTTAAGTACCCGA 660
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Db 898 GTCAGCCACCCCTTC 911

RESULT 15
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DEFINITION mRNA sequence.
ACCESSION BG696015
VERSION BG696015.1 GI:13960717
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 927)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

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[illegible]

Query Match 26.4%; Score 840.8; DB 13; Length 914;  
Best Local Similarity 98.4%; Pred. No. 2.8e-165;  
Matches 870; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 215 CGAGCGGAGGTGTGGTGTCCACCTTCAGCTGGGAGGAGATTCAGAGCATTAACCTGCG 274  
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QY 275 CACCGACAGTGGGCTGGTCAATGACCGCAAGGTTTACCAATCAATGATGATCCATCCA 334  
DB 61 CACCGACAGTGGGCTGGTCAATGACCGCAAGGTTTACCAATCAATGATGATCCATCCA 120

QY 335 GCACCGGGGGGCGACCGGGTCAATCGGCACTACGCTGAGAGAGATGACGAGTGCCTT 394  
DB 121 GCACCGGGGGGCGACCGGGTCAATCGGCACTACGCTGAGAGAGATGACGAGTGCCTT 180

QY 395 CGCGGCTTCCACCTTCAGCTGAAATTCGTGGGCAAGTTCCTTGAACCCCTCTGATGG 454  
DB 181 CGCGGCTTCCACCTTCAGCTGAAATTCGTGGGCAAGTTCCTTGAACCCCTCTGATGG 240

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DB 241 TGAATCGGCGGCGGAGGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300

QY 515 CTTCCGCGGCTTCAGGAGAGCGCTGAGGACATGAACCTGTTCAAGACCAACCACTGTT 574  
DB 301 CTTCCGCGGCTTCAGGAGAGCGCTGAGGACATGAACCTGTTCAAGACCAACCACTGTT 360

QY 575 CTTCCCT 634  
DB 361 CTTCCCT 420

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DB 421 TTAATTTGGCAATGGTGGATTCCTACCTCTACCGGCTTGTCTCTCTCTCTCTCTCTCTCT 480

QY 695 GGGCCCAAGCTGGATGGTGAACATGATATGACCACTGTCTGTCTACAGAAACCCAA 754  
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QY 875 TGTGAACATGTCGACGTGTTGTTCTGGCGAATGCGAGCCCATCGAGTACGGCAAGAA 934  
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QY 935 GAAGCTGAATACCTGCGCTTACATACCAAGCAGCAATCTTCTCTGATTTGGGCGGC 994  
DB 721 GAAGCTGAATACCTGCGCTTACATACCAAGCAGCAATCTTCTCTGATTTGGGCGGC 780

QY 995 GTGTCTCATCCCATGATTTTCAGTACCAAGATCATGACCATGATGATGATCAATGA 1054  
DB 781 GTGTCTCATCCCATGATTTTCAGTACCAAGATCATGACCATGATGATGATGATCAATGA 840

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RESULT 17  
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DEFINITION AL520269 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens  
cDNA clone CS0DB006YML7 3-PRIME, mRNA sequence.  
ACCESSION  
AL520269  
VERSION  
AL520269.2 GI:31038610  
KEYWORDS  
EST.

Source Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1199)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT On Feb 13, 2001 this sequence version replaced gi:12783762.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqres@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6148.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DB006YML7&cluster=6148.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradise Avenue Genoscope, sequence ID : CS0DB006YML7.  
Location/Qualifiers  
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/notes="First strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT 252 a 341 c 245 g 226 t 135 others  
ORIGIN  
Query Match 26.4%; Score 839.6; DB 9; Length 1199;  
Best Local Similarity 97.0%; Pred. No. 5.1e-165;  
Matches 861; Conservative 13; Mismatches 12; Indels 2; Gaps 2;

QY 2275 TGTGACTCAGCAGAGGAGTGGCCACCTTCAGGAGGAGGCGGCTGGCCCTGGAGGCTCAG 2334  
DB 888 TTTTGTAGTACAGAGAGGAGTGGSSASGTTBAGGAGGAGGSCCGGCTGGCTGGAGGCTCAG 829

QY 2335 CCCACCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTCAGAGCAATCTGACC 2394  
DB 828 CCCACCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTCAGAGCAATCTGACC 769

QY 2395 CTTCTCCAAAGCTCTGTATATCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2454  
DB 768 CTTCTCCAAAGCTCTGTATATCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 709

QY 2455 CAGGAG 2514  
DB 708 CA-GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 650

QY 2515 GCCCTCCCACTCTGGGCTCTGTGTGG-ACGGCGCTGCTCAGGCACTCTCCTGTCTG 2573  
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QY 2574 AACCTGCGCTTACTGTGTAACTGTCTCAGGATGCAATTCATGAGAGGAGGAGGAGGAGGAGGAG 2633  
DB 589 AACCTGCGCTTACTGTGTAACTGTCTCAGGATGCAATTCATGAGAGGAGGAGGAGGAGGAGGAG 530

QY 2634 CAGGCTGGGCTTGTGCAATCTGCTTTTCCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2693  
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[illegible]







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721 GTCCAGGCGCCAGGCGCGGGGACAGCAGCCAAACCTTTGGGCGCTTGGAGAGTCTT 780

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841 C 841

RESULT 22

LOCUS BG674567

DEFINITION 602620383F1 NCI\_OGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4745853 5', mRNA sequence.

ACCESSION BG674567

VERSION BG674567.1 GI:13905963

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-WGSC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL) DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LENL at: <http://image.llnl.gov>  
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151 a 301 c 273 g 206 t

BASE COUNT 151 a 301 c 273 g 206 t

ORIGIN

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Best Local Similarity 97.8%; Pred. No. 2.6e-162;  
Matches 891; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

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385 TAAGTACCGGAGGCTCTTTAAAGATGTCAGGGGCCCCAGGCCCGGGGACAGCCAGCC 444

2140 CAAACCTTGGGCGCTTGAAGAGTCTCCACCCCTCACTAGAGTCTCTGACCCCTGGGT 2199

445 CAAACCTTGGGCGCTTGAAGAGTCTCCACCCCTCACTAGAGTCTCTGACCCCTGGGT 504

2200 TTCAGGGGCCCCATTCACCCGCTCCCAACTTGAAGCTGTGACCTTGGGACCAAGGG 2259

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2500 GGAGGTCTCTGCTCCAGCCCTTCCCATCTCGGGGCTGTCTGTGGAGCGGCTGCTCAGG 2559

804 GGAGGTCTCTGCTCCAGCCCTTCCCATCTCGGGGCTGTCTGTGGAGCG--GGCTGCTCAGG 861

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RESULT 23

BU845046

LOCUS BU845046

924 bp mRNA linear EST 16-OCT-2002

[illegible][illegible]

Site 2: XhoI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

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Query Match      25.8%; Score 820; DB 13; Length 1048;
Best Local Similarity 96.6%; Pred. No. 6.4e-161;
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QY      2071 CAGCTCGGTTAGTACCCGAGGCTCTCTTAAGATGTCCAGGGCCCGAGGCCCGGGCA 2130
Db      121 CAGCTCGGTTAGTACCCGAGGCTCTCTTAAGATGTCCAGGGCCCGAGGCCCGGGCA 180
QY      2131 CAGCCAGCCCAACCTTGGGCGCTTGAAGAGTCTTCCACCCCATCACTAGAGTGTCTGA 2190
Db      181 CAGCCAGCCCAACCTTGGGCGCTTGAAGAGTCTTCCACCCCATCACTAGAGTGTCTGA 240
QY      2191 CCTGGGCTTTCAGGGGCGCCATTCCACCGCTCCCGCACTTGAGCTGTGACCTTGGGA 2250
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QY      2311 GGGCGGCTGGCTGAGGCTGACCCACCTCCAGCTTTTCTCAGGGTGTCTGAGGT 2370
Db      361 GGGCGGCTGGCTGAGGCTGACCCACCTCCAGCTTTTCTCAGGGTGTCTGAGGT 420
QY      2371 CCAAGATTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTATCAGCTGGGAGTGC 2430
Db      421 CCAAGATTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTATCAGCTGGGAGTGC 480
QY      2431 AGCCAAATCCCTGGCCATTTGGCCCGCAGGGGAGTGGGCCCTGCAAGGTCGAGAGGCA 2490
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QY      2491 CTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCATCTCGGGGCTGTGTGTGGACGGCG 2550
Db      540 CTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCATCTCGGGGCTGTGTGTGGACGGCG 599
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QY      2611 TGCAATCTGATAGAGGGGCGGAGGCTGGGCTGTGTGAATCTGCTTTTCCACCA 2670
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QY      2671 TGCCCTTGCCCTCGGTGGCCCTGACTGTCTGAGG-AGGGCCAGGAGGCGAGAGGG-AGGG 2728
Db      720 TGCCCTTGCCCTCGGTGGCCCTGACTGTCTGAGGAGGGCCAGGAGGAGGAGGG 779
QY      2729 AGTCTCAGAGGAGGCTG-CCCTGAGGGCTGGGAGGGGGTACCTCATGAGACAGGG 2787
Db      780 AGTCTCAGAGGAGGCTGCCCCCTGAGGGCTGGGAGGGGGTACCTCATGAGGACAGGG 839
QY      2788 TGGAGCTGGAAGAGGAGGAGTGGGGGCTGG--AGGTGCTGTGTAGCTGAGGGGAGCGGC 2845
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DEFINITION 602634223F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779461 5',
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ACCESSION  BG743088
VERSION     BG743088.1 GI:14053741
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1 (bases 1 to 894)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: rsapbs@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
            Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LHAM0636 row: n column: 06
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Matches 874; Conservative 0; Mismatches 18; Indels 4; Gaps 4;
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QY      1312 ACCTTAATCTTCAGATTGAGCACCACTCTTCCCAACCATGCCCCCGGCACTTACACA 1371
Db      121 ACCTTAATCTTCAGATTGAGCACCACTCTTCCCAACCATGCCCCCGGCACTTACACA 180
QY      1372 AGATCGCCCCGCTGGTGAAGTCTCTATGTCCCAAGCATGCAATTGAATACCGAGGAAGC 1431
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QY      1432 CGCTACTGAGGGCCCTGCTGGACATCATCAGGTCCTCTGAAGAGTCTGGGAAGCTGTGGC 1491
Db      241 CGCTACTGAGGGCCCTGCTGGACATCATCAGGTCCTCTGAAGAGTCTGGGAAGCTGTGGC 300
QY      1492 TGGACGCTACCTTCACAAATGAAGCCACAGCCCCCGGACACCGTGGGAGGGGTGCA 1551
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Db 301 TGGAGCGCTACCTTCAAAATGAAGCAACGCCCCGGGACACCGTGGGAGAGGGTGCA 360  
 Qy 1552 GGTGGGGTATGACCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGCTGG 1611  
 Db 361 GGTGGGGTATGACCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGCTGG 419  
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 Db 660 GGTCCATGGTCTGGCCCTGTAGTCTCCCTTGGAGCCCTGCTCACTAGGATCACCCCG 719  
 Qy 1912 CTTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGCA-GGTCTTAGTGGGAGGGCC 1970  
 Db 720 GTTGGTCTTTCAGATGCTCTTGGGGTTCATAGGGGAGGGTCTTAGTGGGAGGGTCC 779  
 Qy 1971 CTGACCTCCCGGCTGGTCTCACTCTCCCTGACGGCTGCATGTTCCACCTTTTCA 2030  
 Db 780 CTGACCTCCCGG-CTGGCTTCAATCTCCCTGACGGTTCATGTTGCCACCTTTTCA 838  
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 VERSION BX440551.1 GI:30781858  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODP008BF03QF1.

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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
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 vector. Library was not normalized."  
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 Matches 814; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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 Qy 1680 CTCGCCCATAGCACCCCTGCCCTTCATGGGACCTGCCCTCCCTCAGCCGTCAGCATCAGC 1739  
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RESULT 27  
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      157 a      296 c      281 g      209 t      5 others
ORIGIN

Query Match      25.5%; Score 811.4; DB 13; Length 948;
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Matches 861; Conservative 5; Mismatches 11; Indels 6; Gaps 4;

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Db      |||
QY 1960 GGGCAGGGCCCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCC 2019
Db      |||
QY 187 GGGCAGGGCCCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGCTGCCATTGGTCC 246
QY 2020 ACCCTTTCATAGAGAGCGCTGCTTGTGTTCAAAAGCTCGGCTCTCCCTCTGAGCTCGGT 2079
Db      |||
QY 247 ACCCTTTCATAGAGAGCGCTGCTTGTGTTCAAAAGCTCGGCTCTCCCTCTGAGCTCGGT 306
QY 2080 TAAGTACCCGAGGCTCTTCTAGATGTCAGAGGCGCCAGGCGCGGCGACAGCCAGC- 2138
Db      |||
QY 307 TAAGTACCCGAGGCTCTTCTAGATGTCAGAGGCGCCAGGCGCGGCGACAGCCAGC 366
QY 2139 --CCAAACCTTGGCCCTTGAAGAGTCTCTCCACCCATCATAGAGTGTCTGACCCCTGG 2196
Db      |||
QY 367 CGCAACGCTTGGCCCTTGAAGAGTCTCTCCACCCATCATAGAGTGTCTGACCCCTGG 426
QY 2197 GCTTTCAGGGCCCATCATACCGCTTCCCACTTGAAGCTGTGAGCTTGGACCCAAAG 2256
Db      |||
QY 427 GCTTTCAGGGCCCATTCACCGCTTCCCACTTGAAGCTGTGAGCTTGGACCCAAAG 486
QY 2257 GGGAGTCCCTGCTCTCTGTGACTCAGCAGAGGAGTGGCCAGCTTCAAGGAGGGCGCG 2316
Db      |||
QY 487 GGGAGTCCCTGCTCTCTGTGACTCAGCAGAGGAGTGGCCAGCTTCAAGGAGGGCGCG 546
QY 2317 GCTGGCTGAGGCTCAGCCCAACCTCCAGCTTTTCTCAGGCTGTCTGAGTCTCAAGA 2376
Db      |||
QY 547 GCTGGCTGAGGCTCAGCCCAACCTCCAGCTTTTCTCAGGCTGTCTGAGTCTCAAGA 606
QY 2377 TTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCCACCA 2436
Db      |||
QY 607 TTCTGGAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCCACCA 666
QY 2437 TCCCTGGCCATTGGCCCGCAGGGGAGCTGGGCCCTCAGCTGAGAGGGGCACTGGAG 2496
Db      |||
QY 667 TCCCTGGCCATTGGCCCGCAGGGGAGCTGGGCCCTCAGCTGAGAGGGGCACTGGAG 725
QY 2497 CTGGAGGCTCTGCTCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGCGGCGCTGCTC 2556
Db      |||
QY 726 CTGGAGGCTCTGCTCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGCGGCGCTGCTC 785
QY 2557 AGGCACTCTCTGTCTGAACCTGCGCTTCTGTTTAACTGTTGTCTCAGAGTGCATT 2616
Db      |||
QY 786 AGGCACTCTCTGTCTGAACCTGCGCTTCTGTTTAACTGTTGTCTCAGAGTGCATT 845
QY 2617 CTGATAGAGGGGGGCGGAGGGCT- GGSCCTTGTGAGAACTCTGCTTTCACCAATGGCC 2675
Db      |||
QY 846 CTGATAGAGGGGGGAGGGGCTTGTGACAACTGCTCTTTCACCAATGGCC 905
QY 2676 TTGCC- TCGGTGGCCCTGACTGTCTCAGGGAGGGCCAGGAGGCA 2717
Db      |||
QY 906 TTGCCCTTGGTGGCCCTGACTGTCTATGTRTGGCAAGAGGCA 948
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RESULT 29
AL559446/c
LOCUS
DEFINITION
Homo sapiens cDNA clone CS0DJ013YD17 3-PRIME, mRNA sequence.
ACCESSION
AL559446
VERSION
AL559446.2 GI:31283578
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12904956.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6148.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ013CB09NP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ013CB09NP1.
FEATURES
Location/Qualifiers
1..928
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DJ013YD17"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      185 a      312 c      249 g      163 t      19 others
ORIGIN

Query Match      25.4%; Score 809.6; DB 9; Length 928;
Best Local Similarity 96.0%; Pred. No. 9.5e-159;
Matches 855; Conservative 8; Mismatches 18; Indels 10; Gaps 3;

QY 2262 GTCCCTCTCTCTTGTGACTCAGCAGAGGAGTGGCCACGTTCAAGGAGGGCGGCTGG 2321
Db      |||
QY 894 GTCCCGWATTCGCGGATCTCAGCAGAGGAGTGGCCACGTTCAAGGAGGGCGGCTGG 835
QY 2322 CTGAGAGGCTAGCCACCTCCAGCTTTCTCAGGGTGTCTGAGTGTCAAGATTCTG 2381
Db      |||
QY 834 CTGAGAGGCTAGCCACCTCCAGCTTTCTCAGGGTGTCTGAGTGTCAAGATTCTG 775
QY 2382 GAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCCCAATCCCT 2441
Db      |||
QY 774 GAGCAATCTGACCTTCTCCAAAGGCTCTGTTATCAGCTGGGCACTGCCCAATCCCT 715
QY 2442 GGCATTTGGCCCGCAGGGGAGCTGGGCCCTTCAGGCTGAGGAGGGGCACTGGAGCTGG 2501
Db      |||
QY 714 GGCATTTGGCCCGCAGGGGAGCTGGGCCCTTCAGGCTGAGGAGGGGCACTGGAGCTGG 656
QY 2502 AGGTCTGTGTCAGCCCTCCCATCTCGGGGCTGTGTGTGAGAGGGCGCTGCTCAGGCA 2561
Db      |||
QY 655 AGGTCTGTGTCAGCCCTCCCATCTCGGGGCTGTGTGTGAGAGGGCGCTGCTCAGGCA 596
QY 2562 CTCTCTGTCTGAACCTGCGCTTACTGTGTTTAACTGTGTTCTGCTCAGGATGCAATCTGAT 2621
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595 CTCTCTGTCTGAACCTGCGCTTACTGTGTTAACTGTGCTCCA-----TCTGAT 544
2622 AGGAGGGGGGGGAGGGCTGGGCTTGTGACATCTGCTTTCACACATGCGCTTGGCT 2681
543 AGGAGGGGGGGGAGGGCTGGGCTTGTGACATCTGCTTTCACACATGCGCTTGGCT 484
2682 CGGTG-CGCTGACTCTACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2740
483 CGGTGCGCTTACTCTACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
2741 AGGCTCCCTGAGGGGCTGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2800
423 AGGCTCCCTGAGGGGCTGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364
2801 AGGAGGAGGTGGGGGCTGGAGGTGCTGTAGTGTAGGGGAGGAGGAGGAGGAGG 2860
363 RGRGGAGGTGGGGGCTGGAGGTGCTGTGTGCTGAGGGAGGAGGAGGAGGAGG 304
2861 GAGGAGGTCTGGGAGGAGTCTGAGTCTGTGTGAGTCTTAACCACTAATCACTTCT 2920
303 GRGGGAGTCTGGGAGGATCTGTGTCTGTGTGAGTCTTAACCACTAATCACTTCT 244
2921 AGATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2980
243 AGATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 184
2981 AGTCCCCCAGCTCTAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3040
183 AGTCCCCCAGCTCTAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 124
3041 CAATGAGCATGCCCGGCTACTGTATGCCCGGAGGAGGAGGAGGAGGAGGAGG 3100
123 CAATGAGCATGCCCGGCTACTGTATGCCCGGAGGAGGAGGAGGAGGAGGAGG 64
3101 TAGGAGGTGATGTAATGTTATCATGTTACTTCCCAACCCCTACATTT 3151
63 TAGGAGGTGATGTAATGTTATCATGTTACTTCCCAACCCCTACATTT 13

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RESULT 30
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LOCUS BQ891931
DEFINITION AGENCOURT_8684379 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377089
5', mRNA sequence.
ACCESSION BQ891931
VERSION BQ891931
KEYWORDS EST.
SOURCE BQ891931.1 GI:22283945
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 950)
NIH-MGC http://imgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2560 row: f column: 02
High quality sequence stop: 632.
Location/Qualifiers
1..950
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6377089"
FEATURES
Source

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/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/notes="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 163 a 286 c 311 g 187 t 3 others
ORIGIN
Query Match 25.3%; Score 804.4; DB 13; Length 950;
Best Local Similarity 95.5%; Pred. No. 1.2e-157;
Matches 871; Conservative 0; Mismatches 33; Indels 8; Gaps 4;
QY 1958 TCGGGCAGGGCCCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGTGCATTGGT 2017
Db 1 TCGGGCAGGGCCCTGACCTCCCGGCTGGCTTCACTCTCCCTGACGGTGCATTGGT 60
QY 2018 CCACCTTTTCATAGAGAGGCTGCTTTGTACAAAGCTCGGGTCTCCCTCCTCAGCTCG 2077
Db 61 CCACCTTTTCATAGAGAGGCTGCTTTGTACAAAGCTCGGGTCTCCCTCCTCAGCTCG 120
QY 2078 GTTAAGTACCCGAGGCTCTCTTTAAGATGTCCAGGGCCCCAGGCCCGGGGCACAGCCAG 2137
Db 121 GTTAAGTACCCGAGGCTCTCTTTAAGATGTCCAGGGCCCCAGGCCCGGGGCACAGCCAG 180
QY 2138 CCACAACTTTGGGCGCTGGAGAGTCTCCACCCCATCACTAGAGTCTCTGACCTCGG 2197
Db 181 CCACAACTTTGGGCGCTGGAGAGTCTCCACCCCATCACTAGAGTCTCTGACCTCGG 240
QY 2198 CTTTCAGGGCCCCCATTTCCACCGCTCCCACTTTGAGCCTTGAGCCTTGGGACCAAGG 2257
Db 241 CTTTCAGGGCCCCCATTTCCACCGCTCCCACTTTGAGCCTTGAGCCTTGGGACCAAGG 300
QY 2258 GGGAGTCCCTCGTCTCTTGTGACTCAGCAGAGCAGTGGCCACGTTTCAGGAGGGCCGG 2317
Db 301 GGGAGTCCCTCGTCTCTTGTGACTCAGCAGAGCAGTGGCCACGTTTCAGGAGGGCCGG 360
QY 2318 CTGGCTTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCAGGGTGTCTCTGAGGTCCAAGAT 2377
Db 361 CTGGCTTGGAGGCTCAGCCACCCCTCCAGCTTTTCTCAGGGTGTCTCTGAGGTCCAAGAT 420
QY 2378 TCTGGAGCAATCTGACCCCTTCTCAAAAGGCTCTGTTATCAGCTGGGAGTGCAGCCAAAT 2437
Db 421 TCTGGAGCAATCTGACCCCTTCTCAAAAGGCTCTGTTATCAGCTGGGAGTGCAGCCAAAT 480
QY 2438 CCCTGGCAATTTGGCCCCCAGGGGAGCCTGGGGCCCTGCAGGCTCAGAGGGGCATCGAGC 2497
Db 481 CCCTGGCAATTTGGCCCCCAGGGGAGCCTGGGGCCCTGCAGGCTCAGAGGGGCATCGAGC 539
QY 2498 TGGAGGTCTGCTCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGCGGCTGCCTCA 2557
Db 540 TGGAGGTCTGCTCCAGCCCTCCCATCTCGGGGCTGTGTGTGAGCGGCTGCCTCA 599
QY 2558 GGCACCTCTGCTGTGAACCTGCTTACTGTCTTTAACTGTTGCTCCAGGATGCATTC 2617
Db 600 GGCACCTCTGCTGTGAACCTGCTTACTGTCTTTAACTGTTGCTCCAGGATGCATTC 659
QY 2618 TGATAGAGGGGGCGGAGGCTGGGCTTGTGACAAATCTGCTTTTCAACACATGSCCTT 2677
Db 660 TGATAGAGGGGGCGGAGGCTGGGCTTGTGACAAATCTGCTTTTCA-CACATGGCTT 718
QY 2678 GCCTCGTGGCTGACTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2737
Db 719 TGCTTCTGCTGCTGACTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 778
QY 2738 AGGAGGCTGCTCTGAGGGG--CTGGGGAGGGGGTACCTCATGAGGAGGAGGAGGAGGAGG 2795

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Db 779 AGGAGCTGCTGAGGGGGCTGGGGAGGGGTACCTCATGAGGACGAGGGTGGAGCTG 838

Qy 2796 AGAA-----GAGGAGGAGGTGGGGCTGGAGGTGCTGAGTGTGAGGGGACGGGCAAGTGA 2851

Db 839 AGAANAAGGAGGAGGGGGGGGGCTTGGAGGGCTGTGTACCTGAGGAGCGGGCAATGG 898

Qy 2852 GAGGGGAGGGAG 2863

Db 899 AAGGGGGAGGG 910

RESULT 31

AL525169/c

LOCUS

DEFINITION

AL525169 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens

CDNA clone CS0DC005YH18 3-PRIME, mRNA sequence.

AL525169

AL525169.2 GI:31043424

EST.

Source

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 884)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 13, 2001 this sequence version replaced gi:12788662.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY Cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6148.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DC005DD09NP1&cluster=6148.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DC005DD09NP1.

Location/Qualifiers

1. 884

/organism="Homo sapiens"

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/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 164 a 292 c 240 g 160 t 28 others

ORIGIN

Query Match 25.1%; Score 799.2; DB 9; Length 884;

Best Local Similarity 95.6%; Pred. NO. 1.4e-156;

Matches 846; Conservative 24; Mismatches 10; Indels 5; Gaps 5;

Qy 2265 COTCTCTCTGTGTCAGAGGAGGTGGCCACGTCAGGGTGTCTGAGGTCCAGATTCTGGAG 2324

Db 884 COTCTCTCTGTGTCAGAGGAGGTGGCCACGTCAGGGTGTCTGAGGTCCAGATTCTGGAG 825

Qy 2325 GGAGGCTCAGCCACCTCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTCTGGAG 2384

Db 824 GGAGGCTCAGCCACCTCTCCAGCTTTTCTCAGGGTGTCTGAGGTCCAGATTCTGGAG 765

Qy 2385 CAATCTGACCTTCTCCAAAGCTCTGTATCAGTGTGGCAGTCCAGCCAAATCCCTGGC 2444

Db 764 CAATCTGACCTTCTCCAAAGCTCTGTATCAGTGTGGCAGTCCAGCCAAATCCCTGGC 705

Qy 2445 CATTTGGCCCCAGGGGAGCTGGGCCCTGTCAGGTGTGAGGAGGGGACCTGGAGCTGGGAGG 2504

Db 704 CATTTGGCCCCA-GGGGACGTGGGGCCCTGCAGGCTGCAGGAGGGCACTGGAGCTGGGAGG 646

Qy 2505 TCTGCTCCAGAGCCTCCCATCTCGGGGCTGCTGTGT-GGACGGGCTT-GCCTCAGGCAC 2562

Db 645 TCTGCTCCAGAGCCTCCCATCTCGGGGCTGCTGTGTGGGACGGGCTGCTGCTCAGGCAM 586

Qy 2563 TCTCTGTCTGAAACCTGCCCTTACTGTGTTAACTGTGTTCTCCAGGATGCAATCTTGATA 2622

Db 585 TCGCTGTCTGAACTGCCCTCACTGTGTTTAACTGCCGCTCCAGGATGCAATCTTGATA 526

Qy 2623 GGAGGGGGCGGACGGGCTGGGCTTGTGACAACTGCTTTCACACATGGGCTTCCCTC 2682

Db 525 GGAGGGGGCGGACGGGCTGGGCTTGTGACAACTGCTTTCACACATGGGCTTCCCTC 466

Qy 2683 GGTGGCCCTCACTGTCTAGGAGGGCCAGGAGGACAGAGGGGAGGAGTCTCAGGAGGAG 2742

Db 465 GGTGGCCCTCACTGTCTAGGAGGGCCAGGAGGACAGAGGGGAGGAGTCTCAGGAGGAG 406

Qy 2743 GCTGCCCTGAGGGGCTGGGAGGGGGTACCTCATGAGGACGAGGTGAGCTCAGAGAGAG 2802

Db 405 GCTGCCCTGAGGGGCTGGGAGGGGGTACCTCATGAGGACGAGGTGAGCTCAGAGAGAG 346

Qy 2803 GAGGAGGTGGGGGCTGGAGGTGCTGTGTAGTGGGACGGGCAAGTGTAGAGGGGAGGGA 2862

Db 345 GAGGAGGKGGGGCTGGAGGTGCTGTGTAGTGGGACGGGCAAGTGTAGAGGGGAGGGA 286

Qy 2863 GGGAGTCTCTGAGGAGGATCTGAGCTGCTGTGAGTCTTAACCCACTCAATCACTGTTCTAG 2922

Db 285 GSGMAGTCTCTGGGAGGAYCCTGAGCTGTGTGAGTCTTAACCCACTCAATCACTGTTCTAG 226

Qy 2923 ATTGAGGAGGAGGACGAGGACCAAACTCAGAACTGGGGGCTTTGGGGGAGGGCGCTAG 2982

Db 225 ATTGAGGAGGAGGACGAGGACCAAACTCAGAACTGGGGGCTTTGGGGGAGGGCGCTAG 166

Qy 2983 TCCCCCAGCTCTTAAGAGCCAGGAGGACCTGATTAAGCATCTGGGTTGCCATGGCA 3042

Db 165 TCCCCCAGCTCTTAAGAGCCAGGAGGACCTGATTAAGCATCTGGGTTGCCATGGCA 106

Qy 3043 ATGGGATCCCCCAGCTTACTGTATGCCCCGACCCCGGAGAGGAGGAGGAGGAGGAGGAGGAG 3102

Db 105 ATGGGATCCCCCAGCTTACTGTATGCCCCGACCCCKACCCCTCAGAGGAGGAGGAGGAGGAG 46

Qy 3103 GGGAGCTCATGTAATGTTTATCATGTTTACTTCCCGACCCCTACA 3147

Db 45 GGGAGCTCATGTAAT-TTTATCATG-TACTTCCCGACCCCTACA 3

RESULT 32

BQ423614

LOCUS

DEFINITION

BQ423614

5', mRNA sequence.

ACCESSION

BQ423614.1 GI:21118929

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1. (bases 1 to 841)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

CDNA Library Prepared by: Life Technologies, Inc.

Tissue Procurement: ATCC

CDNA Library Prepared by: The I.M.A.G.E. Consortium (ILNL)

CDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

http://image.llnl.gov

Plate: LLAM13950 row: n column: 02

QY 1692 ACCTGCGCTCATGGG--ACCTGCGCTCCCTCAGCGGTGAGCC 1732  
 Db 781 ACCTGCGCTCATGGGGACCTGGCCCTCCCTCAGCGGTGAGCC 823  
  
 RESULT 33  
 BX337335  
 LOCUS  
 DEFINITION  
 BX337335 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CSODI040YK05 5-PRIME, mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 EST.  
 BX337335.1 GI:30308549  
 BP 191 91006 EVRY cedex - France  
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6148.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI040AF030P1  
 &cluster=6148.f. Contact : Feng Liang Email : fliang@lifetech.com  
 URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI040AF030P1.  
 Location/Qualifiers  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 255 a 304 c 372 g 189 t  
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 Best Local Similarity 98.8%; Pred. No. 2.8e-156;  
 Matches 843; Conservative 2; Mismatches 4; Indels 4; Gaps 4;  
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 Db 239 CTCCTCAGCGCAGGCGAGAGGCTGGGGAGAGGGCGCGGTGGAGGAGTAGGAGAGAC 238  
 QY 61 AAAAGCCGAAACGAGAGAGGGCCCCGGGTGTCACACACCGCGCTGGAGGAGCAGCGTGTGTG 120  
 Db 299 AAAAGCCGAAACGAGAGAGGGCCCCGGGTGTCACACACCGCGCTGGAGGAGCAGCGTGTGTG 358  
 QY 121 CAGCGAGCAGCGCGCGGGGAGCGCAGTGCACGGGGCGGTACACAGTGGCAGGAGGAGCA 180  
 Db 359 CAGCGAGCAGCGCGCGGGGAGCGCAGTGCACGGGGCGGTACACAGTGGCAGGAGGAGCA 418  
 QY 181 TGGGGAAGGGAGGGAAACAGGGCGAGGGGGCGCGGAGCGCAGGTGTGGTGTCCACCT 240  
 Db 419 TGGGGAAGGGAGGGAAACAGGGCGAGGGGGCGCGGAGCGCAGGTGTGGTGTCCACCT 478  
 QY 241 TCAGCTGGGAGGAGATTGAGAGCATACCTGGCACCGACAGTGGGCTGGTCAATTGACC 300  
 Db 479 TCAGCTGGGAGGAGATTGAGAGCATAACTCGCACCCACACAG-GTGTGGTCAATTGACC 537  
 QY 301 GCAAGGTTTACAACTATCAACAAATGGTTCATCCAGCACCCGGGGGGCCACGCGGTTCATCG 360



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QY 2783 CAGGGTGGAGCTGAGAGAGGAGGAGTGGGGGCTGGAGGTGCTGTAGCTGAGGGGACG 2842
Db 839 CACGGGTGAACCTTGAAGAGAGAGGAGGGGGGGCTTGAAGGTCTTGGTAACAT 898
QY 2843 GGCAGTGTAGAGGGGAGGAGGGA 2866
Db 899 GGAAGGGGAACGGGGCAAGTGGAA 922

RESULT 35
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LOCUS 60263519F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778500 5',
DEFINITION mRNA sequence.
ACCESSION BG742060
VERSION BG742060.1 GI:14052713
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM0634 row: f column: 05
High quality sequence stop: 841.
Location/Qualifiers
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/lab_host="DH10B (T1 phage-resistant)"
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/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 137 a 306 c 249 g 189 t
ORIGIN
Query Match 25.0%; Score 797.2; DB 10; Length 881;
Best Local Similarity 97.8%; Pred. No. 3.7e-156;
Matches 861; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

QY 1706 GACCTGCGCTCCCTCAGCGCTGAGCCATGAGCCATGAGCCCTCCAGGCTCCCTAGGCC 1765
Db 4 GGGACTGCGCTCCCTCAGCGCTGAGCCATGAGCCATGAGCCCTCCAGGCTCCCTAGGCC 63

QY 1766 CTTCTTCCAGGAGCAGAGGTGGCCACCGGGGTGGCTGCTCTACCTCCACTCTCT 1825
Db 64 CTTCTTCCAGGAGCAGAGGTGGCCACCGGGGTGGCTGCTCTACCTCCACTCTCT 123

QY 1826 GCCCTTAAGATGGGAGGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 1885
Db 124 GCCCTTAAGATGGGAGGAGACAGCGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGC 183

QY 1886 AGCTGGTCACTAGGATCACCCCGCTTGGTCTTCAGATGCTCTGGGGTTCATAGG 1945
Db 184 AGCTGGTCACTAGGATCACCCCGCTTGGTCTTCAGATGCTCTGGGGTTCATAGG 243

QY 1946 GGCAGGTCTAGTCGGGAGGAGGCGCCCTGACCCCTCCGGGCTGGCTCACTCTCCCTGACG 2005

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Db 244 GGCAGGTCTAGTCGGGACGGGCCCTTGACCCCTCCGGGCTGCTCACTCTCCCTGACG 303
QY 2006 GCTGCCATTTGGTCCACCCCTTTTCATAGAGAGCTGCTTTGTTTACAAGCTCGGGTCTCC 2065
Db 304 GCTGCCATTTGGTCCACCCCTTTTCATAGAGAGCTGCTTTGTTTACAAGCTCGGGTCTCC 363
QY 2066 TCCTGCAGCTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTGTCCAGGGGCCCCAGAGCCGCG 2125
Db 364 TCCTGCAGCTCGGTTAAGTACCCGAGGCTCTCTTAAGATGTGTCCAGGGGCCCCAGAGCTGC 422
QY 2126 GGGCAGACGACGACCCAAACCTTGGGCCCTTGGAGAGTCTTCCACCCCATCCTAGAGTGC 2185
Db 423 GGGCAGACGACGACCCAAACCTTGGGCCCTTGGAGAGTCTTCCACCCCATCCTAGAGTGC 482
QY 2186 TCTGACCCCTGGGCTTTCACGGGGCCCAATTCACGGGCTCCCACTTGGAGCTGTGACCT 2245
Db 483 TCTGACCCCTGGGCTTTCACGGGGCCCAATTCACGGGCTCCCACTTGGAGCTGTGACCT 542
QY 2246 TGGGACCAAGAGGGGAGTCCCTGCTCTTTGTGACTCAGCAGAGGAGTGGCCAGCTTCA 2305
Db 543 TGGGACCAAGAGGGGAGTCCCTGCTCTTTGTGACTCAGCAGAGGAGTGGCCAGCTTCA 602
QY 2306 GGGAGGGGCGGCTGGGCTGAGGCTCAGCAGCCCTCCAGCTTTCCTCAGGGTGTCT 2365
Db 503 GGGAGGGGCGGCTGGGCTGAGGCTCAGCAGCCCTCCAGCTTTCCTCAGGGTGTCT 661
QY 2366 GAGTCCAAAGATTCTGGAGCAATCTGACCTTTCACAAAGGCTCTGTATCAGCTGGGCA 2425
Db 662 GAGTCCAAAGATTCTGGAGCAATCTGACCTTTCACAAAGGCTCTGTATCAGCTGGGCA 721
QY 2426 GTGCCAGCCCAATCCCTGGCCATTTGGCCCGAGGGGAGCTGGGCCCTGAGGGCTGAGGA 2485
Db 722 GTGCCAGCCCAATCCCTGGCCATTTGGCCCGAGGGGAGCTGGGCCCTGAGGGCTGAGGA 781
QY 2486 -GGGCACTGGAGC--TGGGAGGTCTGTCACAGCCCTCCCACTCTCGGGCTCTGTGTG 2542
Db 782 GGGGCACTGGAGCTTGGGAGGTCTGTCACAGCCCTCCCACTCTCGGGCTCTGTGTG 841
QY 2543 GAGGGGCG-TGGCTCAGGCACTCTCTGTCTGCACTGCC 2581
Db 842 GAGGGGCGCTTGGCTCAGGCACTCTCTGTCTGCACTGCC 881

RESULT 36
BG910799 909 bp. mRNA linear EST 05-JUN-2001
LOCUS 602808526F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4940503
DEFINITION 5', mRNA sequence.
ACCESSION BG910799
VERSION BG910799.1 GI:14291275
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM0879 row: d column: 08
High quality sequence stop: 794.
Location/Qualifiers
1. .909
FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
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/Note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      149 a   318 c   242 g   200 t
ORIGIN

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Query Match      25.0%; Score 795.4; DB 12; Length 909;
Best Local Similarity 96.8%; Pred. No. 8.8e-156;
Matches 866; Conservative 0; Mismatches 21; Indels 8; Gaps 5;

QY 1333 ACCACCTTCTCCACCATCCCGGCACAACTTACACAGATGCGCCGCTGGTGAAGT 1392
DB 1 ACCACCTTCTCCACCATCCCGGCACAACTTACACAGATGCGCCGCTGGTGAAGT 60

QY 1393 CTATATGTGCAAGCATGGCAATTGAATACAGAGAGCGGCTACTGAGGGCCCTGCTGG 1452
DB 61 CTATATGTGCAAGCATGGCAATTGAATACAGAGAGCGGCTACTGAGGGCCCTGCTGG 120

QY 1453 ACATCATCAGTCCCTGAGAGCTGTGGAGAGCTGTGGTGGAGCGCTACCTTCACAAAT 1512
DB 121 ACATCATCAGTCCCTGAGAGCTGTGGAGAGCTGTGGTGGAGCGCTACCTTCACAAAT 180

QY 1513 GAAGCCACAGCCCGCGGCACACCGTGGGGAAGGGGTGCAAGTGGGTGATGGCCAGAGA 1572
DB 181 GAAGCCACAGCCCGCGGCACACCGTGGGGAAGGGGTGCAAGTGGGTGATGGCCAGAGA 240

QY 1573 ATGATGGCTTTGTTCTGAGGGGTGCCAGAGGCTGTGGTATGCACTGCTCAGCGACC 1632
DB 241 ATGATGGCTTTGTTCTGAGGGGTGCCAGAGGCTGTGGTATGCACTGCTCAGCGACC 300

QY 1633 CCATGTTGGATCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1692
DB 301 CCATGTTGGATCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

QY 1693 CCCTGCCCTCATGAGAGCTGCTCCCTCCTCAGCGGTGAGCCATCAGCATGGCCCTCCAG 1752
DB 361 CCCTGCCCTCATGAGAGCTGCTCCCTCCTCAGCGGTGAGCCATCAGCATGGCCCTCCAG 420

QY 1753 TGCCTCTAGCCCTTCTTCCAGAGAGCAGAGAGTGGCCACCGGGGGTGGCTCTCTCTCT 1812
DB 421 TGCCTCTAGCCCTTCTTCCAGAGAGCAGAGAGTGGCCACCGGGGGTGGCTCTCTCTCT 480

QY 1813 ACCTCCACTCTGCTCCCTTAAGATGGAGAGAGCAGCGGTCCATGGGTCTGGCCTGTG 1872
DB 481 ACCTCCACTCTGCTCCCTTAAGATGGAGAGAGCAGCGGTCCATGGGTCTGGCCTGTG 540

QY 1873 AGTCTCCCTCTGACGCTGTGTCACTAGGCATCACCCCGCTTTTGGTTCTTTCAGATGCTCT 1932
DB 541 AGTCTCCCTCTGACGCTGTGTCACTAGGCATCACCCCGCTTTTGGTTCTTTCAGATGCTCT 600

QY 1933 TG-GGGTTCTAAGGGGAGGTCTTAGTGGGAGGCGCCCTGACCCCTCCCGGCTGGCTT 1991
DB 601 TGCGGGTTCTAAGGGGAGGTCTTAGTGGGAGGCGCCCTGACCCCTCCCGGCTGGCTT 660

QY 1992 CACTCTCCCTGACGCTGCCATTTGGTCCACCCCTTTCATAGAGAGGCTGTCTTGTACAA 2051
DB 661 CACTCTCCCTGACGCTGCCATTTGGTCCACCCCTTTCATAGAGAGGCTGTCTTGTACAA 720

QY 2052 AGCTCGGCTCTCCCTCTGAGCTCGGTAAAGTACCCGAGGCTCTCTTAAAGATGTCCAG 2111
DB 721 AGCTCGGCTCTCC--TCTGCACTCGGTAAAGTACCCGAGGCTCTCTTAAAGATGTCCAG 778

QY 2112 GCGCCAGGCGCGGCGACAGCCAGCCAACTTGGGCGCTTGGAGAGTCTTCCACCC 2171

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779 GGCCCCAGGCGCGGCGC-CAGCCAGCCCAA--CCTTGGGCTTGGCAGAGCTTCGCGCC 835
2172 CATCACTAGAGTCTCTGACCTGGGCTTTCAGGGCCCATTCACACGCTCC 2236
836 GATCACTTGAAGTCCCTGACC--TGGGCTTCCGCGGCCCATTCCTCCCGCTCC 888

RESULT 37
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LOCUS 602632689F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:477655 5'
DEFINITION mRNA sequence.
ACCESSION BG742600
VERSION BG742600.1 GI:14053253
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM10632 row: b column: 24
High quality sequence stop: 851.
Location/Qualifiers
1. 877
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/Note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      144 a   288 c   250 g   195 t
ORIGIN

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Query Match      24.9%; Score 792.8; DB 10; Length 877;
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QY 1469 GAAGAGTCTGGAGCTGTGGTGGAGCTTACCTTCAAAATGAAGCCAGCCCGC 1528
DB 1 GAAGAGTCTGGAGCTGTGGTGGAGCTTACCTTCAAAATGAAGCCAGCCCGC 60

QY 1529 GGACACCGTGGGGAAGGGGTGAGTGGGTGATGCCAGAGGAATGATGGCTTTGTT 1588
DB 61 GGACACCGTGGGGAAGGGGTGAGTGGGTGATGCCAGAGGAATGATGGCTTTGTT 119

QY 1589 CTGAGGGGTGTCGAGAGGCTGTGTATGCTACGACCCCATGTTGGATCTTTC 1648
DB 120 CTGAGGGGTGTCGAGAGGCTGTGTATGCTACGACCCCATGTTGGATCTTTC 179

QY 1649 TCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1708
DB 180 TCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239

QY 1709 CTTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1768
DB 240 CTTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 299

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RESULT 39
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LOCUS
DEFINITION
602635575F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780434 5',
mRNA sequence.
ACCESSION
BG743539
VERSION
BG743539.1 GI:14054192
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10639 row: f column: 19
High quality sequence stop: 842.
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/notes="Organ: skin; Vector: pCMV-Sport6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 159 a 251 c 297 g 172 t
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Matches 863; Conservative 0; Mismatches 8; Indels 7; Gaps 6;
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DB 1 CGGTTAAGTACCGAGGCTCTCTTAAGATGTCCA-GGCCCGAGGCTGGGACAGCC 59
QY 2136 AGCCCAACCTTGGGCGCTTGAAGAGTCTCCACCCATCACTAGAGTCTGACCC 2195
DB 60 ASCCCAAACCTTGGGCGCTTGAAGAGTCTCCACCCATCACTAGAGTCTGACCC 119
QY 2196 GCGTTTCAGGCGCCCATCCACCCCTCCCACTGAGCTGTGACCTGGGACCAAA 2255
DB 120 GCGTTTCAGGCGCCCATCCACCCCTCCCACTGAGCTGTGACCTGGGACCAAA 179
QY 2256 GGGGAGTCCCTCGTCTCTTGTGACTCAGCAGGAGTGGCCAGCTTCAGGAGGGGCC 2315
DB 180 GGGGAGTCCCTCGTCTCTTGTGACTCAGCAGGAGTGGCCAGCTTCAGGAGGGGCC 239
QY 2316 GCGTGGCTGGAGGCTCAGCCACCCCTCAGCTTTCTCAGGCTGCTCAGGCTCCAG 2375
DB 240 GCGTGGCTGGAGGCTCAGCCACCCCTCAGCTTTCTCAGGCTGCTCAGGCTCCAG 299
QY 2376 ATTCTGAGCAATCTGACCTTCTCAAAAGGCTCTGTTATCAGCTGGGAGTCCAGCA 2435
DB 300 ATTCTGAGCAATCTGACCTTCTCAAAAGGCTCTGTTATCAGCTGGGAGTCCAGCA 359
QY 2436 ATCCCTGGCCATTGGCGCCACAGGGGACGTGGGGCCCTGCGAGCTCAGGAGGCACTGGA 2495

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Db 360 ATCCCTGGCCATTGGCCCA--GGACGTGGGCGCTGCAGGCTGCAGGAGGCACTGGA 417
QY 2496 GCTGGAGGTCTCTGTCCTCCAGCCCTCCCATCTCGGGGCTCTGTGTGGAGCGGCGCT 2555
Db 418 GCTGGAGGTCTCTGTCCTCCAGCCCTCCCATCTCGGGGCTCTGTGTGGAGCGGCGCT 477
QY 2556 CAGGCACTCTCTGTCCTGTAACCTGCGCTTACTGTGTTAACTGTTGCTCCAGGATGCAT 2615
Db 478 CAGGCACTCTCTGTCCTGTAACCTGCGCTTACTGTGTTAACTGTTGCTCCAGGATGCAT 537
QY 2616 TCTGATAGGAGGCGCGCAGGCGCTGGGCC--TTGTGCAATCTGCTTTCACACATGGC 2674
Db 538 TCTGATAGGAGGCGCGCAGGCGCTGGGCCCTTTGTGCAATCTGCTTTCACACATGGC 597
QY 2675 CTTCCCTCGGTGGCGCTGACTGTCCAGGAGGCGCGCAGGAGGCGGAGGAGTCTC 2734
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QY 2735 AGGAGGAGGCTGCGCTCAGGCGCTGGGAGGCGGTACTCATGAGGACCGAGGTGGAGCT 2794
Db 658 AGGAGGAGGCTGCGCTCAGGCGCTGGGAGGCGGTACTCATGAGGACCGAGGTGGAGCT 717
QY 2795 GAGAGGAGGAGGAG--GTGGGGGCTGGAGGTCTGTGAGCTGAGGAGCGGCAAGTCA-G 2852
Db 718 GAGAGGAGGAGGAGCGGTGGGGGCTGGAGGTCTGTGAGCTGAGGAGCGGCAAGTCA-G 777
QY 2853 AGGGAGGAGGAGGAGTCTCTGGGAGGATCTCTGAGCTCTGTGCGTGTACCCACTAAT 2912
Db 778 AGGGAGGAGGAGGAGTCTCTGGGAGGATCTCTGAGCTCTGTGCGTGTACCACTAAT 836
QY 2913 CAGTTCTTAGATTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2950
Db 837 CAGTTCTTAGATTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 874

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RESULT 40
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LOCUS
DEFINITION
AGENCOURT_10808311 MAPcL Homo sapiens cDNA clone IMAGE:6721119 5',
mRNA sequence.
ACCESSION
CA488914
VERSION
CA488914.1 GI:24951705
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 892)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM14281 row: 1 column: 15
High quality sequence stop: 650.
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, INCaP"
/lab_host="EMDH10B"
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FEATURES

source



/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;  
Subtracted with brain, liver, lung, kidney and muscle.  
Directionally cloned. Priming method: Oligo-dT. Average  
insert size: 1800 bp. Library amplification: 26,000 fold.  
Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
Bungkook Lee & Ira Pastan: Discovery of new breast  
cancer genes encoding membrane and secreted proteins.  
Manuscript submitted."

Job time : 4254 secs

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|---------------------------|--|--|-------|-------|----------|
| BASE COUNT                | 162 a                                  | 284 c  | 240 g | 204 t | 2 others |
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| Query Match               | 24.8%; Score 789.4; DB 14; Length 992; |  |       |       |          |
| Best Local Similarity     | 99.4%; Pred. No. 1.6e-154;             |  |       |       |          |
| Matches 824; Conservative | 0; Mismatches 1; Indels 4; Gaps 3;     |  |       |       |          |
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| Db                        | 1                                      | GGGAGCCCTCCTTTTCTCAACTTCATCAGGTTCTGTGAGAGCCACTGGTTGTGGGT   | 60    |       |          |
| QY                        | 1190                                   | CACACAGATGAATCACATCGTCATGAGATTGACAGAGCCCTACCGTACTGGTTTCAG  | 1249  |       |          |
| Db                        | 61                                     | CACACAGATGAATCACATCGTCATGAGATTGACAGAGCCCTACCGTACTGGTTTCAG  | 120   |       |          |
| QY                        | 1250                                   | TAGCCAGCTGACGACCTGACAGCTGAGAGCTCTTCTTCAACGACTGGTTTCAGTGG   | 1309  |       |          |
| Db                        | 121                                    | TAGCCAGCTGACGACCTGACAGCTGAGAGCTCTTCTTCAACGACTGGTTTCAGTGG   | 180   |       |          |
| QY                        | 1310                                   | ACACCTTAACCTTCAGATTGAGACCACTCTTCCCAACCATGCCCGGCACAACTTACA  | 1369  |       |          |
| Db                        | 181                                    | ACACCTTAACCTTCAGATTGAGACCACTCTTCCCAACCATGCCCGGCACAACTTACA  | 240   |       |          |
| QY                        | 1370                                   | CAAGATGCCCGCTGCTGAGTCTCTATGTGCCAAGCATGGCATTAATACCAAGGAA    | 1429  |       |          |
| Db                        | 241                                    | CAAGATGCCCGCTGCTGAGTCTCTATGTGCCAAGCATGGCATTAATACCAAGGAA    | 300   |       |          |
| QY                        | 1430                                   | GCCTACTAGGGCCCTGTGAGATCATCAGGTCCCTGAAGAAGTCTGGAGGCTGTG     | 1489  |       |          |
| Db                        | 301                                    | GCCTACTAGGGCCCTGTGAGATCATCAGGTCCCTGAAGAAGTCTGGAGGCTGTG     | 360   |       |          |
| QY                        | 1490                                   | GCTGAGCCCTACTTCAATATAGCCACAGCCCGCGGACACCTGGGAGGGGTG        | 1549  |       |          |
| Db                        | 361                                    | GCTGAGCCCTACTTCAATATAGCCACAGCCCGCGGACACCTGGGAGGGGTG        | 420   |       |          |
| QY                        | 1550                                   | CAGTGGGTGATGGCCAGAGGAATGATGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT   | 1609  |       |          |
| Db                        | 421                                    | CAGTGGGTGATGGCCAGAGGAATGATGGCTTTTGTCTGAGGGGTGTCCGAGAGGCT   | 480   |       |          |
| QY                        | 1610                                   | GGTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTTTT | 1669  |       |          |
| Db                        | 481                                    | GGTGTATGCACTGCTCAGGACCCCATGTTGGATCTTTCTCCCTTTCTCTCTCTCTTTT | 540   |       |          |
| QY                        | 1670                                   | CTCTTTCATCTCCCATAGCACCCCTGCTCATGGAGCTGCCCTCCCTCAGCCGTCA    | 1729  |       |          |
| Db                        | 541                                    | CTCTTTCATCTCCCATAGCACCCCTGCTCATGGAGCTGCCCTCCCTCAGCCGTCA    | 600   |       |          |
| QY                        | 1730                                   | GCCATCAGCCATGGCCCTCCAGTGCCTCTCTAGCCCTTTCTTC-CAAGGAGCAGAGGT | 1788  |       |          |
| Db                        | 601                                    | GCCATCAGCCATGGCCCTCCAGTGCCTCTCTAGCCCTTTCTTC-CAAGGAGCAGAGGT | 660   |       |          |
| QY                        | 1789                                   | GGCCACC--GGGGGTGGTCTGTCTACCTCCACTCTGCCCTTAAGATGGAGAGA      | 1846  |       |          |
| Db                        | 661                                    | GGCCACCNGGGGTGGTCTGTCTACCTCCACTCTGCCCTTAAGATGGAGAGA        | 720   |       |          |
| QY                        | 1847                                   | CCAGGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGCAGCCCTGGTCACTAGGCATCAC | 1906  |       |          |
| Db                        | 721                                    | CCAGGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGCAGCCCTGGTCACTAGGCATCAC | 780   |       |          |
| QY                        | 1907                                   | CCCGCTTGGTCTTTCAGATGCTCTT-GGGTTTCATAGGGGAGGTCC             | 1954  |       |          |
| Db                        | 781                                    | CCCGCTTGGTCTTTCAGATGCTCTT-GGGTTTCATAGGGGAGGTCC             | 829   |       |          |

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus p2n model

Run on: December 10, 2003, 18:09:05 ; Search time 1951 Seconds  
(without alignments)  
5531.106 Million cell updates/sec

Title: US-09-719-601-5  
Perfect score: 2438  
Sequence: 1 MGKGNQGEAAREVSVPT.....DIIRSLKSKGLMDAYLHK 444

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-NODEL=frame+ p2n.model -DEV=xlh  
-Q/cn2\_1/USPTO\_spool/US09719601/runat\_09122003\_094908\_21162/app\_query.fasta\_1.583  
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-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em estba:\*  
2: em esthum:\*  
3: em estin:\*  
4: em estmu:\*  
5: em estov:\*  
6: em estpl:\*  
7: em estro:\*  
8: em htc:\*  
9: gb est1:\*  
10: gb est2:\*  
11: gb htc:\*  
12: gb est3:\*  
13: gb est4:\*  
14: gb est5:\*  
15: em estfun:\*  
16: em eston:\*  
17: em gss hum:\*  
18: em gss inv:\*  
19: em gss pin:\*  
20: em gss vrt:\*  
21: em gss fun:\*  
22: em gss nam:\*  
23: em gss mus:\*  
24: em gss pro:\*  
25: em gss rod:\*  
26: em gss phg:\*  
27: em gss vrl:\*  
28: gb gss1:\*

29: gb gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Match % | Query Length | DB ID | Description        |
|------------|--------|---------|--------------|-------|--------------------|
| 1          | 2048   | 84.0    | 2862         | 11    | AK083282 Mus muscu |
| 2          | 1826   | 74.9    | 1201         | 9     | AL530346 AL530346  |
| 3          | 1602   | 65.7    | 884          | 13    | BQ881930 AGENCOURT |
| 4          | 1560   | 64.0    | 1201         | 13    | BQ881930 BX417399  |
| 5          | 1555.5 | 63.8    | 926          | 13    | BQ883702 AGENCOURT |
| 6          | 1553.5 | 63.7    | 924          | 13    | BQ883702 AGENCOURT |
| 7          | 1551.5 | 63.6    | 1689         | 11    | BQ883702 AGENCOURT |
| 8          | 1548   | 63.5    | 914          | 13    | AK080414 Mus muscu |
| 9          | 1545.5 | 63.4    | 3129         | 11    | AK080414 Mus muscu |
| 10         | 1482.5 | 60.8    | 3697         | 11    | AK029318 Mus muscu |
| 11         | 1471   | 60.3    | 3318         | 11    | AK090042 Mus muscu |
| 12         | 1470.5 | 60.3    | 2272         | 11    | AK083959 Mus muscu |
| 13         | 1449   | 59.4    | 820          | 10    | AK076485 Mus muscu |
| 14         | 1412   | 57.9    | 806          | 10    | BG742318 602631469 |
| 15         | 1397   | 57.3    | 909          | 10    | BG742318 602633764 |
| 16         | 1379   | 56.6    | 805          | 10    | BG742318 602632192 |
| 17         | 1379   | 56.6    | 910          | 9     | BG742318 602632908 |
| 18         | 1372   | 56.3    | 802          | 10    | AL522956 AL522956  |
| 19         | 1339   | 54.9    | 933          | 13    | BG742408 602635311 |
| 20         | 1336   | 54.8    | 952          | 13    | BX341258 BX341258  |
| 21         | 1329   | 54.5    | 745          | 10    | BX441083 BX441083  |
| 22         | 1325   | 54.3    | 1091         | 10    | BG739802 602630527 |
| 23         | 1310.5 | 53.8    | 932          | 13    | BF315881 601895828 |
| 24         | 1301.5 | 53.4    | 1246         | 13    | BQ845074 AGENCOURT |
| 25         | 1286   | 52.7    | 829          | 13    | BQ422100 AGENCOURT |
| 26         | 1286   | 52.7    | 938          | 13    | BG741484 602632282 |
| 27         | 1282.5 | 52.6    | 802          | 10    | BUS6567 AGENCOURT  |
| 28         | 1278.5 | 52.4    | 764          | 10    | BF970711 602273891 |
| 29         | 1277   | 52.4    | 832          | 10    | BG741398 602631955 |
| 30         | 1261   | 51.7    | 889          | 10    | BG696305 602659454 |
| 31         | 1251   | 51.3    | 897          | 10    | BG698232 602660143 |
| 32         | 1248   | 51.2    | 796          | 10    | BG596235 60259366  |
| 33         | 1247   | 51.1    | 963          | 13    | BG740017 602630980 |
| 34         | 1244   | 51.0    | 768          | 10    | BUS01667 AGENCOURT |
| 35         | 1243   | 51.0    | 759          | 12    | BG696607 602658902 |
| 36         | 1239   | 50.8    | 799          | 10    | BI752239 603022433 |
| 37         | 1232   | 50.5    | 1022         | 13    | BG743597 602633951 |
| 38         | 1225   | 50.2    | 755          | 10    | BQ071205 AGENCOURT |
| 39         | 1214   | 49.8    | 971          | 14    | BG743135 602634381 |
| 40         | 1212   | 49.7    | 753          | 10    | CA488711 AGENCOURT |
| 41         | 1204   | 49.4    | 1113         | 13    | BQ422998 602450074 |
| 42         | 1194.5 | 49.0    | 851          | 12    | BQ278100 AGENCOURT |
| 43         | 1185   | 48.6    | 968          | 10    | BI332236 602981695 |
| 44         | 1182   | 48.5    | 708          | 10    | BG740405 602634182 |
| 45         | 1178   | 48.3    | 1201         | 13    | BG743224 602634390 |
|            |        |         |              |       | BX418789 BX418789  |

ALIGNMENTS

RESULT 1  
AK083282  
LOCUS  
DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length  
enriched library, clone:C630034B17 product:fatty acid desaturase 2,  
full insert sequence.  
ACCESSION AK083282  
VERSION AK083282.1 GI:26101164  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AK083282 2862 bp mRNA linear HTC 05-DEC-2002  
Mus musculus adult male hippocampus cDNA, RIKEN full-length  
enriched library, clone:C630034B17 product:fatty acid desaturase 2,  
full insert sequence.



QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
 Db 462 ATCGTCATGGAAGCCCTGGCTGCTTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 521  
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
 Db 522 ACCCTCGCTCAGAGCTTTGCTCGTACCTCTCAGGCCCAAGCTGATGCTGCACAT 581  
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
 Db 582 GACTATGGCCACCTTTCTGCTTAAGAAATCCATATGGAAACCGCTGTTCCCAAGTTT 641  
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
 Db 642 GTCATTTGCCACTTAAAGGGTGCCTCAGCCAACTGGTGAACCAACCCGACATTTCCAAAC 701  
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
 Db 702 CATGCCAAGCCCAACATCTTCCCAAGACCCGACATAAAGCCCTGCATGTGTTGTC 761  
 QY 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsn 260  
 Db 762 CTGGCGAGTGGCAGCCCTTGATGGCAAGAAAGCTGAAATACCTGCCCTCAAC 821  
 QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280  
 Db 822 CACCAGCATGATATCTTCTCTGATCGGACCGCGCTGCTCATCCCTATGATCTTCCAG 881  
 QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300  
 Db 882 TACCAGATCATCATGACATGATCAGCGCAGGACTGGGTGGACTTGGCTGGGCCATC 941  
 QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320  
 Db 942 AGCTACTATATGCGTTCTTCTACACCTTACATCCCTTCTACCGCATCTTGGGAGCCCTG 1001  
 QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMet 340  
 Db 1002 GTTTTCTCTCACTTATCAGTTCTCTGAGAGCCACTGTTTGTGTGGTGCACACATG 1061  
 QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360  
 Db 1062 AACCACTTGTCTGAGATTGATCTTGTACACTACCGGACTGGTTCAGCAGCCAGCTG 1121  
 QY 361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380  
 Db 1122 CGAGCCACTGCATGTGAGCAGTCTTCTCAATGACTGTTTGTGAGGGGCACCTCAAT 1181  
 QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400  
 Db 1182 TTCCAGATTGAGCACCACTCTTCCCACTATGCCAGCTCAACACCTGCACAGATTGCC 1241  
 QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420  
 Db 1242 CCACGTGGTGAAGTCTCTCTGCGCCAGCATGGCATTAATACCAAGAGAGCCCTGCTG 1301  
 QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440  
 Db 1302 AGGGCCCTGATGCATTTGTGAGTTTCACTGAAGAAGTCTGGGGAGCTGTGGCTGATGCT 1361  
 QY 441 TyrLeuHisLys 444  
 Db 1362 TACCTCCATAAA 1373  
 RESULT 2  
 LOCUS AL530346 1201 bp mRNA linear EST 23-MAY-2003  
 DEFINITION AL530346 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens  
 CDNA clone CS0DD007J09 5-PRIME, mRNA sequence.  
 ACCESSION AL530346  
 VERSION AL530346.2 GI:31068179  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12793839.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 6148.f For more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DD007CE05QP1&cluster=6148.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DD007CE05QP1.  
 Location/Qualifiers

FEATURES  
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 /clone\_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"  
 /note="Fast strand cDNA was primed with a NotI-oligo (dT)  
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 sites of the pCMVSPORT 6 vector. Library was normalized."  
 BASE COUNT 261 a 345 c 336 g 240 t 19 others

Alignment Scores:  
 Pred. No.: 9,38e-176 Length: 1201  
 Score: 1826.00 Matches: 336  
 Percent Similarity: 96.30% Conservative: 2  
 Best Local Similarity: 95.73% Mismatches: 13  
 Query Match: 74.90% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-719-601-5 (1-444) x AL530346 (1-1201)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
 Db 144 ATGGGGAAGGGAAGGAACCAAGCGGGGGCGGCGAGCGGAGGTGCGGTGCCACC 203  
 QY 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
 Db 204 TTCAGCTGGAGGAGATTTCAGAAGCATACCTGCGCAGCCAGCGKNGCTGCTATTGAC 263  
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
 Db 264 CGCAAGTTTACAAATCATCCAAATGGTCCATCCAGACCCCGGGGGCGAGCGGTCAFC 323  
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
 Db 324 GGGCACTACGCTGGAGAGATGCAACGGATGCTTCCGGCGCTTCCACCTGACCTGGAA 383  
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100  
 Db 384 TTCTGTGGCAAGTTCTTGAACCCCTGCTGTGATGTGTGAACCTGCCCGGAGAGGCCACG 443  
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
 Db 444 CAGGACCAAGGAGAGACTCAAGATCACTAGGACTTCCGGGCCCTGAGGAGAGCGCT 503  
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
 Db 504 GAGGACATGAACCTGTTCAGAACCAACCAACGACGTGTTCCTCTCTCTCTCTCTCTCTCT 563

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141 1leAlaLeuGluSer1leAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160
Db 564 ATCGCCCTGGAGAGCATTCATGGTTCCTACTGCTTTTACTTTGGCAATGGCTGGATTCCT 623
Qy 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
Db 624 ACCCTCATCAGCGCTTTGCTGCTTCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACAT 683
Qy 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTyrPheAsnHisLeuValHisLysPhe 200
Db 684 GATTATGGCCACCTGCTGCTTACAGAAAACCCAGTGGAAACCCACTTGTCCAAATTC 743
Qy 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db 744 GTCAITGGCCACTTAAAGGGTGCCTCTGCAACTGGTGGAAATCATCGCCACTTCAGCAC 803
Qy 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 804 CAGGCCAAGCCTAAACATCTTCACAAAGATCCCGATGTGAACATGCTGCAGTGTGTGT 863
Qy 241 LeuGlyGluTrpGlnProIleGlyTyrGlyLysLysLeuLysTyrLeuProTyrAsn 260
Db 864 CTGGCGGATGCGAGCCCATCGATCGTACGCAAGAAAGAGCTGAATACTGCCCTACAAAT 923
Qy 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
Db 924 CACGACACGAATACTTCTCTGATTGGCGCGCGCTGCTCATCCCATGTATTTCAG 983
Qy 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
Db 984 TACCAGATCATATGACCATGATCGTTCATAGAAAGCTGGTGAGCTGGCGTGGCCGCTC 1043
Qy 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 1044 AGCCATACATCGGTTCTTCATCATCATCCCTTTCTACGGCATCCTGGGAGCCCTC 1103
Qy 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPheValTrpValThrGlnMet 340
Db 1104 CTTTCTCTCMACTTCATCAGGCTCTCTSGAGACATTTGTTTGTGGTGAACAAAWR 1163
Qy 341 AsnHisIleValMetGluLeuAspGlnGluAla 351
Db 1164 AAWMAAAGCTCATRGAGATGAACAAAGAGGCC 1196

RESULT 3
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LOCUS BQ881930
DEFINITION AGENCOURT_8726156 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340921
5', mRNA sequence.
ACCESSION BQ881930
VERSION BQ881930.1 GI:22273938
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mhc.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: gcapsb-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2538 row: c column: 02
High quality sequence stop: 689.
Location/Qualifiers

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source
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/db_xref="taxon:9606"
/clone="IMAGE:6340921"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC library."
BASE COUNT 201 a 271 c 199 g _211 t
ORIGIN
Alignment Scores:
Pred. No.: 4,81e-153 Length: 884
Score: 1602.00 Matches: 291
Percent Similarity: 98.64% Conservative: 0
Best Local Similarity: 98.64% Mismatches: 2
Query Match: 65.71% Indels: 2
DB: 13 Gaps: 0
US-09-719-601-5 (1-444) x BQ881930 (1-884)
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Db 2 TTCACGTGCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCATCAGGCCCTTTGTCTT 61
Qy 169 AlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyr 188
Db 62 GCTACCTCTCAGGCCCAAGCTGGATGGCTGCACATGATTATGGCCACCTGCTGTCTAC 121
Qy 189 ArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAla 208
Db 122 AGAAACCCCAAGTGGAAACACCTTGTCCACAAATTCGTATTGGCCACCTAAAGGGTGCC 181
Qy 209 SerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHis 228
Db 182 TCTGCCAACTGGTGAATCATCGCCACTTCCACACCCAGCCCAAGCTTAACATCTTCCAC 241
Qy 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyTrpGlnProIleGlu 248
Db 242 AAGGATCCCATGTGAACATGCTGCAGCTGTTTGTCTGGCGAATGGCAGCCCATCGAG 301
Qy 249 TyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeu 268
Db 302 TACGCCAAGAAGAAGCTGAAATACCTGCCCTACCAATCACCAGCAGCAATATCTTCTCCTG 361
Qy 269 IleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIle 288
Db 362 ATTGGCGCGCGCTGCTCATCCCATGATATTCAGTACCATCATCATGACCATGATC 421
Qy 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIle 308
Db 422 GTCCATAAAGAACTGGGTGGACCTGGCCCTGGCGCGCTCAGCTACTACATCCGGTCTTCATC 481
Qy 309 ThrTyrIleProPheTyrGlyIleLeuGlyValAlaLeuLeuPheLeuAsnPheIleArgPhe 328
Db 482 ACCTACATCCCTTTCTAGGCAATCCTGGAGCCCTCTCTTTTCTCACTTCATCAGGTTTC 541
Qy 329 LeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAsp 348
Db 542 CTGGAGAGCCACTGGTTTGTGGGTCCACAGATGAATCACATCGTCATGGAGATTGAC 601
Qy 349 GlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGln 368
Db 602 CAGGAGGCGCTTACCTGACTGGTTTCAGTAGCCAGCTGACGCCACCTGCAACAGTGGAGCAG 661

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QY 389 ProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAla 408
DB 722 CCCACCATGCCCGGCACAACTTACACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCC 781
QY 409 LysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAspIleLeuArg 428
DB 782 AAGCATGCAATGATATACAGAGAGCGGCTACTGANGGCCCTTGCGACATCATCANG 841
QY 429 SerLeuLysLysSer-GlyLysLeuTrpLeu-AspAlaTyr 441
DB 842 TCCCTGAAGAAGTCTGGGGAAGCTGTGGCTGGGACGCCCTAC 882

RESULT 4
BX417399
LOCUS
DEFINITION BX417399 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YE07
5-PRIME, mRNA sequence.
ACCESSION BX417399
VERSION BX417399.1 GI:30658393
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li W.B., Gruber C., Jesse J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE009AC04QP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE009AC04QP1.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/tissue_type="PLACENTA"
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/note="Vector: PCWSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 282 a 321 c 306 g 237 t 55 others
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-148 Length: 1201
Score: 1560.00 Matches: 300
Percent Similarity: 91.54% Conservatave: 3
Best Local Similarity: 90.63% Mismatches: 23
Query Match: 63.99% Indels: 8
DB: 13 Gaps: 2

US-09-719-601-5 (1-444) x BX417399 (1-1201)
QY 1 MetGlyLysGlyGlyAsnGlnGlyGluAlaGluArgGluValProThr 20
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DB 142 ATGGGGAAGGAGGAAACCCAGGGCGAGGGGGCGCGAGCGAGGTGTGCGTGCCAC 201
QY 21 PheSerTrpGluGluIleGlnLysHisLeuAsnPhenGlnIleGluValLysLeu 40
DB 202 TTCAGCTGGAGGAGATTTCAGAAAGCATACCTTGCACCCGACGAGGKGNCTGTGCTATTGAC 261
QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyClnArgValIle 60
DB 262 CGCAAGGTTTCAACATCACCAATGGTTCATCCAGCACCCCGGGGGCGAGCGGTCTATC 321
QY 61 GlyHisTyrAlaGlyClnAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
DB 322 GGGCACTAGCTGGAGAGATGCAACGAGATGCTTCCGCGCCTTCCACCTGACCTGGAA 381
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100
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QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
DB 442 CAGGACCAACGGCAAGAACTCAAAGATCACTGAGGACTTCCGGGGCCTTGAGGAGACGGCT 501
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
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DB 622 ACCCTCATCAGCCCTTGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 681
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QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
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QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
DB 802 CAGCCCAAGCCCTAACATCTTCCACAAAGATCCGATGTGAACATGCTGCACGTGTTGTT 861
QY 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsn 260
DB 862 CTGGGCGAATGGCAGCCCATCGAGTACGCGCAAGAAAGAGCTGAAATACCTGCCCTTACAT 921
QY 261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
DB 922 CACCAGCAGATACTTCTCTCTGATTGGGGCGCGCTGCTCATCCCCCATGTATTTCAG 981
QY 281 TyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300
DB 982 TAMCAGATCAWATCACCATCATGATCGTCATATAAAAN-TGGGKGAGCTG-GSCTGGGCGGTA 1039
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleGluAlaLeu 320
DB 1040 RSTAM-TAMATCCGG---TYYTATCACCTAAWYCCITTTWCGGSATCTYGGSRSC--- 1092
QY 321 LeuPheLeuAsnPhenIleArgPheLeuGluSer 331
DB 1093 -----YCTTTTCTCANTTYATMAGTTCT 1116

RESULT 5
BX417399
LOCUS
DEFINITION BX417399 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YE07
5-PRIME, mRNA sequence.
ACCESSION BX417399
VERSION BX417399.1 GI:30658393
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li W.B., Gruber C., Jesse J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE009AC04QP1&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE009AC04QP1.

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YE07"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: PCWSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 282 a 321 c 306 g 237 t 55 others
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-148 Length: 1201
Score: 1560.00 Matches: 300
Percent Similarity: 91.54% Conservatave: 3
Best Local Similarity: 90.63% Mismatches: 23
Query Match: 63.99% Indels: 8
DB: 13 Gaps: 2

US-09-719-601-5 (1-444) x BX417399 (1-1201)
QY 1 MetGlyLysGlyGlyAsnGlnGlyGluAlaGluArgGluValProThr 20
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BQ883702 926 bp mRNA linear EST 16-AUG-2002
AGENCOURT_8152253 Lupsaki_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6179733 5', mRNA sequence.
BQ883702
BQ883702.1 GI:22275710

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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 926)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13561 row: f column: 22
            High quality sequence stop: 586.

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    /clone="IMAGE:6179733"
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    /dev_stage="adult, 36 yr"
    /lab_host="DH10B"
    /clone_lib="Lupski dorsal root ganglion"
    /note="Vector: PCMV-SPORT6 (Life Technologies); Site 1:
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    Directionally cloned using the following adaptors:
    5'-TCGACCCAGCGCTCCG-3' and
    5'-GACTAGTTTACATCGCGAGCGCCCT(15)-3'. Size selected >
    1 kb for average insert length 1.7 kb. This is a primary
    library, non-amplified. Library constructed by Life
    Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
    College of Medicine) and is available through Life
    Technologies."

BASE COUNT  208 a 298 c 203 g 216 t 1 others
ORIGIN
Alignment Scores:
Pred. No.:    2,88e-148      Length:      926
Score:        1555.50        Matches:    287
Percent Similarity: 96.67%    Conservative: 3
Best Local Similarity: 95.67%    Mismatches: 7
Query Match:  53.80%         Indels:     3
DS:           13            Gaps:        1

US-09-719-601-5 (1-444) x BQ883702 (1-926)

QY 105 LysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsn 124
Db 2  AAGAACTCAAGATCACTAGGAGCTTCGGGCCCTGAGGAGAGCGCTGAGGACATGAAC 61
QY 125 LeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGlu 144
Db 62 CTGCTCAAGACCAACACCGTGTCTTCCTCCCTCCTCGGCCACATCATCGCCCTGGAG 121
QY 145 SerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTyrIleProThrLeuIleThr 164
Db 122 AGCATTTGCATGGTTCATCTGCTTTTACTTTGGCAATGGCTGGATTCCTACCTCATCAG 181
QY 165 AlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHisAspTyrGlyHis 184
Db 182 GCCTTTGCTCTGTCTACCTCTCAGGCCCAAGCTGGATGGTGAACATGATTATGGCCAC 241
QY 185 LeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPheValIleGlyHis 204
Db 242 CTGTCTGTCTACAGAAACCAACCAAGTGGACCACTTGTCCACAAATTCGATGGCCAC 301

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205 LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisIleAlaLysPro 224
Db 302 TTAAGAGGTGCTCTGCCAACTGGTGGATCATGCCACTTCCAGCACGACGCAAGCT 361
QY 225 AsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrp 244
Db 362 AACATCTTCCACAAGGATCCCGATGTGAACATGTGCACGTGTGTGTGTGGCGGAATGG 421
QY 245 GlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 264
Db 422 CAGCCCATCATGACGCGCAAGAGCTGAATACCTGCCCTACCAATACACGACCGAA 481
QY 265 TyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIle 284
Db 482 TACTTCTTCTGATTGGGCCCGCGCTGCTCATCCCATGTAATTCAGTACCATCATC 541
QY 285 MetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIle 304
Db 542 ATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGCGCTGAGCTACTACATC 601
QY 305 ArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsn 324
Db 602 CGGTTCTTTCATCACTACATCCCTTCTACGGCATCTTGGGAGCCCTCTTTTCCCTCAC 661
QY 325 PheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleVal 344
Db 662 TTCATCAGGTTCTCGAGAGCCACTGGTTGTGTGGGTCCACAGATGAATCACATCGTC 721
QY 345 MetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCys 364
Db 722 ATGAGATTTGACGAGGCGCTACCGTGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 781
QY 365 AsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGln 384
Db 782 AACGTGGAGCAGCTCTTCTTCCAGCACTGGTTCAGTGGACCCCTTAACCTCCAGATTGA 841
QY 384 uHisHisLeuPhe-ProThrMet---ProArgHisAsnLeuHisLysIleAlaPro 401
Db 842 GGCACACCTTCTTCCCAACCATGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 897

RESULT 6
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LOCUS
DEFINITION AGENCOURT 10412170 NIH MGC.109 Homo sapiens cDNA clone
IMAGE:657575 5', mRNA sequence.
ACCESSION BU845046
VERSION BU845046.1 GI:24029487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ruben Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: Agencourt Bioscience Corporation
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LICM2780 row: i column: 07
            High quality sequence stop: 599.
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            1..924
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
FEATURES
source

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/clone="IMAGE:6578575"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
/notes="Organ: ovary; Vector: pOTB7; Site: 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT      213 a      286 c      202 g      221 t      2 others
ORIGIN

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## Alignment Scores:

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Pred. No.:      4,6e-148      Length:      924
Score:          1553.50      Matches:    290
Percent Similarity: 95.44%      Conservative: 3
Best Local Similarity: 94.46%      Mismatches: 9
Query Match:      63.72%      Indels:      6
DB:              13          Gaps:        2

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US-09-719-601-5 (1-444) x BU845046 (1-924)

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QY 118 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137
Db 2 AAGACGGGTGAGGACATGAACCTGTTCAGACCAACCAACGCTGTTCTCTCTCTCTCTG 61
QY 138 AlaHisIleLeuAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGly 157
Db 62 GCCACATCATCGCCCTGAGAGCAATGATGCTGTTCACTGCTTTTATCTTTGGCAATGCG 121
QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp 177
Db 122 TGGATTCTTACCTCATCAGCGCTTTGTCTTGTCTTCTCTCTCTCTCTCTCTCTCTG 181
QY 178 LeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTyrPheAsnHisLeuVal 197
Db 182 CTGCACATGATATGCGCACCTGTCTGTCTACAGAAACCAACGATGGAACCACTTGTCTC 241
QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTyrPheAsnHisArgHis 217
Db 242 CACAAATTCGTATTGGCCACTTAAGGGTGCCTCTGCCAATCGTGGATCATCGCCAC 301
QY 218 PheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237
Db 302 TTCCAGCACACGCCCAAGCCTAACATCTTCCACAGGATCCCGATGTGAACATGTGTGCAC 361
QY 238 ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeu 257
Db 362 GTGTTTGTCTGGCGAATGGCAGCCCATCGATGATGCGGACAGAGAGCTGATATACCTG 421
QY 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMet 277
Db 422 CCTACATCACCAGCACCAATACTTCTTCTGATTGGCCCGCTGCTCATCCCATG 481
QY 278 TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297
Db 482 TATTCCAGTACAGATCATCATGATCATGATGCTGATGATGATGATGATGATGATGATGATG 541
QY 298 TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLeu 317
Db 542 TGGCGCGTCAGCTACTACATCCGTTCTTCTCATCATCATCATCATCATCATCATCATCATCTG 601
QY 318 GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal 337
Db 602 NGAGCCCTCTTCTCTCACTCATCTCAGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 661
QY 338 ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSer 357
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QY 358 SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGly 377
Db 722 AGCCAGCTACAGCCACCTGCAACGTTGGAGCAGTCTCTTCTTCAACGATGGTTCAGTGA 781
QY 378 HisLeuAspPheGlnIleGluHisLeuPheProThrMet-ProArgHisAsn-LeuH 397
Db 782 CACCTTAACTTCTAG-ATTGAGCACCACCTCTTCTCCCAACATGCCCCCGGCACAACTTAC 840
QY 397 isLysIleAlaProLeuValLys---SerLeuCysAlaLysHis-----GlyIleGlu 414
Db 841 ACGAATCGCCCGCTGGTGAAGTCTTATGTGCCAAGCATGGCATGGCAATTACCA 900
QY 414 yrGlnGluLysProLeu 419
Db 901 GGGAAGAAAGCCGCTT 917

RESULT 7
AK080414
LOCUS
DEFINITION
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730007D17 product:fatty acid desaturase 3,
full insert sequence.
ACCESSION
AK080414
VERSION
AK080414.1 GI:26348536
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamamoto, R.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,

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Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.  
and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)

21085660  
MEDLINE  
PUBMED

# REFERENCE

The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

6 (bases 1 to 1689)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tegawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

# FEATURES

## Source

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GPWVSIIAALILAIISOACWCLQDLGHASIFTSRWNHVAQQVGMQLKGFSAHW
WNEFHQHAQNIETFDPTVAVPFLGLGESVSEYKRRVLPVNHQVLFYFLGIP
PLLTLVNFVENIAYMLVCMQWTELLWAASFYRPLSLVSPFYGANGTLLVAVRVL
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## BASE COUNT

## ORIGIN

Alignment Scores:

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Score: 1551.50 Matches: 277
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Best Local Similarity: 61.56% Mismatches: 105
Query Match: 63.64% Indels: 7
DB: 11 Gaps: 2

US-09-719-601-5 (1-444) x AK080414 (1-1689)

Qy 1 MetClyGlySclyGlyAsnGlnGlyGlyAlaAlaGluArgGlu----- 15
Db 37 ATGGGCGGTCTCGGGAGAGCCGGAGGGGACCCGGCCGGGAGGGGCGGACCGCTG 96
Qy 16 ---VaiserValProThrPheSerTrpGluGluLeuLeuHisAsnLeuArgThrAsp 34
Db 97 GGGGGCGCCCTACCCATCTTCCTCGTGAGAGCAGATCCGCAGCATGACCTACGAGCGAC 156
Qy 35 SerClyLeuValIleAspArgLysValTyraAsnIleThrLysTrpSerIleGlnHisPro 54
Db 157 AAGTGGTGTGTATCATGAGCGCCGTGTCTAGCATCAGCCGTGGCAGCGGACCCCA 216
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Db 217 GGGGTAGCCGCTCATCGGCCACACCGGTGCGAGAGCGCCACGATGCTTCCACGCC 276
Qy 75 PheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuLeuGlyGluLeu 94
Db 277 TTCACCAAGATCTCCATTTTGGCAAGTTCCTGAAACCCCTGTGTATGGAGAGCTA 336
Qy 95 AlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArg 114
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Qy 175 AlaGlyTrpLeuGlnHisAspTyraGlyHisLeuSerValTyraGlyLysProLysTrpAsn 194
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 QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyArgAsp 354  
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RESULT 8  
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 LOCUS AGENCOURT 8294640 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
 DEFINITION IMAGE:6194559 5', mRNA sequence.

ACCESSION BQ717429  
 VERSION BQ717429.1 GI:21856326  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 914)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished

Contact: Robert Strausberg, Ph.D.  
 Email: cgsbbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LUM13599 row: p column: 16  
 High quality sequence stop: 663.

## FEATURES

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 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."

BASE COUNT 208 a 283 c 224 g 199 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1,65e-147 Length: 914  
 Score: 1548.00 Matches: 292  
 Percent Similarity: 96.72% Conservatives: 3  
 Best Local Similarity: 95.74% Mismatches: 6  
 Query Match: 63.49% Indels: 4  
 DB: 13 Gaps: 0

US-09-719-601-5 (1-444) x BQ717429 (1-914)

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RESULT 9
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ACCESSION AK029318
VERSION   1
KEYWORDS  3129 bp mRNA linear HTC 05-DEC-2002
SOURCE   Mus musculus
ORGANISM Mus musculus (house mouse)
REFERENCE 1
  AUTHORS Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE 99279253
  PUBMED  10349636
REFERENCE 2
  AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE 20499374
  PUBMED  11042159
REFERENCE 3
  AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
  JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE 20530913
  PUBMED  11076861
REFERENCE 4
  AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kusakawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustinich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seva,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wyshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S. and Hayashizaki,Y.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL Nature 409 (6821), 685-690 (2001)
  MEDLINE 21085660
  PUBMED  11217851
REFERENCE 5
  AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

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TITLE
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3129)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akashira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
DIRECT SUBMISSION
SUBMITTED (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
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ACCESSION AK090042
VERSION AK090042.1 GI:26105704
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ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3697)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitho, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
 Location/Qualifiers

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 ORIGIN

Alignment Scores:  
 Pred. No.: 5, 07e-140 Length: 3697  
 Score: 1482.50 Matches: 275  
 Percent Similarity: 74.45% Conservative: 63  
 Best Local Similarity: 60.57% Mismatches: 105  
 Query Match: 60.81% Indels: 11  
 DB: 11 Gaps: 2

US-09-719-601-5 (1-444) x AK090042 (1-3697)

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 Db 164 ATGGCGCGTCTCGGGAGCGCGGAGCGGACCGCGGCGGGAGGGCGCGCGCGTGTG 223  
 Qy 16 --ValSerValProThrPheSerTrpGluGluLeuLeuGlnLysHisAsnLeuArgThrAsp 34  
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 Qy 35 SerGlyLeuValIleAspArgLysValThrAsnIleThrLysTrpSerIleGlnHisPro 54  
 Db 284 AAGTGGCTGGTCTATCGAGCGCGGTGTCTACGACATCAGCGCTGGGCGAGCGGCCA 343

Qy 55 GlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAla 74  
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 Qy 114 GAlaLeu-ArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheL 134  
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 Qy 273 uLeuIleProMetTyr-PheGlnTyrGlnIleIleMetMetIleValHisLysAsnTr 293  
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 Qy 293 pValAspLeuAlaTrpAlaValSerTyrTrpIleA-gPhePheIleThrTyrIleProPh 313  
 Db 1061 GACGACTTGTGTGGCTGCCAGTTTCTACTCCCGCTTTTCTGCTCTACTCTCCCTT 1120  
 Qy 313 eTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTr 333  
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 Qy 333 pPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrAr 353  
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| QY                     | 433   | rGlyYsLeuYspTrpLeuAspAlaTyLeuHisLys                         | 444  |
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| LOCUS                  | AK083959  |   |      |
| DEFINITION             | Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI30069P05 product:DELTA-5 DESATURASE, full insert sequence.  |   |      |
| ACCESSION              | AK083959  |   |      |
| VERSION                | AK083959.1  | GI:26350884   |      |
| KEYWORDS               | HTC, CAP trapper.   |   |      |
| SOURCE                 | Mus musculus (house mouse)  |   |      |
| ORGANISM               | Mus musculus  |   |      |
| REFERENCE              | 1   |   |      |
| AUTHORS                | Carninci, P. and Hayashizaki, Y.  |   |      |
| TITLE                  | High-efficiency full-length cDNA cloning  |   |      |
| JOURNAL                | 99279253  |   |      |
| MEDLINE                | 10349636  |   |      |
| PUBLISHED              | 1999  |   |      |
| REFERENCE              | 2   |   |      |
| AUTHORS                | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  |   |      |
| TITLE                  | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  |   |      |
| JOURNAL                | Genome Res. 10 (10), 1617-1630 (2000)   |   |      |
| MEDLINE                | 20499374  |   |      |
| PUBLISHED              | 11042159  |   |      |
| REFERENCE              | 3   |   |      |
| AUTHORS                | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  |   |      |
| TITLE                  | RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer   |   |      |
| JOURNAL                | Genome Res. 10 (11), 1757-1771 (2000)   |   |      |
| MEDLINE                | 20530913  |   |      |
| PUBLISHED              | 11076861  |   |      |
| REFERENCE              | 4   |   |      |
| AUTHORS                | Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saio, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Frieschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stauble, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bjunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashina, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Togo, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y. |   |      |
| TITLE                  | Functional annotation of a full-length mouse cDNA collection  |   |      |
| JOURNAL                | Nature 409 (6921), 685-690 (2001)   |   |      |
| MEDLINE                | 21085660  |   |      |
| PUBLISHED              | 11217851  |   |      |
| REFERENCE              | 5   |   |      |
| AUTHORS                | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  |   |      |
| TITLE                  | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  |   |      |
| JOURNAL                | Nature 420, 563-573 (2002)  |   |      |
| REFERENCE              | 6 (bases 1 to 3318)   |   |      |
| AUTHORS                | Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, I., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nomura, K., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.   |   |      |
| TITLE                  | Direct Submission   |   |      |
| JOURNAL                | Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045 Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp, tel: 81-45-503-3222, fax: 81-45-503-9216)  |   |      |
| COMMENT                | cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/   |   |      |
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| polyA_site             |   |   |      |
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| Pred. No.:             | 6.58e-139   | Length:   | 3318 |
| Score:                 | 1471.00   | Matches:  | 263  |
| Percent Similarity:    | 76.11%  | Conservative:   | 62   |
| Best Local Similarity: | 61.59%  | Mismatches:   | 98   |



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| Query Match:                                | 60.34% | Indels:  | 4    |
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| Db  | 90     | TTTACTTGGAGAGGTGGCGAGCGCTCCGGGGGGAAGAGCGATGGCTGGTATC         | 149  |
| Qy  | 40     | AspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgVal | 59   |
| Db  | 150    | GACCGGAAGGTGTACAACTACGAGACTTCAGCGCGCCACCCCGGGGGCTCCCGGTC     | 209  |
| Qy  | 60     | IleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeu | 79   |
| Db  | 210    | ATCAGCCACTACGGGGTTCAGATGCCAGGATCTCTTTGTGGCATTCACATCAACAAG    | 269  |
| Qy  | 80     | GluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluPro | 99   |
| Db  | 270    | GGTCTTTGGAGAAAGTATATGAACCTCTCTTGATTTGGAGAGCTGGCTCCGGAGCAACC  | 329  |
| Qy  | 100    | SerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThr | 119  |
| Db  | 330    | AGCTTTGAACCCCAAGAAATAAGCGCTAACTGATGAATTCGGGAGCTGGCGGCCACA    | 389  |
| Qy  | 120    | AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis    | 139  |
| Db  | 390    | GTAGAGCAATGGCGCTCATGAAGGCCAACCACTCTCTCTGGTCTACCTGGCTTCCAC    | 449  |
| Qy  | 140    | IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrpIle | 159  |
| Db  | 450    | ATCCTGTGTGTGGTGTGGCTGGCTCACCTTTGGATCTTTGGAACTTCCTTGGTG       | 509  |
| Qy  | 160    | ProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGluAlaGlyTrpLeuGln | 179  |
| Db  | 510    | CCCTTATCTCTGTGAGTACTGTCTAGTACAGTTCAGCTCAGCGACGTTGGCTACAG     | 569  |
| Qy  | 180    | HisAspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsnHisLeuValHisLys | 199  |
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| Qy  | 200    | PheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGln | 219  |
| Db  | 630    | TTTGTGATTGGCACCTGAAGGGGGCCCCCGCAGCTGTGGACCAACATGATTTCCAG     | 689  |
| Qy  | 220    | HisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis       | 237  |
| Db  | 690    | CACCATGCCAAGCTTAACCTGCTCCGCAAGGACCCCGATATCAACATG---CACCCCTC  | 746  |
| Qy  | 238    | ValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLysLysLysLysLysLys | 257  |
| Db  | 747    | TTCTTCGCCCTGGGAAGGTCCTTCTGTGGAGCTCGGGAGGAAAGAAAGAACGACATG    | 806  |
| Qy  | 258    | ProTrpAsnHisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeuLeuProMet | 277  |
| Db  | 807    | CCATACCAACCATCAGCACAGTACTTCTCTCATCGGACCCCGCCCTGTGCTGCTCA     | 866  |
| Qy  | 278    | TyrPheGlnTrpGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla | 297  |
| Db  | 867    | TACTTCCAGTGATATATTTCTATTTTGTGGTTTCAGCGGAAATAATGGGTGGACTTGGC  | 926  |
| Qy  | 298    | TrpAlaValSerTrpTrpIleArgPhePheIleThrTrpIleProPheTrpGlyIleLeu | 317  |
| Db  | 927    | TGGTGTCTAGCTTCTATGTCGGCATCTTTCTTCTATCATGCGGTGGTGGGCTGAA      | 986  |
| Qy  | 318    | GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal | 337  |
| Db  | 987    | GGCTTCTGGGCTTTTCTTCTTCTTCTGAGTCTTCTGGAAGCAACTGGTTGTGGTGG     | 1046 |
| Qy  | 338    | ThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTrpArgAspTrpPheSer | 357  |
| Db  | 1047   | ACACAGATGAACCATATCCCATGACATGATCATCAGCCGGAATGTGACTGGTCTCTC    | 1106 |

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|--|------|--|------|
| Qy   | 358  | SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGly | 377  |
| Db   | 1107 | ACCCAGCTGCAGGCAACCTGCAACGTTCCACCAATGACCTTCAACCAACTGGTTCAGTGC | 1166 |
| Qy   | 378  | HisLeuAsnPheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHis    | 397  |
| Db   | 1167 | CACCTAAATTTCCAGATTGAACACCACTCTTCCCCACCATGCGCGGCACCACTACAC    | 1226 |
| Qy   | 398  | LysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrpGlnGluLys | 417  |
| Db   | 1227 | AAAGTGGACCCCTAGTACAACTCCCTGTGCGCAAGTACGGCATCAAGTATGATGTCAG   | 1286 |
| Qy   | 418  | ProLeuLeuArgAlaLeuLeuAspIleArgSerLeuLysLysSerGlyLysLeuTrp    | 437  |
| Db   | 1287 | CCCTGTCTCAGCCITCGGGACATTTTACTCTCCTGAAGGAGTCAGGCAACTCTGG      | 1346 |
| Qy   | 438  | LeuAspAlaTrpLeuHisLys  | 444  |
| Db   | 1347 | TTGAGCGCTTACCTTACCACAA                                       | 1367 |
| RESULT 12  |      |  |      |
| AK076485   |      |  |      |
| LOCUS  |      |  |      |
| DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:483423E24 product:unclassified, full insert sequence.   |      |  |      |
| ACCESSION AK076485.1 GI:26096835   |      |  |      |
| VERSION  |      |  |      |
| KEYWORDS HTC; CAP trapper.   |      |  |      |
| SOURCE Mus musculus (house mouse)  |      |  |      |
| ORGANISM Mus musculus  |      |  |      |
| REFERENCE  |      |  |      |
| 1 Carninci, P. and Hayashizaki, Y.   |      |  |      |
| High-efficiency full-length cDNA cloning   |      |  |      |
| Meth. Enzymol. 303, 19-44 (1999)   |      |  |      |
| JOURNAL 98279253   |      |  |      |
| MEDLINE  |      |  |      |
| PUBMED 10349636  |      |  |      |
| REFERENCE  |      |  |      |
| 2  |      |  |      |
| Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.   |      |  |      |
| Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes   |      |  |      |
| Genome Res. 10 (10), 1617-1630 (2000)  |      |  |      |
| JOURNAL  |      |  |      |
| MEDLINE  |      |  |      |
| PUBMED 20499374  |      |  |      |
| REFERENCE  |      |  |      |
| 3  |      |  |      |
| Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Masumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Tanaka, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  |      |  |      |
| RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer  |      |  |      |
| Genome Res. 10 (11), 1757-1771 (2000)  |      |  |      |
| JOURNAL  |      |  |      |
| MEDLINE  |      |  |      |
| PUBMED 20530913  |      |  |      |
| REFERENCE  |      |  |      |
| 4  |      |  |      |
| Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Suzuki, R., Quackenbush, J., Schriml, L.M., Stauber, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldairelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., |      |  |      |

Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,  
 Marchionni, L., Mashima, J., Mazzatelli, J., Mombaerts, P., Nordone, P.,  
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H.,  
 Sato, K., Schenbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H.,  
 Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L.,  
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontecki, S.,  
 and Hayashizaki, Y.

**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409 (6821), 685-690 (2001)  
**MEDLINE** 21085660  
**PUBMED** 11217851

# **REFERENCE** **AUTHORS**

The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.

**TITLE** Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs

**JOURNAL** Nature 420, 563-573 (2002)  
**REFERENCE** 6 (bases 1 to 2272)

**AUTHORS** Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp).  
 URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216

**COMMENT** cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>

# **FEATURES** **source**

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**BASE COUNT** 686 a 457 c 513 g 616 t

# **ORIGIN**

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**Best Local Similarity:** 59.00% **Mismatches:** 99  
**Query Match:** 60.32% **Indels:** 2  
**DS:** 11 **Gaps:** 0

US-09-719-601-5 (1-444) x AK076485 (1-2272)

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 Db 578 TATGCTGGCAAGATGCAACCGATGTTTCAGGGCCATGCACTGGATGGCGATGGTG 637  
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 Qy 143 LeuGluSerIleAlaThrPheThrValPheThrPheGlyAsnGlyTyrIleProThrLeu 162  
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 Qy 163 IleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyr 182  
 Db 878 CTTATTTCTTCTCTCTACAGTGCTCTCAGGCTCAATGTTCAATTTTACACATGACTTA 937  
 Qy 183 GlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIle 202  
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Db      1597 GTGAGTCACTTTTGCCAGCATGGATTGCGAGTATATAAATAGCCCATATTGAAGGCC 1656
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LOCUS   BG742318
DEFINITION 6026311469F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:477689 5',
mRNA sequence.
ACCESSION BG742318
VERSION   1
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0629 row: j column: 18
High quality sequence stop: 811.
Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 191 a 255 c 180 g 194 t
ORIGIN

Alignment Scores:
Pred No.: 1.86e-137 Length: 820
Score: 1449.00 Matches: 265
Percent Similarity: 98.53% Conservative: 3
Best Local Similarity: 97.43% Mismatches: 3
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US-09-719-601-5 (1-444) x BG742318 (1-820)

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mRNA sequence.
ACCESSION BG740873
VERSION   1
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov  
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/clone\_lib="NCI CGAP\_Skn3"

Note="Organ: Skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 187 a 246 c 175 g 198 t

## ORIGIN

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 Best Local Similarity: 96.65% Mismatches: 8  
 Query Match: 57.92% Indels: 3  
 DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG740873 (1-806)

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 QY 207 GlyAlaSerAlaAsnTrrPheAsnHisArgHisPheGlnHisHisAlaLysProAsnIle 226  
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 Db 360 TTCTTGATTTGGGCGCGCGCTGTCTATCCCATGATTTCCAGTACCAATCATCATGACC 419  
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 Db 420 ATGATCGTCCATAAAGAACTGGGTGACCTGCGCTGGCGCTGACGCTACATCCGCTTC 479  
 QY 307 PheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIle 326  
 Db 480 TTCAATCACTATCCCTTTTCACGGCATCTCGGGAGCGCTCTTTTCTCAACTTCATC 539  
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 QY 407 CysAlaLysHisGlyIleGlyTyrGln 415  
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## RESULT 15

BG674926

LOCUS

DEFINITION

602621092F1 NCI CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4746670 5',

mRNA sequence.

ACCESSION

BG674926

VERSION

BG674926.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 909)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/

TITLE

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaabs@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10595 row: g column: 23

High quality sequence stop: 750.

FEATURES

Location/Qualifiers

1..909

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/mol\_type="mRNA"

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/clone="IMAGE:4746670"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP\_Skn3"

/note="Organ: Skin; Vector: pCMV-SPORT6; Site: 1: NotI;

Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 207 a 279 c 217 g 206 t

ORIGIN

Alignment Scores:

Pred. No.: 4,38e-132 Length: 909

Score: 1397.00 Matches: 288

Percent Similarity: 96.77% Conservative: 2

Best Local Similarity: 96.06% Mismatches: 7

Query Match: 57.30% Indels: 6

DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG674926 (1-909)

QY 158 TrrPheProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrr 177

Db 2 TGGATTCT-ACCTCATCAGCG-TTTGTCTTGTAACTTCAGGCCCAAGCTGGATGG 59

QY 178 -LeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrrAsnHisLeuVa 197

Db 60 GCTGCACATGATTATGGCCACCTGTCTGTCTACAGAAACCCAGTGAACACCTTGT 119

QY 197 lHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrrPheAsnHisArgHi 217

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Db 120 CCACAAATTCGTCATGGCCACTTAAAGGGTCCCTCTCCCACTGGTGGATCATCGCCA 179
Qy 217 sPheGlnHisHisAlaLysProAsnHisLysPheHisLysAspProAspValAsnMetLeuHi 237
Db 180 CTTTCAGCACCAACGCGCAAGCTTAAACATCTTCCACAAGGATCCGATGTGAACATGCTGCA 239
Qy 237 sValPheValLeuGlyGluTrpGlnProlleGluTrpGlyLysLysLysLeuLysTyrLe 257
Db 240 CCGTGTGTTGTTCTGGCGAATGCGCCCATCGAGTACGCGCAAGAGAGCTGAATACCT 299
Qy 257 uProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMe 277
Db 300 GCGCTACATACACACGACGATATCTTCTCTGATGGCGCGCTGCTCATCCCCAT 359
Qy 277 tTyrPheGlnTyrGlnHisLysMetThrMetileValHisLysAsnTrpValAspLeuAl 297
Db 360 GATATTCAGTACCAGATCATATGACCATGATGTCCTAAGAACTGGTGGACCTGGC 419
Qy 297 aTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLe 317
Db 420 CTGGGCGGTGAGTACTACATCGGTCTTCTCATCATCATCATCATCATCATCATCATCAT 479
Qy 317 uGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVa 337
Db 480 GGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 538
Qy 337 lThrGlnMetAsnHisLysValMetGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 357
Db 539 CACACAGATGAATCATCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 598
Qy 357 eSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerG 377
Db 599 GTAGCAGCTGACGACCACTGCACTGAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 658
Qy 377 lHisLeuAsnPheGlnIleGluHisLysLeuPheProThrMetProArgHisAsnLeuH 397
Db 659 GACACCTTAACTTCCAGATTGACACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
Qy 397 isLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluL 417
Db 718 ACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCATGTCATGTCATGTCATGTCATGTC 777
Qy 417 ysProLeuLeuArgAlaLeuLeuAspIleArgSerLeuLysLysSerGly 434
Db 778 GCGCGCTACTGAGGCGCTGTCGACATCATCGTCTGTCGTCGTCGTCGTCGTCGTCGTCG 830

RESULT 16
BG742694
LOCUS 602632908F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4778329 5',
DEFINITION mRNA sequence.
ACCESSION BG742694
VERSION BG742694.1 GI:14053347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10633 Row: 0 Column: 02
High quality sequence stop: 798.
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FEATURES
source
Location/Qualifiers
1..805
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778329"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 194 a 245 c 191 g 175 t
ORIGIN
Alignment Scores:
Pred. No.: 2,58e-130 Length: 805
Score: 1379.00 Matches: 254
Percent Similarity: 98.84% Conservative: 1
Best Local Similarity: 98.45% Mismatches: 1
Query Match: 56.56% Indels: 1
DB: 10 Gaps: 0
US-09-719-601-5 (1-444) x BG742694 (1-805)
Qy 189 ArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLys-GlVal 208
Db 1 AGAAACCCCAAGTGGAGAACCACTTGTCCCAAAATTCGTATTGGCCACTTAAGAGGTGC 60
Qy 208 aSerAlaAsnTrpTrpAsnHis-ArgHisPheGlnHisAlaLysProAsnIlePheH 228
Db 61 CTCTGCCAACTGTGTGAATCATCGCCACTTCCAGCACCAAGCCCAAGCTTAACATCTTCC 120
Qy 228 isLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleG 248
Db 121 ACAAGGATCCCGATGTGAACATGCTGCACGTGTGTCTCTGGCGCAATGACACCCATCG 180
Qy 248 luTyrGlyLysLysLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 268
Db 181 AGTACGCGCAAGAGAGCTGAATACCTGCGCTTACAATCACCAGCAGCAATATCTTCTCC 240
Qy 268 eulleGlyProProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 288
Db 241 TGATTGGCGCGCGCTGCTCATCCCATGATTTTCCAGTACCAGATCATCATGACCATGA 300
Qy 288 leValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheI 308
Db 301 TCGTCCATAGAACTGGGTGACCTGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 308 leThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuLeuLeuLeuLeuLeuLeuLeu 328
Db 361 TCACCTACATCCCTTCTACGGCATCTCTGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Qy 328 heLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleA 348
Db 421 TCCCTGGAGAGCCACTGGTTGTGGGTGCACACAGATGATCATGCTCATGAGATTG 480
Qy 348 spGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluG 368
Db 481 ACCAGAGGCGCTACCGTGACTGTGTAGTACCCAGCTGACAGCCACCTGCAAGCTGGAGC 540
Qy 368 lnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuP 388
Db 541 AGTCTCTCTTCAACAGCTGGTTGAGTGGACACCTTAATCTTCCAGATTGAGCACCATCTCT 600
Qy 388 heProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysA 408
Db 601 TCCCACCATCCCGG-CACAACTTACCAAGATCGCCCGCTGGTGGTGAAGTCTCTATGTG 659
Qy 408 laLysHisGlyIleGluTyrGlnGlySerProLeuLeuArgAlaLeuLeuAspIleIleA 428
Db 660 CCAAGCATGGCATTGAATACCGAGAGAGCGCTCTCTGAGGGCCCTCTCTGGACATCATCA 719
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QY 428 tgsrLeuLysSerGlyLysLeuTrpLeuAspAlaTrpLeuHisLys 444  
 Db |||||  
 720 GTCCTCTGAAGAGTCTGGAGCTGTGCTGGACGCTACCTTCAAAA 769

RESULT 17  
 AL522956 910 bp mRNA linear EST 22-MAY-2003  
 LOCUS 4522956 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens  
 DEFINITION cDNA clone CS0DB009F18 5-PRIME, mRNA sequence.  
 ACCESSION AL522956  
 VERSION AL522956.2 GI:31041219  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 910)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12786449.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6148.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DB009DC09QP1&cluster=6148.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL : Corporation 1600  
 http://fulllength.invitrogen.com/ invitroGen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DB009DC09QP1.  
 Location/Qualifiers  
 1..910  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="CS0DB009F18"  
 /tissue\_type="NEUROBLASTOMA COT 10-NORMALIZED"  
 /clone\_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo (dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and Bclor V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 BASE COUNT 212 a 263 c 258 g 175 t 2 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 3,03e-130 Length: 910  
 Score: 1379.00 Matches: 252  
 Percent Similarity: 99.21% Conservative: 0  
 Best Local Similarity: 99.21% Mismatches: 2  
 Query Match: 56.56% Indels: 0  
 DB: 9 Gaps: 0

US-09-719-601-5 (1-444) x AL522956 (1-910)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluAlaGluArgGluValSerValProThr 20  
 Db |||||  
 147 ATGGGGAAGGAGGGAACACAGGCGGAGGGGGCGGCGGAGGTGTGGTGGCCACC 206

QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
 Db |||||  
 207 TTCAGCTGGAGGAGATTCAAAGCATACCTCGCCACGACGAGTGTGTCTATTGAC 266

QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlnArgValIle 60  
 Db |||||  
 267 CGCAGGTTTACAACATCAACAAATGGTCCATCCAGACCCCGGGGGCGAGCGGTGATC 326

QY 61 GlyHisTyrAlaGlyLysAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
 Db |||||  
 327 GGGCACTAGCTGGAGAGATGCAACGGATGCTTCCGCGCCTTCCACCTGACCTGGAA 386

QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100  
 Db |||||  
 387 TTCGTGGGCAAGTCTTTGAACCCCTGCTGATTTGTTGAAGTGGCCCGGAGAGGCCACC 446

QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
 Db |||||  
 447 CAGGACACGGCAAGAACTCAAAGATCACTAGGAGCTTCCGGGGCCCTGAGGAGAGCGGT 506

QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
 Db |||||  
 507 GAGGACATGAACCTGTTCAARACCAACACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 566

QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
 Db |||||  
 567 ATCGCCTCGAGAGCATTCATGGTTTCACTGCTCTTTTACTTTGGCAATGGCTGGATTCT 626

QY 161 ThrIleuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpIleuGlnHis 180  
 Db |||||  
 627 ACCCTCATCAGGCTTTTCTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 686

QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
 Db |||||  
 687 GATTATGGCCACCTGCTCTCTACAGAAACCAAGTGGACCACTTGTCCACAAATTC 746

QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
 Db |||||  
 747 GTCATTTGGCCACTTAAAGGCTGCTCTGCTCAATCGTGGAAATCATCGCCACTTCCAGCAC 806

QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240  
 Db |||||  
 807 CAGCCCAAGCTTACATCTTCCACAGGATCCGATGTGACATGCTGCGCTGTTGTT 866

QY 241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLeu 254  
 Db |||||  
 867 CTGGGCGAATGGCAGCCCATCGAGTACGGCAAGAGAGCTG 908

RESULT 18  
 BG742408 802 bp mRNA linear EST 15-MAY-2001  
 LOCUS 602635311F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4780395 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG742408  
 VERSION BG742408.1 GI:14053061  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 802)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (LINL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.lnl.gov  
 Plate: L1AM10639 row: e column: 04  
 High quality sequence stop: 802.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4780395"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Skn3"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

FEATURES  
 source

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT  
ORIGIN

180 a 252 c 192 g 178 t

#### Alignment Scores:

Pred. No.: 1,33e-129 Length: 802  
Score: 1372.00 Matches: 264  
Percent Similarity: 97.78% Conservative: 0  
Best Local Similarity: 97.78% Mismatches: 3  
Query Match: 56.28% Indels: 5  
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG742408 (1-802)

QY 54 ProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArg 73  
Db 1 CGGGGGGGCAGGGGTCTCGGGCACTACGCTGGAGAAGATGCAACGGATCCCTTCGCG 60  
QY 74 AlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGlu 93  
Db 61 GCCTCCACCTGACCTGGAATTCGTGGCAAGTCTTGAACCCCTGCTGATTGGTGA 120  
QY 94 LeuAlaProGluCluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPhe 113  
Db 121 CTGGCCCGGAGAGCCCGCAGGACCCAGCAAGACTCAAGATCACTGAGGACTTC 180  
QY 114 ArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePhe 133  
Db 181 CGGGCCCTGAGGAAGACGGCTGAGGACATGAACCTGTTCAGACCAACCGTGTCTTC 240  
QY 134 LeuLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTy 153  
Db 241 CTCCTCTCTCGGCCACATCATCGCCCTGGAGAGATTGCATGTTCACTGCTCTTTTA 300  
QY 153 rPhe-GlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnA 173  
Db 301 CTTTGGCAAGGTGTGGATTCTACCTCATACGCGCTTTGCTTGTACTCTCAGG 360  
QY 173 laGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysT 193  
Db 361 CCCAAGCTGATGGCTGCACATGATTATGGCCACCTGTCTGTACAGAAACCCAAAGT 420  
QY 193 rPAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyValAlaSerAlaAsnTrp 213  
Db 421 GGAACCACTTGTCCACAATTCGTATTGGCCACTTAAGGGTGCCCTTGCCAACTGCT 480  
QY 213 rPAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspV 233  
Db 481 GGAATCATCGCACTTCCAGCACCCAGCCCAAGCCTAACATCTCCACAGGATCCCGATG 540  
QY 233 aAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysL 253  
Db 541 TGAACATGCTGCACGTGTA-GTTCTGGCGAATGGCGCCCATCGAGTACGGCAGAAGA 599  
QY 253 ySLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProL 273  
Db 600 AGCTGAATACCTGCGCTTCAATCACCAGCAGCAATATCTTCTGATTGGCGCGC-C 658  
QY 273 euLeuIleProMetTyrPheGlnTyr-GlnIleIleMetThrMetIleValHisLysAsn 292  
Db 659 TGTCTATCCCACTGATATTTCAGTACCCAGATCATCATGACCATGCTCCATAGAAC 718  
QY 293 TrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIlePro 312  
Db 719 TGGGTGACCTGGCTGGCGCGTCACTACTACTACCTCCGTTCTTCATCATCACTACCTCCT 778  
QY 313 PheTyrGlyIleLeuGlyAlaLeu 320  
Db 779 TTCTACGGCATCTCTGGAGCCCTC 802

RESULT 19

EX341258

LOCUS

DEFINITION

EX341258 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED

ACCSSION

EX341258

VERSION

EX341258.1 GI:30343944

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Homo sapiens

REFERENCE

1 (bases 1 to 933)

AUTHORS

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6148.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

csi-bin/cluster.cgi?seq=CS0DJ014AB11QPI&cluster=6148.f. Contact :

Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/

Paradey Avenue Genoscope sequence ID : CS0DJ014AB11QPI.

Location/Qualifiers

1..933

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DJ014YC21"

/cell\_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/cell\_line="JURKAT"

/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT

10-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with NotI and cloned into the NotI and EcoRV

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 231 a 258 c 204 g 194 t 46 others

ORIGIN

#### Alignment Scores:

Pred. No.: 3.82e-126 Length: 933  
Score: 1339.00 Matches: 252  
Percent Similarity: 86.90% Conservative: 0  
Best Local Similarity: 86.90% Mismatches: 38  
Query Match: 54.92% Indels: 0  
DB: 13 Gaps: 0

US-09-719-601-5 (1-444) x BX341258 (1-933)

QY 155 GlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGln 174

Db 58 GGGATTGGCTGGATTCCTAMCCTCATCAGCGCTTTGTCTCTACCTCTTCAGGCCAA 117

QY 175 AlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsn 194

Db 118 CTTGGAAGGCTGGCAACAWGATTATGCCCACTGTCTGTCTAMAPAAAAMCCAAAGTGAAC 177

QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsn 214

Db 178 CAMCTTCTCCAAAAAAGCGTCATWTGGCCACTTAARGGTGCTCTGCCCACTGGTGAAG 237

QY 215 HisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234

Db 238 CACGCCCACTCCAGCACCCAMGCCACCTTAAMWCTTCCAMAAAGATCCCGATGTGAAM 297

QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeu 254

Db 298 AWGTGCACTGTGTTGTTCTGGCGAATGGCAGCCCATCGATAMGGCAAAAAAAGCTG 357



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QY 255 LysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGlyProProLeuLeu 274
Db 358 AAAAAMCTGGCCCTAAACACACARVACGAAWACTTCTTCGATGGCGCCGCTGCTC 417
QY 275 IleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTyrVal 294
Db 418 ATCCCATGATATTCCAGTACCAACAWCATCAWAGCAGCAWAGCGTCCATARAACATGGGTG 477
QY 295 AspLeuAlaTyrAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyr 314
Db 478 GACCTGGCCCTGGCGCGTCAAGTAMTAMATCCGGTCTTCACACCTAMAWCCCTTTCTAC 537
QY 315 GlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPhe 334
Db 538 GGCATCTCGGAGCGCCCTCTTCTCAACTCAATCAATCAAGTTCCTGGAGAGCACTGGTT 597
QY 335 ValTyrValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAsp 354
Db 598 GTGTGGGTCAACACAGATGAATCAATGCTCATGAGATTGACAGAGGCGCTACCGGTGAC 657
QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTyr 374
Db 658 TGGTTCACTAGCAGCTGACAGCCACCTGCAACGTGGAGCAGTCTCTTCTCAGCACTGG 717
QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisIlePheProThrMetProArgHis 394
Db 718 TTCAGTGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCGACCATGCCCGGCAC 777
QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyr 414
Db 778 AACITACAWARATCGCCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCATTAATAC 837
QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGly 434
Db 838 CAGGAGAGCGCGCTACTGAGGCGCCCTGCTGACATCAWAGGTCCCTGAAGAGTCTGGG 897
QY 435 LysLeuTyrLeuAspAlaTyrLeuHisLys 444
Db 898 AAGCTGTGGCTGGAGCGCTACTCTTCAAAA 927

RESULT 20
BX441083
LOCUS
DEFINITION
BX441083 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF014YM11 5-PRIME, mRNA sequence.
ACCESSION
BX441083
VERSION
BX441083.1 GI:30787936
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 952)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6148.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF014AG06QPI&cluster=6148.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF014AG06QPI.
Location/Qualifiers
1 .952
/morganism="Homo sapiens"
/mol_type="mRNA"
FEATURES
source

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/clone="CS0DF014YM11"
/tissue_type="FETAL BRAIN"
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/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 237 a 280 c 236 g 168 t 31 others
ORIGIN

```

```

Alignment Scores:
Pred. No.: 7,94e-126 Length: 952
Score: 1336.00 Matches: 248
Percent Similarity: 92.94% Conservatives: 2
Best Local Similarity: 92.19% Mismatches: 19
Query Match: 54.80% Indels: 1
DB: 13 Gaps: 0
US-09-719-601-5 (1-444) x BX441083 (1-952)
QY 1 MetGlyLysGlyClyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20
Db 147 ATGGGGAAAGGAGGAAACAGGGCGAAGGGCGCGAAGCGAAAGTGTGGTATCCACC 206
QY 21 PheSerTyrGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40
Db 207 TTCARCTGGAGGAGAAWTCAAAAGCATACCTGCCGACCGACAGKGC-CTGTCATTGAM 265
QY 41 ArgLysValTyrAsnIleThrLysTyrPheSerIleGlnHisProGlyGlyGlnArgValIle 60
Db 266 CGCAAGGTTTAAACATACATCAAAAWGGTCCAAWCCAGCACCCCGGGGGCGAGCGGTCTATC 325
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80
Db 326 GGGCACTAGCTGGAGAGATCAAGGATGCTTCCAAACAAACACCTGACCTGACMTGGA 385
QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSer 100
Db 386 TWCCTGGGCAARTTCTTGAACCCCTGCTGATGTTGTAACCTGGCCCGGAGGAGCCAGC 445
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db 446 CAGGACCAACGGCAAGAACTCAAAAACWCTGARGACTTCCGGGGCCCTGAGGAACGGCT 505
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db 506 GARGACATGAACCTGTTCAAAACCAACCAACGACGTTGTTCTCTCTCTCTGCGCCACATC 565
QY 141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTyrIlePro 160
Db 566 ATCGCCCTGGAGACATTCGATGGTTCACTGCTTTTACTTTGGCAATGGCTGGATTCTCT 625
QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTyrLeuGlnHis 180
Db 626 ACCCTCATCAGCGCTTTGTCTCTCTACTCTCAGGCCCAACCTGATGGTGGTCAACAT 685
QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPhe 200
Db 686 GATTATAGCACCTGCTGCTTACAGAAACCAAGTGGAAACCAACCTTGTCCACAAATTC 745
QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHis 220
Db 746 GTCATTTGGCCACTTAAGGGTGGCTCTGCCAACTGGTGGATCATCGCCACTTCAGCAC 805
QY 221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db 806 CACGCCAAGCCTTAACTCTTCCACAAAGGATCCGATGTAACATGCTGACGCTGTTTCTT 865
QY 241 LeuGlyGluTyrProIleGluTyrGlyLysLysLeuLysLeuTyrLeuProTyrAsn 260

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Db      866 CTGGCGGATGGCAGCCCATCGAGTACGGCAAGAGAGTGAATACCTGCCCTACAAT 925
Qy      261 HisGlnHisGlnTyrPhePhePheLeu 269
Db      926 CACGACGAGTACTTCTTCCTGATT 952

RESULT 21
LOCUS   BG739802
DEFINITION 602630527F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4775791 5',
mRNA sequence.
ACCESSION BG739802
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 745)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10627 row: e column: 08
High quality sequence stop: 743.
FEATURES
source
Location/Qualifiers
1..745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4775791"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/Note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dn.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 172 a 234 C 159 G 180 T
ORIGIN

Alignment Scores:
Pred. No.: 2,99e-125 Length: 745
Score: 1329.00 Matches: 245
Percent Similarity: 98.79% Conservative: 0
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 54.51% Indels: 3
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG739802 (1-745)

Qy      151 ValPheTyrPheGlyAsnGlyTrrPileProThrLeuIleThrAlaPheValLeuAlaThr 170
Db      3 GTCTTTTACTT-GGCAATGGCTGGATTCTTACCTCATCAGCGCTT-GTCCITGCTACC 60
Qy      171 SerGlnAlaGlnAlaGlyTrrPleuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db      61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCCACTGTCTGTCTACAGAAA 120
Qy      191 ProLysTyrAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyValAsnAla 210
Db      121 CCCAAGTGAACACCACTTGTCCAAATTCCTGATTGGCCACTTAAGGGTGGCTCTGCC 180
Qy      211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db      181 AACTGGTGGATCATCGCACTTCCAGCACCACCAAGCCTACATCTTCCACAAGGAT 240

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Qy      231 ProAspValAsnMetLeuHisValPheValLeuGlyLtrPdnPtoileGluTyrGly 250
Db      241 CCGATGTGAACATGCTGCACCTGTT-GTTCCTGGCGAATGGCAGCCCATCGAGTACGC 299
Qy      251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270
Db      300 AAGAAGAAGTGAATACCTGCCTCTACATCACCAGCACGAATACTTCTTCCTGATTGGG 359
Qy      271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290
Db      360 CCGCGCTGCTCATCCCATGATTTCAGTACAGATCATCATGACCATGATCGTCCAT 419
Qy      291 LysAsnTrpValAspLeuAlaTrrAlaValserTyrTrrIleArgPhePheIleThrTyr 310
Db      420 AAGAACTGGGTGGACCTGGCGCTGGCGCTCAGTACTACATCGGTTCCTTCATCACCTAC 479
Qy      311 IleProPheTyrGlyIleLeuGlyValAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db      480 ATCCCTTTCACGGCACTCTGGGAGCCCTCTTTCTCAACTTCATCAGGTTCTCTGGAG 539
Qy      331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db      540 AGCCACTGGTTTGTGGTCCACACAGATGAATCACATCGTCATGGAGATTGACACGAG 599
Qy      351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db      600 GCCTACCGTGACTGGTTCAGTAGCCAGTCAGCCACCTGCAACGTGGAGCAGTCTCTTC 659
Qy      371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390
Db      660 TTCAACGACTGGTTCAGTGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCCACC 719
Qy      391 MetProArgHisAsnLeuHisLys 398
Db      720 ATGCCCGCGCACAACTTACACAAG 743

RESULT 22
LOCUS   BF315881
DEFINITION 6018989828F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125342 5',
mRNA sequence.
ACCESSION BF315881
VERSION BF315881.1 GI:11264175
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1091)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW1013 row: g column: 07
High quality sequence stop: 725.
FEATURES
source
Location/Qualifiers
1..1091
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4125342"
/cisue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/Note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:

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EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 271 a 317 c 288 g 213 t 2 others  
ORIGIN

## Alignment Scores:

Pred. No.: 1,266-124 Length: 1091  
Score: 1325.00 Matches: 257  
Percent Similarity: 93.64% Conservative: 8  
Best Local Similarity: 90.81% Mismatches: 13  
Query Match: 54.35% Indels: 6  
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BF315881 (1-1091)

QY 5 GlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGlu 24  
Db 1 GGGATCAGGGCGAGGGCGCGCGAGCGAGGTGTCGGTCCACCTTCAGCTGGAG 60  
QY 25 GluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyr 44  
Db 61 GAGATTCAGAGCATACCTCGCACCCAGCGAGGTGGCTGATTCAGCCGCAAGGTTTAC 120  
QY 45 AsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAla 64  
Db 121 AACATCACCAGATGTCTCCATCAGACCGGGGGCCAGCGGTCATCGGCATACGCT 180  
QY 65 GlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLys 84  
Db 181 GGAGAAGATGCAACGGATGCTTCGCGCCCTCCACCTGACCTGGAATTCGTGGGCAAG 240  
QY 85 PheLeuLysProLeuLeuIleGlyLeuAlaProGluGluProSerGlnAspHisGly 104  
Db 241 TTCTTGAAACCTCTGATGGTGAATCGCCCGAGGAGCCCGAGGACACCGGC 300  
QY 105 LysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsn 124  
Db 301 AAGAACTCAAGATCCTCAGGACTTCGCGGCCCTCAGGAAGACGGGTGAGGACATGAAC 360  
QY 125 LeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGlu 144  
Db 361 CTGTTCAAGACCAACACCGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
QY 145 SerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTyrIleProThrLeuIleThr 164  
Db 421 AGCATTCGATGGTTCACCTGCTTTTACCTTTGGCAATGGCTGGATTCCTACCTCATCAG 480  
QY 165 AlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHis 184  
Db 481 GCCTTTGCTTGTCTTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATATGGCCAC 540  
QY 185 LeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHis 204  
Db 541 CTGTCGTCTACAGAAACCAACCAAGTGAACACCTTGTCCCAATTCGTCATTTGGCCAC 600  
QY 205 LeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysPro 224  
Db 601 TTAAGGGTGCTCTGCAACCTTGTGGATCATCGCCATTCAGCCACCGCCCAAGCCT 660  
QY 225 AsnIlePheHisLysAsp-ProAspValAsnMetLeu-HisValPhe-ValLeuGlyGlu 243  
Db 661 AACATCTTCCACAGGATCCCGATGTGAACATGCTGGCAGCTGTTGATCTGGGGGAA 720  
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysTyrLeuProTyrAsnHisGlnHis 263  
Db 721 TGGGAGGCCATCGAGTACGGGAGGAAGATG-AAATTTACTGGGCTATATGACACCGGC 779  
QY 264 GluTyr-PhePheLeu-IleGlyProProLeuLeuIleProMetTyr-PheGlnTyrGln 282

Db 780 GAATACTTCTCTCTAGTTGGCCCGGATGGTCCATCCCTGGTTTCCGACCAA 838

RESULT 23  
BU845074

LOCUS DEFINITION BU845074 932 bp mRNA linear EST 16-OCT-2002  
IMAGE: 6578608 5', mRNA\_sequence.

ACCESSION BU845074.1 GI:24029515

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 932)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLC2780 row: j column: 16

High quality sequence stop: 768.

## FEATURES

source

1..932  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6578608"  
/tissue\_type="teratocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_109"  
/note="Organ: ovary; Vector: pOTB7; Site: 1: EcoRI; Site 2:  
XhoI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

BASE COUNT 204 a 285 c 260 g 178 t 5 others

## ORIGIN

Alignment Scores:  
Pred. No.: 3,116-123 Length: 932  
Score: 1310.50 Matches: 249  
Percent Similarity: 91.46% Conservative: 8  
Best Local Similarity: 88.61% Mismatches: 15  
Query Match: 53.75% Indels: 9  
DB: 13 Gaps: 3

US-09-719-601-5 (1-444) x BU845074 (1-932)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
Db 80 ATGGGGAAGAGGAGGAACAGGGCGAGGGCGCGAGGTGTGCGTGGCCAC 139  
QY 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
Db 140 TTCAGCTGGAGGAGGAGTTTCAGAGCATACCTTCGCGCCGACGACGAGTGGTGTGATGAC 199  
QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
Db 200 CGCAAGGTTTACAACATCATCACCAGTGGTTCATCCAGCACCCCGGGGGCGAGCGGTATC 259  
QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80

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Db      260 GGCACCTACCTGGAGAGATGCAACGATGCTTCGCGCTTCCACCTGACCTGGAA 319
Qy      81 PheValGlyLysPheLeuLysProLeuLeuLeuGlyGluLeuAlaProGluProSer 100
Db      320 TTCGTGGCAAGTTCATTGAACCCCTGCTGATTGTTGAATCGCCCGGAGGAGCCAGC 379
Qy      101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120
Db      380 CAGACACGCGAAGAACCTCAAGATCACTGAGGACTTCGCGCCCTGAGGAAGCGGT 439
Qy      121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140
Db      440 GAGGACATGAACCTGTTCAAGACCAACACCGTGTCTCTCTCTCTCTCTCTCTCTCT 499
Qy      141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyPheGlyAsnGlyTrpIlePro 160
Db      500 ATCGCCCTGGAGAGCATGATGCTGCTACAGAAACCCAGTGAACACCTTGTCCACAAATTC 559
Qy      161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180
Db      560 ACCCTCATCAGCGCTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Qy      181 AspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHisLysPhe 200
Db      620 GATTATGGCCACCTGCTGCTCTACAGAAACCCAGTGAACACCTTGTCCACAAATTC 679
Qy      201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220
Db      680 GTCATTTGGCCACTTAAGGGTGGCTCTGCCAATCTGGTGAATCATCGCCACTTCCAGCAC 739
Qy      221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeu---HisValPhe 239
Db      740 CAGCGCAAGCCTAACATCTTCCACAAAGGATCCCGATGTGAACATGTGTGGCAGCTGTTGT 799
Qy      240 ValLeuGlyGluTrpGln---ProIleGluTyGlyLysLysLysLysLysTyLeuProT 259
Db      800 TNCCTGGCGCAATGGCAGCCCTATCCGAGTACGGCAAGAAANGAANGCCTGAAATACCT 859
Qy      259 yr-----AsnHisGlnHisGluTyPhePheLeu---IleGlyProPro 272
Db      860 GGCNNCCTACATCAATCACCAGCAAGAAATACCTTCTCTCTCTCTCTCTCTCTCTCT 918

RESULT 24
LOCUS   B0422100 1246 bp mRNA linear EST 23-MAY-2002
DEFINITION AGENCOURT_7766465 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6021978
5', mRNA sequence.
ACCESSION B0422100
VERSION   B0422100.1 GI:21117415
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1246)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: DCTD/DTP/Gazdar
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM13228 row: 1 column: 19
          High quality sequence start: 71
          High quality sequence stop: 659.
FEATURES             Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6021978"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site: 1; NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 306 a 383 c 281 g 276 t
ORIGIN
Alignment Scores:
Pred. No.: 3,78e-122 Length: 1246
Score: 1301.50 Matches: 269
Percent Similarity: 85.85% Conservative: 10
Best Local Similarity: 82.77% Mismatches: 27
Query Match: 53.38% Indels: 19
Db: 13 Gaps: 8
US-09-719-601-5 (1-444) x B04222100 (1-1246)
Qy 93 GluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAsp 112
Db 58 GAATCGTGCAGCCAGCGCTCGTGCAGC-----GTCCGCTCAAGATCACTGAGGAC 108
Qy 113 PheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhe 132
Db 109 TTCGGGCGCTTGAGGAAGCGGTGAGGACATGAACCTGTTCAAGACCAACCACTGTTTC 168
Qy 133 PheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPhe 152
Db 169 TTCCTCTCTCTCTGCGCCACATCATCGCTCGAGAGCAATTCATCGTGTCTCTCTCTTT 228
Qy 153 TyPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGln 172
Db 229 TACTTTTGGCAATGCTGGATTCCTACCTCATCAGCGCTTTTGTCTTGTCTCTCTCTCAG 288
Qy 173 AlaGlnAlaGlyTrpLeuGlnHisAspTyGlyHisLeuSerValTyArgLysProLys 192
Db 289 GCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTACAGAAAACCAAG 348
Qy 193 TrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrp 212
Db 349 TGGAAACACCTTGTCCACAAATTCGTCATTGGCCACTTAAAGGGTGCCTCTGCCAACTGG 408
Qy 213 TrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAspProAsp 232
Db 409 TGGAAATCATGCCACTTCCAGCACCAGCCCAAGCCTAACATCTTCCACAAGGATCCGAT 468
Qy 233 ValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyGlyLysLys 252
Db 469 GTGAACATGCTGCACGTGTTTGTCTGGCGCAATGGCAGCCCATCAGATACGCGAGAAG 528
Qy 253 LysLeuLysTyLeuProTyAsnHisGlnHisGluTyPhePheLeuIleGlyProPro 272
Db 529 AAGTGTAAATACCTGCCCTTACATCACCAGCAGATATCTTCTCTCTGATTTGGCGCGC 588
Qy 273 LeuLeuIleProMetTyPheGlnTyGlnIleIleMetThrMetIleValHisLysAsn 292
Db 589 CTGCTCATCTCCCATGATTTCAGATACCATCATCATCATCATCATCATCATCATCATCAT 648
Qy 293 TrpValAspLeuAlaTrpAlaValSerTyTrpTyIleArgPhePheIleThrTyIlePro 312
Db 649 TGGGTGAGCACTGGCGCTGGCGCGTACGACTACTATCATCGGTCTCTCATCATCATCCCT 708
Qy 313 PheTyGlyLeuLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu-SerH 332
Db 709 TTCACGCGCATCTCTGGGAGCCCTCTTTTCTCTCACTTTCATCAGGTTCCTCGAAGAGCC 768
Qy 332 isTrpPheValTrpVal-ThrGlnMetAsnHisIleValMet---GluIleAspGlnGlu 350

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Db      769 ACTGTTGGGTGGTCCCCCGACATGAATCACAATCCTCATGGGAAATTTGACAGGAG 828
Qy      351 AlatyArgAsp-TpPheSer--SerGlnLeuThraL-ThrCysAsn-ValGluGln 368
Db      829 GCTACCCGGGAAGACTGGTTTCACTAACCCTGTGACGCCCTTGCACCCACCTGCAACGGGGGAACAG 888
Qy      369 SerPhe---PheAsnAspTTP-PheSerGlyHis---LeuAsnPheGln-----IleG1 384
Db      889 TCCCTTCTTCAACCAACTGGGTTCAGTGGGAACACCTTTAACTTCCCGAGATTGAGGAA 948
Qy      384 uHisHisLeuPhe-ProThrMet----ProArgHisAsnLeuHis---LysIleAlaPro 401
Db      949 CCACCTCTTTTCCCAACAATGGCCCGGGATACAACTTTAAACCAAAAATTCGCCCC 1007

RESULT 25
LOCUS   BG741484
DEFINITION BG741484 829 bp mRNA linear EST 15-MAY-2001
VERSION   BG741484
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs@mail.nih.gov
          CDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
          Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L14M10631 row: d column: 22
          High quality sequence stop: 824.
          Location/Qualifiers
            1..829
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:4777317"
              /lab_host="DH10B (T1 phage-resistant)"
              /clone_lib="NCI CGAP Skn3"
              /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
              Average insert size 1.5kb. Library constructed by Life
              Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 187 a 247 c 237 g 158 t
ORIGIN
Alignment Scores:
Pred. No.: 8-5e-121 Length: 829
Score: 1286.00 Matches: 242
Percent Similarity: 96.85% Conservatives: 4
Best Local Similarity: 95.28% Mismatches: 6
Query Match: 52.75% Indels: 3
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG741484 (1-829)

Qy      1 MetGlyVsGlyAsnGln-GlyGluGlyAlaGluArgGluValSerValProTh 20
Db      72 ATGGGAAGGAGGAGGAAACAGTGGCGAGGGGCGCCGAGCGAGGTGTCGGTCCAC 131
Qy      20 rPheSerTPGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAs 40

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Db      132 CTTTCAGTCGGAGGAGATT'CAGAAGCATAA'CTCGCCACCGACAGGTGGTGGTCATTGA 191
Qy      40 pArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValI 60
Db      192 CCACAAGGTTTACACATCACCATAATGGTTCATTCACGACCCCGGGGGGCGAGGGTCA 251
Qy      60 eGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuG1 80
Db      252 CGGGCACTAGCTGGAGAGATGCAACGATGCTTCGCGGCTTCACCCCTGACCTGGA 311
Qy      80 uPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGluProSe 100
Db      312 ATTCTGGGGCAAGTTCTTGAACCCCTGCTGATGGTGAACCTGGCCCGGAGAGGCCAG 371
Qy      100 rGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAl 120
Db      372 CCAGGACCCAGGCAAGACTCAAGATCACTGAGGACTTCGCGGCTTCGAGGAAGACGC 431
Qy      120 aGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisI 140
Db      432 TGAGGACATGAACCTGTTCAAGACCAACCAACCGTGTCTTCCTCCTCCTCCTGCCCACAT 491
Qy      140 eIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePr 160
Db      492 CATCGCCCTGGAGAGCATTCGATGTTCACTGTCCTTTTACTTTGGCAATGGCTGATTCC 551
Qy      160 oThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHi 180
Db      552 TACCCTCATCAGCGCCTTTGTCTTCTGCTACCTCTCAGGCCCAAGCTGGATGCTGCAACA 611
Qy      180 sAspTyrGlyHis-LeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysP 200
Db      612 TGATTATGGCCACCATGCTGCTCTACGAACCCCAAGTGGAAACCACTTGTCCCAAT 671
Qy      200 heValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnH 220
Db      672 TCGTCATTGGCCACTTAAAGGTGCTCTGCAACTGCTGGAATCATCGCCACTTCACG 731
Qy      220 iHisAlaLysProAsnIlePheHisLysAspProAspValLenMetLeuHisValPheV 240
Db      732 ACCAGCCCAAGCCTTAACATCTTCCAGGGATCCGATGTGAACATGTCACGCTGATT 791
Qy      240 alLeuGlyGluTrpGlnProIleGluTyrGlyLysLys 252
Db      792 GTCTGGCGAATGGCAGCATC-GAGTACGGCAGAAGA 828

RESULT 26
LOCUS   BU856567
DEFINITION AGENCOURT_10472773 NIH_MGC_109 Homo sapiens cDNA clone
ACCESSION BU856567
VERSION   BU856567.1 GI:24041557
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NTH-MGC http://mgi.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs@mail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Rubin Laboratory
          CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L14M2884 row: n column: 21
          High quality sequence start: 25

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High quality sequence stop: 567.

## FEATURES

Location/Qualifiers

source

1..938  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6646293"  
 /tissue\_type="teratocarcinoma, cell line"  
 /lab\_host="PH108 (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_109"  
 /note="Organ: ovary; Vector: pORF7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 219 a 293 c 204 g 219 t 3 others

## ORIGIN

Alignment Scores:

Pred. No.: 9,996-121 Length: 938  
 Score: 1266.00 Matches: 262  
 Percent Similarity: 88.63% Conservative: 3  
 Best Local Similarity: 87.63% Mismatches: 19  
 Query Match: 52.75% Indels: 16  
 DB: 13 Gaps: 5

US-09-719-601-5 (1-444) x BU856567 (1-938)

QY 118 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137  
 DB 34 AAGACGGCTGAGACATGAACTGTTCAAGACCAACACCGTGTCTTCTCTCTCTCTG 93  
 QY 138 AlaHisIleAlaLeuGluSerIleAlaTTPheThrValPheTyrPheGlyAsnGly 157  
 DB 94 GCCCC-ATCATGCCCTGGAGCATGTGATGTTCACTGTCTTTACTTGGCAATGGC 152  
 QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrp 177  
 DB 153 TGGATTCCATCCCTCATCGCCGCTTGTCCCTGTACCTCTCAGGCCCAACGCTGGATGG 212  
 QY 178 LeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuVal 197  
 DB 213 CTCACACATGATTATGGCCACCTGTCTGTCTACAGAAACCCAGTGGACCACTTGTCT 272  
 QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHis 217  
 DB 273 CACAAATTCGTCTATTGGCCACTTAAAGGGTGCCTCTGCCAACTGTGTGAATCATGCCAC 332  
 QY 218 PheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHis 237  
 DB 333 TTCACGACCAACCCAGCCTACATCTTCCACAGATCCCGATGTGAACTGTGTGAC 392  
 QY 238 ValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysTyrLeu 257  
 DB 393 GTCTTTGTCTGGCGAATGGCAGCCCATCGAGTACCGCAAGAAAGCTGAATACCTG 452  
 QY 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeuIleProMet 277  
 DB 453 CCTTCAATCACCAGACCGAATACTTCTCTGATTGGGCGCGCTGTCTATCCCCATG 512  
 QY 278 TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297  
 DB 513 TATTTCAGTACCATCATCATGACCATGATCGTCCATAAGAACTGGGTGACCTGGCC 572  
 QY 298 TrpAlaValSerTyrTrpIleArgPhePheIleThrTyrIle-ProPheTyrGlyIle 317  
 DB 573 TGNCGCGTACGTACATACCGGTCTCTCATCACCTATACCTCCCTTCTACGGATCCT 632  
 QY 317 uGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVa 337

DB 633 GNGAGCCCTCTTTTCTCACTCATCAGTTCTCTGGAGAGCACTGGTTTGTGGGT 692  
 QY 337 lThrGlnMetAsnHisIleValMetGluLeuAspGlnGluAla-TyrArgAspTrpPhe 357  
 DB 693 CACACAGATGAATCATCGTATGAGATTGACAGGAGGCCCTACCTGACTGNTCA 752  
 QY 357 erSer-GlnLeuThrAla-ThrCysAsnValGluGlnSer---Phe-PheAsnAspTrp 375  
 DB 753 ATAGCCAGCTGACAGCCACCTGCAAGTGTGGAGCAGTCCCTCTTTCACAGCTGG 812  
 QY 375 heSerGly---His--LeuAsnPheGln---lleGluHisHisLeuPhe-----Pr 389  
 DB 813 GTTCAGGGGAACACCTTTAACTTCAGGATTGGAGCAACACCTTCTTCCCAACC 872  
 QY 389 oThrMetProArgHisAsnLeu-----HisLysIleAlaPro 401  
 DB 873 ATTGGCCCGGGAGCAAACTTAAACACAAACAAAANTCCCCC 915

RESULT 27  
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 LOCUS 602273891F1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4361855 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF970711  
 VERSION BF970711.1 GI:12337926  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: ggaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM10005 row: e column: 24  
 High quality sequence stop: 712.  
 Location/Qualifiers  
 1..802  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4361855"  
 /tissue\_type="adrenal cortex carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_84"  
 /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site 1:  
 NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT  
 primed. Average insert size 1.229 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH MGC Library."

BASE COUNT 193 a 241 c 187 g 181 t

## ORIGIN

Alignment Scores:

Pred. No.: 1,856-120 Length: 802  
 Score: 1282.50 Matches: 245  
 Percent Similarity: 96.09% Conservative: 1  
 Best Local Similarity: 95.70% Mismatches: 6  
 Query Match: 52.60% Indels: 6  
 DB: 10 Gaps: 1

US-09-719-601-5 (1-444) x BF970711 (1-802)

QY 190 LysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSer 209

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Db 3 AAACCAAGTGAACCACTTGTGCACAAATGGTCATGTGGCCACTTAAGAGGTGCCTCT 62
QY 210 AlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLys 229
Db 63 GCCAACTGGTGAATCATCGGCACCTTCAGACACACCCAGCCCAAGCTTCCCAAG 122
QY 230 AspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyr 249
Db 123 GATCCGATGGAACATGCTGCACGTGTTGTCTGGGGAATGGCAGCCCATCGAGTAC 192
QY 250 GlyLysLysLysLeuLysTyrLeuProTyrAsnHisGln---HisGluTyrPhePheLeu 268
Db 183 GGCAGAGAGAGAGCTGAATACCTGCCCTACAAATCACCAGCCACGAAATTAATCTTCTG 242
QY 269 IleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIle 288
Db 243 ATTGGGCGCGCTGCTCATCCCATGTAATTCAGTACGATCATCATGACCATGATC 302
QY 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg-PhePheI 308
Db 303 GTCCATAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTACTACATCCGGGTTCTTCAT 362
QY 308 eThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPh 328
Db 363 CACCTACATCCCTTCTACGGCAGTCCCTGGAGCCCTCTCTTCTCACTTCATCAGTT 422
QY 328 eLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAs 348
Db 423 CCTGGAGAGCCACTGGTTTGTGGTGCACACAGATGAATCAGATCGTCATGGAGATTGA 482
QY 348 pGluGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluI 368
Db 483 CCAGAGGCCCTACCGTGACTGGTTCAGTAGCCAGCTCAGACCCACCTGCAACGTGGAGCA 542
QY 368 nSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPh 388
Db 543 GTCCCTTCTCAACGACTGGTTCAGTGGACACTTAATCTCCAGATTGAGCACCACCTCTT 602
QY 388 eProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAl 408
Db 603 CCCACCATGCCCCGGGCAACACTTACCAAGATCGC-CCGCTGGTGAAGTCTCTATGTGC 661
QY 408 aLysHis-GlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp-IleIle 427
Db 662 CAAGCATGGGATTTGAATACCAAGAGAGACCGTA-CTGAGGGCCCTCTGACCATCATC 720
QY 428 ArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyr 441
Db 721 AGGTCCCTGAAAAATTTTGGGAAACTGTGGTTGAAGCTTAC 762

RESULT 28
LOCUS BG741398
DEFINITION BG741398 764 bp mRNA linear EST 15-MAY-2001
mRNA sequence.
ACCESSION BG741398
VERSION BG741398.1 GI:14052051
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 764)
NTH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLNMI0830 row: n column: 13

High quality sequence stop: 764.

Location/Qualifiers

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1. .764

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4777164"

/lab\_host="DHIOB (T1 phage-resistant)"

/clone\_lib="NCI CGAP Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 179 a 232 c 184 g 169 t

ORIGIN

Alignment Scores:

Prod. No.: 4.46e-120 Length: 764

Score: 1278.50 Matches: 236

Percent Similarity: 97.52% Conservative: 0

Best Local Similarity: 97.52% Mismatches: 5

Query Match: 52.44% Indels: 2

DB: 10 Gaps: 1

US-09-719-601-5 (1-444) x BG741398 (1-764)

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QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
Db 3 CACTTAAGAGGTGGCTTCGCCAACTGGTGGAAATCATGCCACTTCCAGCACCCCAAG 62
QY 224 ProAsnIlePheHis---LysAspProAspValAsnMetLeuHisValPheValLeuGly 242
Db 63 CCTAACATCTTCCACTAAGGGATCCCTGATGGAACATGCTGCAGCTGTTGTTCTGGGC 122
QY 243 GluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLys 262
Db 123 GAATGGAGCCCATCGAGTACGGCAAGAGAGTGAATACCTCCCTCCATCAATCACCAG 182
QY 263 HisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGln 282
Db 183 CACGAATACTTCTCTGATGGGCGCGCTGCTCATCCCATGATATTTCAGTACCAG 242
QY 283 IleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 302
Db 243 ATCATCATGACCATGATCGTCATAAGAACTGGGTGGACCTGGCCCTGGGCGCTCAGCTAC 302
QY 303 TyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPhe 322
Db 303 TACATCCGGTCTTTCATCACCTACATCCCTTCTACGGCATCTCTGGAGCCCTCTCTTTC 362
QY 323 LeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHis 342
Db 363 CTCAACTTTCATCAGGTTCTCTGAGAGCCACTGGTTGTGGTGCACACAGATGAATCAC 422
QY 343 IleValMetGluLeuAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAla 362
Db 423 ATCGTCATGGAGATTGACAGAGGCCCTACCGTACTGTTTCAGTAGCAGCTGACGCC 482
QY 363 ThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGln 382
Db 483 ACCTGCAACGTGGAGCAGTCTCTCTTCAACGACTGGTTCAGTGGAGCCCTTAACCTCCAG 542
QY 383 IleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeu 402
Db 543 ATTAGCACCCTCTCTCCCAATGCCCCGAGCAACTTACACAAATCGC-CCGCTG 601
QY 403 ValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAla 422
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/clone lib="NCI CGAP_Skn3"
/notes="Organ: sKln; Vector: PCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 167 a 214 c 148 g 160 t
ORIGIN
Alignment Scores:
Pred. No.: 2,39e-118 Length: 689
Score: 1261.00 Matches: 225
Percent Similarity: 99.12% Conservative: 1
Best Local Similarity: 98.71% Mismatches: 2
Query Match: 51.72% Indels: 1
DB: 10 Gaps: 0
US-09-719-601-5 (1-444) x BG696235 (1-689)
QY 171 SerGlnAlaGlnAlaGlyTrrPLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 5 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCCACCTTGTCTCTACAGAAA 64
QY 191 ProlysTrrAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 65 CCCAAGTGAACCACTTGTCCACAAATTCGTATTGGCCCACTTAAAGGGTGCCTCTGCC 124
QY 211 AsnTrrTrrAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 125 AACTGGTGGATCATCGCCACTTCAGCACCAAGCCCAAGCTTAAACATCTTCCACAGGAT 184
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrrGlnProIleGluTrrGly 250
Db 185 CCCGATGTGAACATGCTCAGCTGTTTCTTGGCGAATGCGACCCATCGAGTACGGC 244
QY 251 LysLysLysLeuLysTrrLeuProTrrAsnHisGlnHisGluTrrPhePheLeuIleGly 270
Db 245 AAGAGAGAGCTGAATACCTGCCCTACATCACCAGCACGATACCTTCTCTGATTGGG 304
QY 271 ProProLeuLeuIleProMetTrrPheGlnTrrGlnIleIleMetThrMetIleValHis 290
Db 305 CGCGCGCTGCTCATCCCATGTATTTCAGTACCATCATCATGATCATGATGCTCAT 364
QY 291 LysAsnTrrValAspLeuAlaTrrAlaValSerTrrTrrIleArgPhePheIleThrTyr 310
Db 365 AAGAAGTGGTGGACCTGGCCCTGGCCCTGACTACTACATCCGGTCTTCTCATCCTAC 424
QY 311 IleProPheTrrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db 425 ATCCCTTTCTACGGCATCTGGGAGCCCTCTTTCTCTCAACTTCATCAGGTTCCTGGAG 484
QY 331 SerHisTrrPheValTrrValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db 485 AGCCACTGGTT-GTGTGGGTACACAGATGAATCATCATCGTCATGGAGATTGACAGAG 543
QY 351 AlaTrrArgAspTrrPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db 544 GCCTACCGTACTGCTTTCAGTAGCAGCTGACAGCCACCTGCAAGCTGGAGACGCTCTTC 603
QY 371 PheAsnAspTrrPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
Db 604 TTCACGACTGGTTTCAGTGGACACTTAACTTCCAGATTGAGCCACCTCTTCCCCAAC 663
QY 391 MetProArgHisAsnLeuHisLys 398
Db 664 ATGCCCCCGAACAATTACACAG 687
RESULT 31
BG696235
LOCUS
DEFINITION 602659366F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802272 5',
mRNA sequence.
ACCESSION BG696235
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VERSION BG696235.1 GI:13961176
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 697)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Invitrogen, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10696 row: d column: 17
High quality sequence stop: 695.
FEATURES
Location/Qualifiers
1..697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4802272"
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/clone_lib="NCI CGAP_Skn3"
/notes="Organ: sKln; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 166 a 214 c 170 g 147 t
ORIGIN
Alignment Scores:
Pred. No.: 2,55e-117 Length: 697
Score: 1251.00 Matches: 229
Percent Similarity: 98.71% Conservative: 0
Best Local Similarity: 98.71% Mismatches: 2
Query Match: 51.31% Indels: 1
DB: 10 Gaps: 0
US-09-719-601-5 (1-444) x BG696235 (1-697)
QY 34 AppSerGlyLeuValIleAspArgLysValTrrAsnIleThrLysTrrSerIleGlnHis 53
Db 2 GACAGTGGCTGGTCTATTGCCGCAAGTTTACAACATCACCAATGGTCCATCCAGCAC 61
QY 54 ProGlyGlyGlnArgValIleGlyHisTrrAlaGlyGluAspAlaThrAspAlaPheArg 73
Db 62 CCGGGGGGCGACGGGGTCTATCGGGCTACCTGAGAGATGCAACGATGCTTCCG 121
QY 74 AlaPheHisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGlu 93
Db 122 GCCTTCCACCTGACCTGGAATTCGTGGCAAGTCTTGAACCCCTGCTGATGGTGA 181
QY 94 LeuAlaProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPhe 113
Db 182 CTGGCCCCGAGAGAGCCAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGG 241
QY 114 ArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePhe 133
Db 242 CGGGCCCTGAGGAAGACGGCTGAGGACATGAACCTGTTCAAGACCAACCCAGCTTCTTC 301
QY 134 LeuLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrrPheThrValPheTyr 153
Db 302 CTCTCTCTCTGGCCACATCATCGCCCTGGAGAGCAATGCAATGGTTCCTGCTTTTAC 361
QY 154 PheGlyAsnGlyTrrIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAla 173
Db 362 TTTGGCAATGGCTGGATTCTTACCTCATCAGGCCCTTGTCTTGCTTCTCTCAGGCC 421
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QY 174 GlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrAcLysProLysTrp 193  
 Db 422 CAAAGTGGATGCTGCAACATGATTAATGCGCACCTGTCTGTCTACAGAAAACCCAGTGG 481  
 QY 194 AsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrp 213  
 Db 482 AACCACTTGTCCACAAATTCGTCATTTGCCACTTAAGGGTGCCTCTGCCAACTGGTGG 541  
 QY 214 AsnHisAspHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspVal 233  
 Db 542 AATCATCGCCACTTCAGCACCCAGCCCAAGCCTAACATCTTCCAAAGATCCCGATGTG 601  
 QY 234 AsnMetLeuHisValPhe-ValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLY 253  
 Db 602 AACATGCTGACGTGTTGGTCTGGCGAATGGCAGCCATCGAGTACGCGCAAGAA 661  
 QY 253 IleuLysTyrLeuProTyrAsnHisGlnHisGlu 264  
 Db 662 GCTGAAATACCTGCCCTACAATCACACAGCAGAA 695

RESULT 32  
 BG740017 796 bp mRNA linear EST 15-MAY-2001  
 LOCUS 602630980F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4776427 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG740017  
 VERSION BG740017.1 GI:14050670  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [rgapbs-x@mail.nih.gov](mailto:rgapbs-x@mail.nih.gov)

Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLNL0628 row: 0 column: 20  
 High quality sequence stop: 737.  
 Location/Qualifiers  
 1..796

## FEATURES

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4776427"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Skn3"  
 /note="Organ: Skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI CGAP Library."  
 184 a 244 c 174 g 193 t I others

## BASE COUNT

## ORIGIN

## Alignment Scores:

Pred. No.: 6.14e-117 Length: 796  
 Score: 1248.00 Matches: 252  
 Percent Similarity: 93.38% Conservative: 7  
 Best Local Similarity: 92.65% Mismatches: 2  
 Query Match: 51.19% Indels: 13  
 DB: 10 Gaps: 2

US-09-719-601-5 (1-444) x BG740017 (1-796)

QY 152 PheTyrPheGlyVasnglyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSer 171  
 Db 2 TTTTACTTTGGCAATGGCTGGATTCTACCTCATCAAGGC-ITTGCTCTTGTCTACCTCT 60  
 QY 172 GlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysPro 191  
 Db 61 CAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACTGTCTGTCTACAGAAAACCC 120  
 QY 192 LysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsn 211  
 Db 121 AAGTGGAACCACTTGTCCACAAATTCGTCAITGGCCACTTAAGGGTGCCTCTGCGCAAC 180  
 QY 212 TrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspPro 231  
 Db 181 TGTGTGAATCATGCCACTTCCAGCACCCAGCCCAAGCCTAACATCTTCCACAGGATCCC 240  
 QY 232 AspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGlyLys 251  
 Db 241 GATGTGAACATGCTGCACGTGTTGTTCTGGCGAATGGCAGCCCATCGAGTACGCGCAAG 300  
 QY 252 LysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyPro 271  
 Db 301 AAGAAGCTGAATACCTGCCCTACAATCACACGACGAAATACTTCTTCTGATTGGCGCG 360  
 QY 272 ProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHisLys 291  
 Db 361 CCGCTGCTCATCCCAATGATATNTCCAGTACCAGATCATCATGACCATGATCGTCCATAG 420  
 QY 292 AsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIle 311  
 Db 421 AACTGGGTGGACCTGGCGCTGGCGCTGAGTACTACATCGGTCTTCTCATCACTCAATC 480  
 QY 312 ProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSer 331  
 Db 481 CCTTTCTACCGGACTCTGGGAGCCCTCTTTCTCACTTCACTGAGTTCCTGGAGAGC 540  
 QY 332 HisTrpPheValTrpValThr-GlnMetAsnHisIleValMetGluIleAspGlnGluAl 351  
 Db 541 CACTGGTTTGTGGGTCAACACAGATGAATCATCATGCTCATGGAGATTGACCGAGGAGC 600  
 QY 351 aTyrArgAspTrp-PheSerSerGlnLeuThrAla-ThrCysAsnValGluGlnSer-Ph 370  
 Db 601 CTACCGGTGACTGGGTTTCACTAGCCAGCTGACGCCACCTGACACCTGACGAGTCCCTT 660  
 QY 370 ePheAsnAsp-TrpPhe-SerGlyHisLeuAsnPheGlnIleGluHisHis-LeuPhePr 389  
 Db 661 CTTCACGACTTGGTTTCAAGTGGACACCTTAA-TTCCAGATAGACACCACTCTT---CC 716  
 QY 389 oThrMetProArgHisAsnLeuHis---LysIleAlaProLeuValLysSer-LeuCysA 408  
 Db 717 CACCATGCCCGGAACAACTTACACCAAGAAATTGCCCGCTGGTGAAGTCTCTTATGTG 776  
 QY 408 laLys-HisGlyIleGlu 413  
 Db 777 CCAAGGCATGSCATTGAA 794

## RESULT 33

## BUS01667

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

BUS01667 963 bp mRNA linear EST 12-SEP-2002  
 AGENCOURT 8868718 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6341523  
 5', mRNA sequence.

BUS01667 GI:22804803  
 BUS01667.1

EST.  
 Homo sapiens (human)

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 963)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.



QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
 Db 68 ATGGGGAAGGAGGAGAACCAAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 127  
 QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
 Db 128 TTCAAGTGGGAGGAGATTGAGAAGCATACCTCGCCAGCCAGCCAGAGTGGTGCATTGAC 187  
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
 Db 188 CGCAAGGTTTACAACTACCAAAATGGTCCATCCAGACCCCGGGGGGGGGGGGGGGTATC 247  
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
 Db 248 GGGCACTACCTGGAGAGATGCAACGAGTGCCTTCGGCGCTTCACACCTGACCTGAA 307  
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluLysProSer 100  
 Db 308 TTGCTGGGCAAGTTCTTGAACCCCTGCTGATGTGTGAACCTGGCCCCGGAGGAGCCAGC 367  
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
 Db 368 CAGGACCAAGCAAGAACTCAAGATCACTGAGGACTTCGGGGCCCTGAGGAAGACGGCT 427  
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
 Db 428 GAGGACATGAACCTGTTCAGACCAACACCGTGTCTTCTCTCTCTCTCTCTCTCTCTCT 487  
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
 Db 488 ATCGCCCTGGAGAGCATTCATGTTCACTGTCTTTTACTTTGGCAATGGCTGGATTCT 547  
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
 Db 548 ACCCTCATCAGCGCTTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 607  
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLysPhe 200  
 Db 608 GATTATGGCCACCTGTCTGTCTACAGAAACCCAGTGGAGCAACCTTGTCCACAAATC 667  
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
 Db 668 GTCAATGGCCACTTAAGGGTGCCTCTGCAATGGTGGAAATCATCGCCACTTCCAGCAA 727  
 QY 221 HisAlaLysProAsnIlePheHisLysAspProAspVal 233  
 Db 728 CCAGCCAGCCCTAACATCTTCCCAAGATCCCGATGTG 766

## RESULT 35

BI752239

LOCUS

60302433F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5192744 5',  
 mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLAM11482 row: b column: 09  
 High quality sequence stop: 759.  
 Location/Qualifiers  
 1. 759

## FEATURES

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5192744"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_114"  
 /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 019. Note:  
 this is a NIH MGC library."

BASE COUNT 168 a 233 c 213 g 145 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 1-87e-116 Length: 759  
 Score: 1243.00 Matches: 228  
 Percent Similarity: 98.70% Conservatives: 0  
 Best Local Similarity: 98.70% Mismatches: 3  
 Query Match: 50.98% Indels: 0  
 DB: 12 Gaps: 0

US-09-719-601-5 (1-444) x BI752239 (1-759)

QY 1 MetGlyLysGlyGlyAsnGlnGlyGluGlyAlaAlaGluArgGluValSerValProThr 20  
 Db 67 ATGGGGAAGGAGGAGAACCAAGTCCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 126  
 QY 21 PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
 Db 127 TTCAGCTGGGAGGAGATTGAGAAGCATACCTCGCCAGCCAGAGTGGTGGTGCATTGAC 186  
 QY 41 ArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
 Db 187 CGCAAGTGGGAGGAGATTGAGAAGCATACCTCGCCAGCCAGAGTGGTGGTGCATTGAC 246  
 QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
 Db 247 GGGCACTACCTGGAGAGATGCAACGAGTCCCTTCGGCGCTTCCACCTGACCTGGAA 306  
 QY 81 PheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluLysProSer 100  
 Db 307 TTGCTGGGCAAGTTCTTGAACCCCTGCTGATGTGTGAACCTGGCCCGGAGGAGCCAGC 366  
 QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
 Db 367 CAGGACCAAGGAGAGACTCAAGATCACTGAGACTTCCGGGCCCTCGAGGAAGCGCT 426  
 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
 Db 427 GAGGACATGAACCTGTTCAGAGCAACCAACCGTGTCTTCTCTCTCTCTCTCTCTCTCT 486  
 QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
 Db 487 ATCGCCCTGGAGAGCATTCATGTTCACTGTCTTTTACTTTGGCAATGGCTGGATTCT 546  
 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
 Db 547 ACCCTCATCAGCGCTTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 606  
 QY 181 AspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisArgHisPheGlnHis 200  
 Db 607 GATTATGGCCACTTGTCTGTCTACAGAAACCCAGTGGAGCAACCTTGTCCACAAATC 666  
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220

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Db      667 GTCAATTGCCACTTAAAGGGTGCCTCTGCCAACTGGTGAATCATGCCACTTCCAGCAC 726
QY      221 HisAlaLysProAsnIlePheHisLysAspPro 231
Db      727 CACGCCAAGCCTAAACATCTTCCCAAGATCCC 759

RESULT 36
BG743597
LOCUS   602633951F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778892 5',
DEFINITION mRNA sequence.
ACCESSION BG743597
VERSION   BG743597.1 GI:14054250
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 799)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10635 row: f column: 13
High quality sequence stop: 795.
Location/Qualifiers
1. 799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778892"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 182 a 236 c 205 g 176 t
ORIGIN

Alignment Scores:
Pred. No.: 5,13e-116 Length: 799
Score: 1239.00 Matches: 224
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.82% Indels: 0
D: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG743597 (1-799)

QY      221 HisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVal 240
Db      2 CACGCCAAGCCTAACATCTTCCACAGAGTCCGATGCAACATGTCGACGCTTTGTT 61
QY      241 LeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsn 260
Db      62 CTGGCGCAATGGCAGCCCATCGAGTACGCGCAAGAAGAGCTGAATACCTGCCCTACAAT 121
QY      261 HisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGln 280
Db      122 CACCGACGACGATATCTTCTCTGATTGGCGCGCTCATCCCGATGATTTCCAG 181
QY      281 TyrGlnIleLeuMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaVal 300

```

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Db      182 TACCAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGCACCTGGCCCTGGGCCCTC 241
QY      301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db      242 AGCTACTCATCCGGTCTTTCATCACCTACATCCCTCTTACGGCATCTCTGGAGCCCTC 301
QY      321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisTyrPheValTrpValThrGlnMet 340
Db      302 CTTTTCCTCAACTTCACTCAGGTTCCTGGAGAGCCACTGGTTGTGTGGGTACACAGATG 361
QY      341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db      362 AATCACTCATGTCAGATTACACAGAGGCTACCTGACTGGTTTCAGTAGCCAGCTG 421
QY      361 ThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db      422 ACAGCCACCTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTCACTGGACACCTTAAC 481
QY      381 PheGlnIleGluHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db      482 TTCCAGATTGACACACCACTCTTCCCACCATGCCCCGGCACAACTTACACAGATCGCC 541
QY      401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db      542 CCGCTGGTGAAGTCTCTATGTGCCAAGCATGCGATTGAATACACAGAGAGCGCTACTG 601
QY      421 ArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAla 440
Db      602 AGGGCCCTCTCGACATCATCAGGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGACGCC 661
QY      441 TyrLeuHisLys 444
Db      662 TACCTTCACAAA 673

RESULT 37
BG071205
LOCUS   AGENCOURT 6853101 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5927574
DEFINITION 5', mRNA sequence.
ACCESSION BG071205
VERSION   BG071205.1 GI:19900251
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1022)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2102 row: 1 column: 07
High quality sequence stop: 656.
Location/Qualifiers
1. 1022
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5927574"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'

```

FEATURES  
source

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 224 a 313 c 283 g 202 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3,67e-115 Length: 1022  
Score: 1232.00 Matches: 244  
Percent Similarity: 83.28% Conservative: 10  
Best Local Similarity: 80.00% Mismatches: 22  
Query Match: 50.53% Indels: 30  
DB: 13 Gaps: 5

US-09-719-601-5 (1-444) x BQ071205 (1-1022)

QY 1 MetGlyLeuGlyAsnGlnGlyGluAlaGluArgGluValserValProThr 20  
Db 80 ATGGGAAGGGAGGAACAGAGCGGAGGGGGCGCGAGCGAGGTGTGGTGGCCACC 139  
QY 21 PheSerTrpGluLeuGlnGlyHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40  
Db 140 TTCAGCTGGAGGAGATTGAGAGCATACCTCGCCAGCCAGAGGTGGTGTGCTATTGAC 199  
QY 41 ArgLeuValIleAsnLeuThrTrpSerIleGlnHisProGlyGlyGlnArgValIle 60  
Db 200 CGCAAGGTTTACAAATCATCAACCAATGGTCCATCCAGCACCGCGGGGGCGAGCGGTGTCATC 259  
QY 61 GlyHisValIleGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsnLeuGlu 80  
Db 260 GGGCACTACCTGGAGGAAGATGACGAGTGCCTTCGGCGCTTCACCTGACCTGGAA 319  
QY 81 PheValGlyLeuPheLeuLeuProLeuLeuLeuGlyGluLeuAlaProGluProSer 100  
Db 320 TTCGTGGGCAAGTTCCTGAAACCCCTGCTGATTGGTGAATGGCCCGGAGGAGCCAGC 379  
QY 101 GlnAspHisGlyLeuAsnSerIleThrGluAspPheArgAlaLeuArgIleThrAla 120  
Db 380 CAGGACACGCGCAAGAACTCAAGATGACTGAGGACTTCGGGCGCTGAGGAGCGGT 439  
QY 121 GluAspMetAsnLeuPheLeuThrAsnHisValPhePheLeuLeuLeuLeuAlaHisIle 140  
Db 440 GAGGACATGAACCTGTTCAGACACCAACCGAGTGTCTTCTCTCTCTCTCTCTCTCTCT 499  
QY 141 IleAlaLeuGluSerIleAlaTrpPheThrValPheTrpPheGlyAsnGlyTrpIlePro 160  
Db 500 ATCGCCCTGGAGAGCATTTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 559  
QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHis 180  
Db 560 ACCCTCATCAGCCCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 619  
QY 181 AspTrpGlyHisLeuSerValIleArgLeuProLysTrpAsnHisLeuValHisLysPhe 200  
Db 620 GATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGAACCACTTGTCTCCACAA-TTC 678  
QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHis 220  
Db 679 GTCAATGGCCACTTAAAGGTGCTCTGCAACCTGTGGTAATCATGCCACTTCCAGCAC 738  
QY 221 HisAlaLysProAsnIle-PheHisLysAspProAspValAsnMetLeuHisVal----- 238  
Db 739 CACGCCAAGCTTAACATCTTCCACAGATCCCGAGGGGAACATGCTGACGTGGTTTG 798  
QY 239 -----PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLys----- 255  
Db 799 TTCTCTGGCGAAGGGCAGCCCATCCA---AGTACGGGCAAGAGAACTGAATATAC 855  
QY 256 -----TyrLeuPro-----Ty 859

Db 856 CTGGCCCTAAATTCGCCGCCGGAATAAATTCCTTCCCTGAATGGGGCGCGCCGCT 915  
QY 259 rAsnHisGlnHisGluTrpPhePhe-----LeuIleGlyProPhe 273  
Db 916 GCTTCATTCGCCCATGTATATTCCTTACCCAAATCTCTCTGGACCCCTGT 975  
QY 273 uLeuIleProMet 277  
Db 976 ATCGTCCCGCTT 988

RESULT 38  
BG743135

LOCUS 755 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602634281F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4779189 5', mRNA sequence.

ACCESSION BG743135

VERSION BG743135.1 GI:14053788

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 755)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10636 row: b column: 22

High quality sequence stop: 751.

FEATURES

source

1..755

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clones="IMAGE:4779189"

/lab\_host="DH10B (TI phage-resistant)"

/clone\_lib="NCI\_CGAP\_Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6, Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.

Average insert size 1.5kb Library constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 166 a 233 c 212 g 144 t

ORIGIN

Alignment Scores:

Pred. No.: 1.28e-114 Length: 755

Score: 1225.00 Matches: 225

Percent Similarity: 98.68% Conservative: 0

Best Local Similarity: 98.68% Mismatches: 3

Query Match: 50.25% Indels: 0

DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x BG743135 (1-755)

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QY 21 PheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAsp 40

Db 132 TTCAGCTGGAGGAGATTGAGAGCATACCTCGCCAGCCAGAGGTGGTGGTTCATTGAC 191

QY 41 ArgLysValIleAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIle 60

Db 192 CGCAAGGTTTACAAATCATCAACAAATGGTTCATCCAGCACCGCGGGGGCGAGCGGTGTCATC 251



QY 61 GlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAspLeuGlu 80  
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 QY 101 GlnAspHisGlyLysAsnSerLysLthrGluAspPheArgAlaLeuAtgLysThrAla 120  
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 QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
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 QY 141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTrrIlePro 160  
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 QY 161 ThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrrLeuGlnHis 180  
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 Db 612 GATTATGGCCACCTGCTGCTTACAGAAAACCCCAAGTGAACCACTTGTTCACAAATTC 671  
 QY 201 ValIleGlyHisLeuLysGlyAlaSerAlaAsnTrrPrrAsnHisArgHisPheGlnHis 220  
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 VERSION CA488711.1 GI:24951219  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 1 (bases 1 to 971)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contract: Robert Strausberg, Ph.D.  
 Email: c9abbs-remail.nih.gov  
 Tissue Procurement: Kristi A. Eglund, Ira Pastan  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM14281 row: b column: 23  
 High quality sequence start: 25  
 High quality sequence stop: 562.  
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FEATURES  
 SOURCE

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 Score: 1214.00 Matches: 215  
 Percent Similarity: 98.17% Conservative: 0  
 Best Local Similarity: 98.17% Mismatches: 4  
 Query Match: 49.79% Indels: 0  
 DB: 14 Gaps: 0

US-09-719-601-5 (1-444) x CA488711 (1-971)  
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 QY 187 ValTyrArgLysProLysTrrAsnHisLeuValHisLysPheValIleGlyHisLeuLys 206  
 Db 70 GTCTACAGAAAACCCCAAGTGAACCACTTGTGCCAAATTCCTCATTTGGCCACCTTAAAG 129  
 QY 207 GlyAlaSerAlaAsnTrrPrrAsnHisArgHisPheGlnHisHisAlaLysProAsnIle 226  
 Db 130 GGTGCTCTGCGCAACTGGTGGAAATCATCGCCACTTCCAGCACACGCCAAGCTTAACTC 189  
 QY 227 PheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrrGlnPro 246  
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 Db 250 ATCGATGATCGGCAAGAAAGAGCTGAAATACCTTGCCTTCAATCACACAGCACGAATCTTC 309  
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 QY 287 MetIleValHisLysAsnTrrValAspLeuAlaTrrAlaValSerTyrTyrIleArgPhe 306  
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 QY 307 PheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIle 326  
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 QY 327 ArgPheLeuGluSerHisTrrPheValTrrValThrGlnMetAsnHisIleValMetGlu 346  
 Db 490 AGGTTCTCTGGAGAGCCACTGGTTGTGTGGGTGCACACAGATGAATCACAATCGCTCATGGAG 549  
 QY 347 IleAspGlnGluAlaTyrArgAspTrrPheSerSerGlnLeuThrAlaThrCysAsnVal 366  
 Db 550 ATTGACCAAGAGGCTTACCTGACTGTTTCACTACCTACCTGAGCCACCTTGCACACGTTG 609  
 QY 367 GluGlnSerPhePheAsnAspTrrPheSerGlyHisLeuAsnPheGlnIleGluHis 385  
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 DEFINITION mRNA sequence.  
 ACCESSION BG422898

602450074F1 NTH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4586387 5',  
 mRNA sequence.  
 BG422898

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 Directionally cloned. Priming method: oligo-dT. Average  
 insert size: 1800 bp. Library amplification: 26,000 fold.  
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
 Bungkook Lee & Ira Pastan: Discovery of new breast  
 cancer genes encoding membrane and secreted proteins.  
 Manuscript submitted."

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VERSION      BG422898.1  GI:13329404
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 753)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: gcapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM320 row: d column: 20
High quality sequence stop: 677.
FEATURES
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                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 175 a 224 c 190 g 164 t

#### Alignment Scores:

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Pred. No.: 2,72e-113 Length: 753
Score: 1212.00 Matches: 223
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 1
Query Match: 49.71% Indels: 1
DB: 10 Gaps: 0
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US-09-719-601-5 (1-444) x BG422898 (1-753)

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Db 62 GTGTT-GTTCTGGCGAATGGCAGCCCATCGAGTACGGCAAGAAAGCTGAATACCTG 120
Qy 258 ProTyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProPheLeuLeuProMet 277
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Qy 278 TyrPheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAla 297
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Qy 298 TrpAlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeu 317
Db 241 TGGCCCGTCAGCTACTACATCCGGTTCTTCATCACCTACATCCCTTCTACCGCATCCCG 300
Qy 318 GlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpVal 337
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Qy 358 SerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGly 377
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Qy 378 HisLeuAsnPheGlnIleGluHisHisIleuPheProThrMetProAspHisAsnLeuHis 397
Db 481 CACCTTAACTTCCAGATTGAGCACCACTCTTCCACCACTGCCCGCCACACTTACAC 540
Qy 398 LysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLys 417
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Search completed: December 10, 2003, 20:05:52

Job time : 1981 secs



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Db 2055 TCTCTTGTGACTCAGCAGAGGAGTGGCCAGCTTTCAGGAGGGGCGGCGGCTGCGCTGGAGG 2114  
Qy 2330 CTCAGCCACCGCTCTCAGCTTTTCTCAGGCTGCTCTGAGGTCAGGTCAGGTCAGGTCAGG 2389  
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Qy 2390 TGACCTCTCTCCAAAGGCTCTGTTATCAGCTGGGAGTGGCCAGTTCCTCTGGCCATTT 2449  
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## RESULT 2

US-10-191-513A-7  
; Sequence 7, Application US/0191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1843  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-7

Query Match 57.5%; Score 1830.4; DB 15; Length 1843;  
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| Db | 1    | GTCTTTTACTTTGGCAATGCTGATTCCTACCTCATACAGCGCTTTGTCCTTGTAC        | 60   |
| Qy | 690  | TCTCAGCCCAAGCTGCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAA           | 749  |
| Db | 61   | TCTCAGGCCCAAGCTGCTGCAACATGATTATGGCCACCTGCTGTCTACAGAAA          | 120  |
| Qy | 750  | CCCAAGTGGAAACCACTTTGTCACAAATTCGTATTGGCCACATTAAGAGGTGCTCTGCC    | 809  |
| Db | 121  | CCCAAGTGGAAACCACTTTGTCACAAATTCGTATTGGCCACATTAAGAGGTGCTCTGCC    | 180  |
| Qy | 810  | AACGTGGTGAATCATCGCCACTTCCAGCACACGCGCAAGCTTAACATCTCCACAGGAT     | 869  |
| Db | 181  | AACGTGGTGAATCATCGCCACTTCCAGCACACGCGCAAGCTTAACATCTCCACAGGAT     | 240  |
| Qy | 870  | CCCCGATGTGAACATGCTGCAGCTGTTTGTCTGGGCGAATGGCAGCCCATCGAGTACGGC   | 929  |
| Db | 241  | CCCCGATGTGAACATGCTGCAGCTGTTTGTCTGGGCGAATGGCAGCCCATCGAGTACGGC   | 300  |
| Qy | 930  | AAGAAGAGCTGAATACCTGCCCTACAAATCAGCACGACCAAGCTTAACATCTTCCTGATTGG | 989  |
| Db | 301  | AAGAAGAGCTGAATACCTGCCCTACAAATCAGCACGACCAAGCTTAACATCTTCCTGATTGG | 360  |
| Qy | 990  | CCGCGGTGCTCATCCCATGATATTTCCAGTACAGATCATCATGACCATGATCGTCCAT     | 1049 |
| Db | 361  | CCGCGGTGCTCATCCCATGATATTTCCAGTACAGATCATCATGACCATGATCGTCCAT     | 420  |
| Qy | 1050 | AAGAAGCTGGGTGGACCTGGCGTGGCGGTAGCTACTACATCCGGTTCTTCATCACCTAC    | 1109 |
| Db | 421  | AAGAAGCTGGGTGGACCTGGCGTGGCGGTAGCTACTACATCCGGTTCTTCATCACCTAC    | 480  |
| Qy | 1110 | ATCCCTTTCTAGGCTACCTGGGAGCCCTCTTTCTCACTTCACTCAGTTCCCTGGAG       | 1169 |
| Db | 481  | ATCCCTTTCTAGGCTACCTGGGAGCCCTCTTTCTCACTTCACTCAGTTCCCTGGAG       | 540  |
| Qy | 1170 | AGCCACTGGTTGTGTGGGTCAACAGATGAATCAATGCTGATGGAGATTGACAGGAG       | 1229 |
| Db | 541  | AGCCACTGGTTGTGTGGGTCAACAGATGAATCAATGCTGATGGAGATTGACAGGAG       | 600  |

|    |      |  |      |
|----|------|--|------|
| Qy | 1230 | GCCTACCGTGACTGTTTCACTAGCCAGTGCAGAGCCACCTGCAACGTTGGAGCAGTCTTCT  | 1289 |
| Db | 601  | GCCTACCGTGACTGTTTCACTAGCCAGTGCAGAGCCACCTGCAACGTTGGAGCAGTCTTCT  | 660  |
| Qy | 1290 | TTCAACGACTGGTTTCACTAGCAGACCTTAACTTCCAGATTGAGCAGCAGCTTCTTCCCACC | 1349 |
| Db | 661  | TTCAACGACTGGTTTCACTAGCAGACCTTAACTTCCAGATTGAGCAGCAGCTTCTTCCCACC | 720  |
| Qy | 1350 | ATGCCCGGACAACTTACCAAGATCGCCCGCTGCTGCTGAAGTCTCTATGTGCCAAGCAT    | 1409 |
| Db | 721  | ATGCCCGGACAACTTACCAAGATCGCCCGCTGCTGCTGAAGTCTCTATGTGCCAAGCAT    | 780  |
| Qy | 1410 | GGCATTTGAATACAGAGAGAGCCCTACTAGAGCCCTGCTGGACATCATCAGTCTCCCTG    | 1469 |
| Db | 781  | GGCATTTGAATACAGAGAGAGCCCTACTAGAGCCCTGCTGGACATCATCAGTCTCCCTG    | 840  |
| Qy | 1470 | AAGAAGTCTGGGAAAGCTGTGCTGAGAGCCCTTACCTTCACAAAATGAAGCCACAGCCCCGG | 1529 |
| Db | 841  | AAGAAGTCTGGGAAAGCTGTGCTGAGAGCCCTTACCTTCACAAAATGAAGCCACAGCCCCGG | 900  |
| Qy | 1530 | GACACCGTGGGAAAGGGTGCAGTGGGGTATGGCCAGAGGAATGATGGCTTTTGTTC       | 1589 |
| Db | 901  | GACACCGTGGGAAAGGGTGCAGTGGGGTATGGCCAGAGGAATGATGGCTTTTGTTC       | 960  |
| Qy | 1590 | TGAGGGGTGTCGAGAGAGCTGCTGTATGCACTGTCTACGGACCCCATGTTTGGATCTTCT   | 1649 |
| Db | 961  | TGAGGGGTGTCGAGAGAGCTGCTGTATGCACTGTCTACGGACCCCATGTTTGGATCTTCT   | 1020 |
| Qy | 1650 | CCCTTTCT   | 1709 |
| Db | 1021 | CCCTTTCT   | 1080 |
| Qy | 1710 | CTGCCCTCCCTCAGCGTCAGCCATCAGCCATGAGCCCTCCAGAGCTCTCCCTAGCCCTTC   | 1769 |
| Db | 1081 | CTGCCCTCCCTCAGCGTCAGCCATCAGCCATGAGCCCTCCAGAGCTCTCCCTAGCCCTTC   | 1140 |
| Qy | 1770 | TTCCAAGGAGCAGAGAGTGGCCACCGGGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  | 1829 |
| Db | 1141 | TTCCAAGGAGCAGAGAGTGGCCACCGGGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  | 1200 |
| Qy | 1830 | CTAAGATGGGAGGAGACCGGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGGAGCC        | 1889 |
| Db | 1201 | CTAAGATGGGAGGAGACCGGGTCCATGGGTCTGGCTGTGAGTCTCCCTTGGAGCC        | 1260 |
| Qy | 1890 | TGGTCACTAGGCATCACCCCGCTTTTGGTTCTTTCAGATGCTCTTGGGGTTCTATGGGCA   | 1949 |
| Db | 1261 | TGGTCACTAGGCATCACCCCGCTTTTGGTTCTTTCAGATGCTCTTGGGGTTCTATGGGCA   | 1320 |
| Qy | 1950 | GGTCTAGTCCGGAGGAGCCCTGACCTCCGGGCTGGCTTCACTCTCCCTGAGCGGTG       | 2009 |
| Db | 1321 | GGTCTAGTCCGGAGGAGCCCTGACCTCCGGGCTGGCTTCACTCTCCCTGAGCGGTG       | 1380 |
| Qy | 2010 | CCATTGGTCCACCCCTTTCTAGAGAGGCTGCTTTTGTATCAAAAGCTCGGGTCTCCCTCT   | 2069 |
| Db | 1381 | CCATTGGTCCACCCCTTTCTAGAGAGGCTGCTTTTGTATCAAAAGCTCGGGTCTCCCTCT   | 1440 |
| Qy | 2070 | GCAGTCTGGTTAAGTACCCGAGGCTCTCTTAAAGTGTCAAGGCCCCCAGGCCCCGGGC     | 2129 |
| Db | 1441 | GCAGTCTGGTTAAGTACCCGAGGCTCTCTTAAAGTGTCAAGGCCCCCAGGCCCCGGGC     | 1500 |
| Qy | 2130 | ACAGCCAGCCCAAACTTTGGGCTTGGAGAGTCTCTCCACCCCATCACTAGAGTCTCTG     | 2189 |
| Db | 1501 | ACAGCCAGCCCAAACTTTGGGCTTGGAGAGTCTCTCCACCCCATCACTAGAGTCTCTG     | 1560 |
| Qy | 2190 | ACCCTGGGTTTCAAGGCCCCCATTCACCGCTCCCCCACTTTGAGCCTGTGACCTGGG      | 2249 |
| Db | 1561 | ACCCTGGGTTTCAAGGCCCCCATTCACCGCTCCCCCACTTTGAGCCTGTGACCTGGG      | 1620 |
| Qy | 2250 | ACCAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCAGAGGAGTGGCCACCTTCAGGGA      | 2309 |
| Db | 1621 | ACCAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCAGAGGAGTGGCCACCTTCAGGGA      | 1680 |
| Qy | 2310 | GGGGCGGCTGGCTGGAGGCTCAGCCCAACCCCTCAGCTTTTCTCAGGGTGTCTGAGG      | 2369 |

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Db 1681 GGGGCGGCTGGCTGGAGGCTCAGCCACCCCTCCAGCTTTCTCAGGGTGTCTGAGG 1740
Qy 2370 TCCAAAGATTCTGAGCAATCTGACCTCTTCCAAAGGCTCTGTATCAGCTGGGAGTGC 2429
Db 1741 TCCAAAGATTCTGAGCAATCTGACCTCTTCCAAAGGCTCTGTATCAGCTGGGAGTGC 1800
Qy 2430 CAGCCAAATCCCTGGCCATTGGGCCCCCAGGGGGACGTGGGCCCTG 2473
Db 1801 CAGCCAAATCCCTGGCCATTGGGCCCCA-GGGGACGTGGGCCCTG 1843

RESULT 3
US-10-191-513A-6
; Sequence 6, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-6

Query Match 52.6%; Score 1675; DB 15; Length 1686;
Best Local Similarity 99.9%; Fred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 787 GCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCACTTCCAGCACACGCCA 846
Db 1 GCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATCGCACTTCCAGCACACGCCA 60
Qy 847 AGCCTAACATCTTCCAAAGGATCCGATGTGACATGCTGCAGCTGTTTGTCTGGGCG 906
Db 61 AGCCTAACATCTTCCAAAGGATCCGATGTGACATGCTGCAGCTGTTTGTCTGGGCG 120
Qy 907 AATGGCAGCCCATCGAGTACGCAAGAAAGAGCTGAAATACCTGCCCTACAAATCACCAGC 966
Db 121 AATGGCAGCCCATCGAGTACGCAAGAAAGAGCTGAAATACCTGCCCTACAAATCACCAGC 180
Qy 967 AGCAATACTTCTCTGATTGGGCGCGCTGCTCATCCCATGATTTTCAGTACACCAGA 1026
Db 181 AGCAATACTTCTCTGATTGGGCGCGCTGCTCATCCCATGATTTTCAGTACACCAGA 240
Qy 1027 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGAGCTGGCCCTGGGCGCTCAGCTACT 1086
Db 241 TCATCATGACCATGATCGTCCATAAGAACTGGGTGGAGCTGGCCCTGGGCGCTCAGCTACT 300
Qy 1087 ACATCCGGTCTTTCATCATCTCATCCCTTTTACGGGATCTGGGAGCCCTCTTTTCC 1146
Db 301 ACATCCGGTCTTTCATCATCTCATCCCTTTTACGGGATCTGGGAGCCCTCTTTTCC 360
Qy 1147 TCAACTTTCATCAGTTTCTCGAGAGCCACTGTTTGTGGGTTCACAGATGATATCACA 1206
Db 361 TCAACTTTCATCAGTTTCTCGAGAGCCACTGTTTGTGGGTTCACAGATGATATCACA 420
Qy 1207 TCGTCAATGAGATTGACAGGAGGCGCTACCGTGACTGGTTAGTAGCCAGCTGACAGCCA 1266
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Db 421 TCGTCAATGAGATTGACAGGAGGCGCTACCGTACCTGGTTCTAGTAGCAGCTGACAGCCA 480
Qy 1267 CTTGCAACGCTGGAGCAGTCTCTTTCAACGACTGGTTCTAGTGGACACCTTAACTTCCAGA 1326
Db 481 CTTGCAACGCTGGAGCAGTCTCTTTCAACGACTGGTTCTAGTGGACACCTTAACTTCCAGA 540
Qy 1327 TTGAGCAGCAGCTCTTCCACCACCATGCGCGGCACACCTTACACAGATCGCCCGCTGG 1386
Db 541 TTGAGCAGCAGCTCTTCCACCACCATGCGCGGCACACCTTACACAGATCGCCCGCTGG 600
Qy 1387 TGAAGTCTCTATGTGCCAAGCATGGCAATTGAATACCAAGGAGAGCCGCTACTGAGGGCCC 1446
Db 601 TGAAGTCTCTATGTGCCAAGCATGGCAATTGAATACCAAGGAGAGCCGCTACTGAGGGCCC 660
Qy 1447 TGCTGGACATCATCAGTCTCCCTGAGAGTCTGGGAGCTGTGGCTGGAGCGCTTACCTTC 1506
Db 661 TGCTGGACATCATCAGTCTCCCTGAGAGTCTGGGAGCTGTGGCTGGAGCGCTTACCTTC 720
Qy 1507 ACAATGAAGCCACAGCCCCCGGACACCCGTGGGGAGAGGGGTGCAGGTGGGGTGAATGCC 1566
Db 721 ACAATGAAGCCACAGCCCCCGGACACCCGTGGGGAGAGGGGTGCAGGTGGGGTGAATGCC 780
Qy 1567 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGCTGTGTATGCACTGCTCA 1626
Db 781 AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGCTGTGTATGCACTGCTCA 840
Qy 1627 CGGACCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686
Db 841 CGGACCCCATGTTGGATCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Qy 1687 ATAGCACCTGCTCCCTCATGGGACCTGCCCTCCCTCAGCCGTGAGCCATCAGCCATGSCC 1746
Db 901 ATAGCACCTGCTCCCTCATGGGACCTGCCCTCCCTCAGCCGTGAGCCATCAGCCATGSCC 960
Qy 1747 TCCCAAGTGCCTCTAGCCCCCTTTCTCCAAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1806
Db 961 TCCCAAGTGCCTCTAGCCCCCTTTCTCCAAAGAGCAGAGAGTGGCCACCGGGGTGGCTC 1020
Qy 1807 TGTCTTACCTCCACTCTCTGCCCCCTAAAGATGGGAGGAGACCGCGGTGCCATGGGTCTGG 1866
Db 1021 TGTCTTACCTCCACTCTCTGCCCCCTAAAGATGGGAGGAGACCGCGGTGCCATGGGTCTGG 1080
Qy 1867 CTTGTGAGTCTCCCTTGACGCTGCTCACTAGGATCACCCCGCTTTGGTTCTTTCAGA 1926
Db 1081 CTTGTGAGTCTCCCTTGACGCTGCTCACTAGGATCACCCCGCTTTGGTTCTTTCAGA 1140
Qy 1927 TGTCTTGGGGTTCATAGGGGAGTCTTGTGCGGAGGGGCTTGAACCTTCCCGGCT 1986
Db 1141 TGTCTTGGGGTTCATAGGGGAGTCTTGTGCGGAGGGGCTTGAACCTTCCCGGCT 1200
Qy 1987 GGTTCACCTCTCCCTGACGCTGCCATTGGTCCACCTTTTATAGAGAGGCTGCTTTGT 2046
Db 1201 GGTTCACCTCTCCCTGACGCTGCCATTGGTCCACCTTTTATAGAGAGGCTGCTTTGT 1260
Qy 2047 TACAAAGCTCGGGTCTCTCCCTGACGCTCGGTAAAGTACCCGAGGCTCTCTTAAAGT 2106
Db 1261 TACAAAGCTCGGGTCTCTCCCTGACGCTCGGTAAAGTACCCGAGGCTCTCTTAAAGT 1320
Qy 2107 TCAGGGGCCCCAGGCCCCGGGACACAGCAGCCCAACCTTGGGCTCGGAGAGTCTCTC 2166
Db 1321 TCAGGGGCCCCAGGCCCCGGGACACAGCAGCCCAACCTTGGGCTCGGAGAGTCTCTC 1380
Qy 2167 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCACGGGCCCCATTTCCACCGGCTCCC 2226
Db 1381 CACCCCATCACTAGAGTGTCTGACCCCTGGGCTTTTCACGGGCCCCATTTCCACCGGCTCCC 1440
Qy 2227 CAACTTGAAGCTGTGACCTTGGAGCAAAAGGGGAGTCCCTGTCTCTTGTGACTCAGCA 2286
Db 1441 CAACTTGAAGCTGTGACCTTGGAGCAAAAGGGGAGTCCCTGTCTCTTGTGACTCAGCA 1500
Qy 2287 GAGCAGTGGCCACGTTTCAGGGAGGGGCGGCTGGGCTGAGGAGCTCAGGCCACCCCTCCAG 2346
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Db 1501 GAGCAGTGGCCACGTTTCAGGAGGGGCGGCTGGGCTGGAGGCTCAGCCCAACCTCCAG 1560  
QY 2347 CTTTCTCCTCAGGGTGCTCAGGTCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG 2406  
Db 1561 CTTTCTCCTCAGGGTGCTCAGGTCAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG 1620  
QY 2407 CTTCTGTTATCAGTGGGAGTGGCAGCCAAATCCCTGGCCATTGGCCCCCAGGGGACGTG 2466  
Db 1621 CTTCTGTTATCAGTGGGAGTGGCAGCCAAATCCCTGGCCATTGGCCCCCA-GGGGACGTG 1679  
QY 2467 GGGCCCTG 2473  
Db 1680 GGGCCCTG 1686

RESULT 4  
US-10-102-806-232  
; Sequence 232, Application US/10102806  
; Publication No. US2003005421A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P103P1C1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 232  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1337)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1355)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1377)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-102-806-232

Query Match 43.4%; Score 1383.2; DB 15; Length 1474;  
Best Local Similarity 97.2%; Pred. No. 0;  
Matches 1433; Conservative 4; Mismatches 35; Indels 3; Gaps 3;

QY 652 GGATTCTACCTCATCAGCGCCCTTGTCTGTCTACCTCTCAGGCCCAAGCTGGATGGC 711  
Db 1 GGATTCTACCTCATCAGCGCCCTTGTCTGTCTACCTCTCAGGCCCAAGCTGGATGGC 60  
QY 712 TGCACATGATATGCGCACTGTCTGTCTACAGAAACCCAAAGTGGAAACCACTTGTC 771  
Db 61 TGCACATGATATGCGCACTGTCTGTCTACAGAAACCCAAAGTGGAAACCACTTGTC 120  
QY 772 ACAATTTCGTCATGCGCACTTAAAGGTGCTCTGCGCACTGTGGAAATCATCGCCACT 831  
Db 121 ACAATTTCGTCATGCGCACTTAAAGGTGCTCTGCGCACTGTGGAAATCATCGCCACT 180  
QY 832 TCCAGCACCAAGCCCAAGCTTAACATCTTCCAAAGGATCCGATGTGAAACATGCTGCA 891  
Db 181 TCCAGCACCAAGCCCAAGCTTAACATCTTCCAAAGGATCCGATGTGAAACATGCTGCA 240  
QY 892 TGTGTTCTCGGCGAATGGAGCCCATCGAGTACGCGCAAGAAAGCTGAATACCTGC 951  
Db 241 TGTGTTCTCGGCGAATGGAGCCCATCGAGTACGCGCAAGAAAGCTGAATACCTGC 300

QY 952 CCTACAAATCAACGACAGCAATACCTTCTTCTGATTGGGCGCGCTGCTCATCCCATGT 1011  
Db 301 CCTACAAATCAACGACAGCAATACCTTCTTCTGATTGGGCGCGCTGCTCATCCCATGT 360  
QY 1012 ATTTCCAGTACCAAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGAGACCTGGCCT 1071  
Db 361 ATTTCCAGTACCAAGATCATCATGACCATGATCGTCCATAAGAACTGGGTGAGACCTGGCCT 420  
QY 1072 GGGCCGTGAGTACTATCATCCGGTTCCTCATCACTTACATCCCTTCTTCTAGGATCTCTGG 1131  
Db 421 GGGCCGTGAGTACTATCATCCGGTTCCTCATCACTTACATCCCTTCTTCTAGGATCTCTGG 480  
QY 1132 GAGCCCTCCTTTTCTCAACTTCATCAGGTTCTTGAGAGCCCACTGTTTGTGTGGTCA 1191  
Db 481 GAGCCCTCCTTTTCTCAACTTCATCAGGTTCTTGAGAGCCCACTGTTTGTGTGGTCA 540  
QY 1192 CACAGATGAATCATCATCGTCAATGGAGATTGACACAGAGGCGCTACCGTACTGTTCACTA 1251  
Db 541 CACAGATGAATCATCATCGTCAATGGAGATTGACACAGAGGCGCTACCGTACTGTTCACTA 600  
QY 1252 GCCAGCTGACAGCCACCTGCAACCTGGAGCAGTCTTCTTCAACGACTGGTTCAGTGGAC 1311  
Db 601 GCCAGCTGACAGCCACCTGCAACCTGGAGCAGTCTTCTTCAACGACTGGTTCAGTGGAC 660  
QY 1312 ACCTTAACTTCCAGATTGAGCAACCACTTCTTCCCACTGCCCCGCGCACACTTACACA 1371  
Db 661 ACCTTAACTTCCAGATTGAGCAACCACTTCTTCCCACTGCCCCGCGCACACTTACACA 720  
QY 1372 AGATGCGCCCGCTGCTGAGTCTCTATGTCGAGCATGTCATTAATACAGAGGAGC 1431  
Db 721 AGATGCGCCCGCTGCTGAGTCTCTATGTCGAGCATGTCATTAATACAGAGGAGC 780  
QY 1432 CGTACTGAGGGCCCTGCTGAGCATCATCAGTCCCTGAAGAACTCTGGGAAGCTGTGGC 1491  
Db 781 CGTACTGAGGGCCCTGCTGAGCATCATCAGTCCCTGAAGAACTCTGGGAAGCTGTGGC 840  
QY 1492 TGGAGCCCTACTTTCACAAATGAAGCCACAGCCCGCGGACACCTGGGAGGAGGTGCA 1551  
Db 841 TGGAGCCCTACTTTCACAAATGAAGCCACAGCCCGCGGACACCTGGGAGGAGGTGCA 900  
QY 1552 GGTGGGGTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGTGG 1611  
Db 901 GGTGGGGTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGTGG 960  
QY 1612 TGTATGCACTGCTACGAGCCCACTGTTGATCTTCTCCCTTCTCTCTCTCTCTCTCTCT 1671  
Db 961 TGTATGCACTGCTACGAGCCCACTGTTGATCTTCTCCCTTCTCTCTCTCTCTCTCTCT 1020  
QY 1672 CTTCACTCTCCCAATAGCACCTTCCCTCATGCGGACCTGCCCTCCCTCAGCCGTGAGC 1731  
Db 1021 CTTCACTCTCCCAATAGCACCTTCCCTCATGCGGACCTGCCCTCCCTCAGCCGTGAGC 1080  
QY 1732 CATCAGCATGGCCCTCCAGTGCTCTAGCCCTTCTTCCAGAGGACAGAGAGGTGGC 1791  
Db 1081 CATCAGCATGGCCCTCCAGTGCTCTAGCCCTTCTTCCAGAGGACAGAGAGGTGGC 1140  
QY 1792 CACCGGGGTGGCTGCTGCTTACCTTCCACTCTCTGCCCCCTAAAGATGGGAGAGACCCAGC 1851  
Db 1141 CACCGGGGTGGCTGCTGCTTACCTTCCACTCTCTGCCCCCTAAAGATGGGAGAGACCCAGC 1200  
QY 1852 GGTTCATGGGTCTGGCTGTGAGTCTCCCTTGGAGCCTGTGCTCATAGGCACTACCCCGC 1911  
Db 1201 GGTTCATGGGTCTGGCTGTGAGTCTCCCTTGGAGCCTGTGCTCATAGGCACTACCCCGC 1260  
QY 1912 CTTTGGTCTTCAGATGCTCTTGGGTTTCATAGGGGAGGTCTAGTC-GGGCAGGGGCC 1970  
Db 1261 CTTTGGTCTTCAGATGCTCTTGGGTTTCATAGGGGAGGTCTAGTCGGGGCARGGGCC 1320  
QY 1971 CTGACCCCTCCCGCCCTGGCTTCACTCTCCCTG-ACGGCTGCCATTTGGTCCACCTTTTCA 2029  
Db 1321 CTGACCCCTCCCGCCCTTNGCTTAAATCTCCCTGAAACGTTNGCAATTTGGTCCACCTTTNCA 1380  
QY 2030 AGAGAGGCGCTGTTTGTGTACAAAGCTCGGGTCTCCCTCTCGAGCTCGGTAAAGTACCGG 2089



Db 1381 AAAAAGGCTGCTGTATCAAAAGTTCGGGTTTTCCTTCTGACATCGGTTAA-FAACCG 1439  
Qy 2090 AGCCCTCTCTTAAGATGTCAGGCGCCCGAGGCGCG 2124  
Db 1440 AAGGCTCTCTTAAGATGTTTCAAGGCGCCCAAGGCGG 1474

RESULT 5  
US-10-262-617-2  
; Sequence 2, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 1717  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CB1  
US-10-262-617-2

Query Match 21.9%; Score 697.8; DB 15; Length 1717;  
Best Local Similarity 70.7%; Pred. No. 8.2e-190;  
Matches 943; Conservative 0; Mismatches 387; Indels 3; Gaps 1;

Qy 198 CAGGCGAGGGGGCGCGGAGCGGAGTGTCGGTGCCTCCACCTTCAGCTGGAGGAGATT 257  
Db 99 CGCGGGAGGGACCCGCGACCGGCGACGAGTGGCTGTCATCGAGCGCGCGTCTACGACATC 158  
Qy 258 CAGAAAGTAACTGTCGCGACCGACAGTGGGCTGTCATTGATCCGCAAGGTTTACAAATC 317  
Db 159 CGCGGCGACGACCGCGCGGCGACGAGTGGCTGTCATCGAGCGCGCGTCTACGACATC 218  
Qy 318 ACCAAATGTTCCATCCAGACCGCGGCGGCGGCGGCTCATCGGCGACTACGCTGGAGAA 377  
Db 219 AGCCGCTGGGACAGCGGCGACCCAGGGGGGAGCCGCTCATCGGCGACCCAGCGCGCTGAG 278  
Qy 378 GATGCAAGGATGCTTCGCGGCGCTTCCACCTGACCTGGAATTCGTGGCAAGTTTCTTG 437  
Db 279 GACGCGAGGATGCTTCGCGGCTTCCATCAAGATCTCAATTTGTGCGCAAGTTCTTA 338  
Qy 438 AAACCCCTGCTGATTTGGTGAATGCTCCCGGAGGAGCCGAGCGGCGGCGGCGGCGGCGG 497  
Db 339 CAGCCGCTGTTGATTTGAGAGTGGCTCGGAGAGACCCAGCGGCGGCGGCGGCGGCGGCGG 398  
Qy 498 TCAAGATCACTGAGGACTTCGCGGCGCTGAGGAGAGCGGCTGAGGACATGAACCTGTTC 557  
Db 399 GCGGAGCTGTCGAGGACTTCGAGGCGCTGACACGCGGCGGCGGCGGCGGCGGCGGCGG 458  
Qy 558 AAGACCAACACGCTGCTTCT 617  
Db 459 GATGCGAGTCCCACTTCT 518  
Qy 618 GATGCTTCACTGCTTCT 677  
Db 519 GCTGCTCTCTTACT 578  
Qy 678 GTCCTTGTCT 737  
Db 579 ATCCTGGCCATCT 638

Qy 738 GTCTACAGAAAAACCAAGTGGAAACCACTTGTCCAAATTCGTCATTGGCCACTTAAAG 797  
Db 639 ATCTTCAAGAAGTCTCTGGTGAACCAAGTGGCCAGAAAGTTCGTCATTGGGCGAGCTAAAG 698  
Qy 798 GGTGCTCTGCAACTGGTGAATCATCGCCACTTCCAGCACGACCAAGCCTAAACATC 857  
Db 699 GGTCTTCCGCGCACTGGTGAATCTTCCGCACTTCCAGCACGACCAAGCCTAAACATC 758  
Qy 858 TTCCACAAGGATCCCGATGTGAACATCTGCAAGTGTTCCTTGGGCGAATGGCAGCCC 917  
Db 759 TTCCACAAGGATCCCGATGTGAACATCTGCAAGTGTTCCTTGGGCGAATGGCAGCCC 815  
Qy 918 ATCAGTACGCGAAGAGAGTGAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 977  
Db 816 GTCAGTATGCGAAGAGAGAGTGAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 875  
Qy 978 TTCTGTATTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1037  
Db 876 TTCTGTATTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935  
Qy 1038 ATGATGCTCAATAAGAACTGGTGGAGCTGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCT 1097  
Db 936 ATGCTGTGTGTCATGCAAGTGGGCGGAGTTGCTGCTGGGCGCGGAGTTGCTGCTGGGCG 995  
Qy 1098 TTCTGTATTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1157  
Db 996 TTCTGTATTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055  
Qy 1158 AGTTTCCTGGAGAGCACTGGTTTGTGGGTGTCACAGATGAATCATGCTCATGGAG 1217  
Db 1056 AGGTCCTTGGAAAGCACTGGTTTGTGGGTGTCACAGATGAATCATGCTCATGGAG 1115  
Qy 1218 ATTGACCAAGAGGCGCTACCGTGAATTCAGTGGTTCAGTGAACAGTGAACAGTGAAC 1277  
Db 1116 ATCGCGCGAGAGAGCACTGGTTTGTGGGTGTCACAGATGAATCATGCTCATGGAG 1175  
Qy 1278 GAGCAGTCTTCTTCAACGAGCTGGTTCAGTGAACAGTGAACAGTGAACAGTGAACAG 1337  
Db 1176 GAGCCTCTACATTTTCAACAGTGGTTCAGTGAACAGTGAACAGTGAACAGTGAACAG 1235  
Qy 1338 CTCTTCCCGACCATCCCGCGGCGACAACTTACAAAGATCGCGCGCTGGTGAAGTCTCTA 1397  
Db 1236 CTCTTCCCGAGATGCGGAGACAACTTACAGCGGCTGGCGCGCTGGTGAAGTCTCTA 1295  
Qy 1398 TGTGCGCAAGCTGGATTAATACAGGAGAAAGCGCTTACTGAGGCGCTGCTGAGCATC 1457  
Db 1296 TGTGCGCAAGCTGGATTAATACAGGAGAAAGCGCTTACTGAGGCGCTGCTGAGCATC 1355  
Qy 1458 ATCAGTCTCTGAAAGTCTGGGAGCTGCTGGAGCTGCTGGAGCTGCTGGAGCTGCTGGAG 1517  
Db 1356 GTCAGTCTCTGAAAGTCTGGGAGCTGCTGGAGCTGCTGGAGCTGCTGGAGCTGCTGGAG 1415  
Qy 1518 CACAGCGCGCGG 1530  
Db 1416 CAACACCGCGG 1428

RESULT 6  
US-10-262-617-4  
; Sequence 4, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 1928  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CB1  
US-10-262-617-4

Query Match 19.1%; Score 608.2; DB 15; Length 1928;  
Best Local Similarity 66.0%; Pred. No. 5.1e-164; Indels 3; Gaps 1;  
Matches 896; Conservative 0; Mismatches 458;

200 GGCGCAGGCGCGCGCGAGCGAGGTGTCGGTCCCGCCACCTTCAGCTGGAGGAGATCA 259  
101 GGCGCGGAGACCGCGGCTCAGGACCTACCCCGCGCTACTTCACCTGGGAGGAGTGC 160  
260 GAAGCATACCTCGCACCGACAGTGGGTGCTCATTTGACCGCAAGGTTTCAACATCAC 319  
161 CCAGCGCTCAGGTCGGAGAGCGGTGCTAGTATGATCGACCGTAAAGGTGTACAAATCAG 220  
320 CAAATGCTCATCAGACACCGCGGGGCGCAGCGGGTTCATCGGCGCATACGCTGGAGAAGA 379  
221 CGAGTTCAACCGCGGATCCAGGGGGCTCCCGGGTTCATCAGCCATCAGCGCGGACGA 280  
380 TGCAACGAGATGCTTCGGCGCTTCACCGCTGACCTGGAATTCGTGGGCAAGTCTTGAA 439  
281 TGGCAGGATCCCTTTGTGGCTTCACATCAACAAGGGCTTTGTGAAGATATATGAA 340  
440 ACCCTGCTCATTTGGTGAATCGCCCGGAGGAGCCAGCGAGGACCGCAAGAACTC 499  
341 CTCTCTCTGATTTGGAGACTGTCTCCAGAGCAGCCAGCTTTGACCCACCAAGATTA 400  
500 AAAGATCACTGAGGATTCCTCGGCGCTCGAGAGAGCGGTGAGGACATGAACCTGTTCAA 559  
401 AGAGCTGACAGATGATTCGGGAGGTTCGGGCGCACAGTGGAGCGGATGGGCTCATGAA 460  
560 GACCAACAGTGTCTTCCTCTCTCTCTCGGCGCACATCATCGCCCTCGAGAGCATTCG 619  
461 GGCCAAACATGTCTTCTCTGTGTACCTGTGTCGACATCTGCTCTGTGATGGTGCAGC 520  
620 ATGCTTCACTGTCTTCTTACTTTGGCAATGGCTGATTCCTTACCTCATCAAGCGCTTGT 679  
521 CTGCTCAACCTTTGGGTCTTTGGAGCTCTTTTGGCGCTCTCTCTCTCTCTCTCTCT 580  
680 CTTGTCTACTCTCAGGCGCAAGCTGGATGGTGCACATGATTATGGCCACCTGTCTGT 739  
581 GCTCAGTGCAGTTTGGCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 640  
740 CTACAGAAACCCCAAGTGGAAACCACTTGTCCAAATTCGTCAATTTGGCCACTTAAAGG 799  
641 CTTCAGCACTTCAAGTGGAAACCATCTGTACATCATTTTGTGATTTGGCCACCTGAAGG 700  
800 TGCCTCTGCCAATCTGTGGAAATCATCCGCACTTCCAGCACCGCCCAAGCTTAACATCT 859  
701 GGCCCCCGCAGTTGGTGGAAACCATCTGTACATCTTCCAGCACCTGCGCAAGCTTGTCT 760  
860 CCACAGGATCCGATGTGAACATGTCTGCACGT---GTTTGTCTGGCGCAATGGCAGCC 916  
761 CCGCAAGACCCGACATCAACATGATCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 820  
917 CATCGATGACGCGAAGAAAGTGAATACCTGCGCTCAATCAACAGCACCAATACATTT 976  
821 TGTGGAGTTTGGGAAACAGAAAGAAATATATGCGGTACAAACCAACAGCAAAATACAT 880  
977 CTTCTGATTTGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATCATCATGAC 1036  
881 CTTCTTAATTTGGGCCCGCAGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 940  
1037 CATGATCGTCCATGAATCGGTGGACCTGGCTGGCGGTGTAGCTACTACATTCGGTT 1096

## RESULT 7

US-09-822-849A-485/C  
; Sequence 485, Application US/09822849A  
; Patent No. US20020045170A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakar  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6403  
; CURRENT APPLICATION NUMBER: US/09/822,849A  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/195,582  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 598  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 485  
; LENGTH: 1972  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-849A-485

Query Match 19.1%; Score 608.2; DB 9; Length 1972;  
Best Local Similarity 66.0%; Pred. No. 5.2e-164;  
Matches 896; Conservative 0; Mismatches 458; Indels 3; Gaps 1;

200 GGCGGAGGCGCGCGCGAGCGGAGGTGTGGTCCCGCCACCTTCAGCTGGGAGGAGATCA 259  
1865 GGCGCGGAGACCGCGGCTCAGGGACCTTACCCCGCGCTACTTCTACCTGGGACGAGTGC 1806  
260 GAAGCATACCTGCGCACCGGACAGTGGGCTGGTCTATTGACCGCAAGGTTTACAAATCAC 319

Db 1305 CCAGCGCTCAGGTTGCGAGGAGCGGTGGCTAGTGTATCGACCGTAAAGTGTACACATCAG 1746  
Qy 320 CAATATGTTCCATCCAGCACCCGGGGGCGACGCGGTATCGGGCACTACCTGGGAGAGA 379  
Db 1745 CGAGTTCAACCGCGCGCATCCAGGGGGCTCCCGGGTATCAGCCACTACGCGGGCAGGA 1686  
Qy 380 TGCACCGATGCTTCCGCGCTTCCACCTGACCTGGAATTCGTGGCAAGTTCCTTGA 439  
Db 1685 TGCACCGATGCTTCCGCGCTTCCACATCAACAGGGGCTTGTGAAGATGATATGA 1626  
Qy 440 ACCCGCTGATTTGGTGAATCTGGCCCGGAGGACCCAGCCAGGACCAAGCAAGAACTC 499  
Db 1625 CTCTCTCTGATTTGGAGAACTGTCTCCAGAGACGCCAGCTTTGAGCCCAAGAAATA 1566  
Qy 500 AAAGATCACTGAGACTTCGGGCGCTTGGAGAGCGCTGAGACATGAACCTGTTC 559  
Db 1565 AGAGCTGACATGAGTTCCGGGAGCTCGGGGCCACAGTGGAGCGGATGGGCTCATGA 1506  
Qy 560 GACCAACACATGTTCT 619  
Db 1505 GGCCAAACATGCT 1446  
Qy 620 ATGGTTCACTGCT 679  
Db 1445 CTGGCTCACCTTTGGGCTTTGGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1386  
Qy 680 CTTGCTACCTCTCAGGCGCAAGCTGGATGCTGCAACATGATATGCGCCACCTGTCTGT 739  
Db 1385 GCTCAGTCAGTTGAGGCGGAGCTGGCTGCTGCTGACATGACITTTGGCACCTGTCTGT 1326  
Qy 740 CTACAGAAACCCAGTGGAAACCACTTGTCTCCAAATTTGTCTATTCGCGCACITTAAGGG 799  
Db 1325 CTTACGACCTCAAGTGGAAACCACTTGTCTACATCATTTTGTGATGGCCACCTGGAAGG 1266  
Qy 800 TGCCTCTGCACTGCTGGTGAATCATCGGCATCTCCAGCACCCAGCCAGCCATCACTTT 859  
Db 1265 GCGCCCGCGCAGTTGGTGGAAACCACTGCACTTCCAGCACCATGCGCAAGCCCACTGCTT 1206  
Qy 860 CCACAGGATCCGATGTGAACATGCTGC---AGTGTGTTGTTGGCGAATGGCAGCC 916  
Db 1205 CGGCAAGACCCAGACATCAACATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1146  
Qy 917 CATCAGTACGCAAGAGAGAGCTCAATATCTGCTCTCAATCACCAGCAGCAATACTT 976  
Db 1145 TGTGAGCTTGGAAACAGAGAAATATATGCGGTACACACACAGCACAATACTT 1086  
Qy 977 CTTCTGATTTGGCGCGCTGCTCATCCCAATGATTTCCAGTACCAAGATCATCATGAC 1036  
Db 1085 CTTCTTAATTTGGGCGCCAGCCCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1026  
Qy 1037 CATGATCGTCCATAGAGCTGGTGGAGCTGCGCTGGCGGCTGCTACTACTACCTCGGTT 1096  
Db 1025 TGTATCCAGCGAAAGAGTGGTGGACCTTGGCGCTGGATGATTAACCTTCTAGCTCGCTT 966  
Qy 1097 CTTTCATCACTACCTCTCTCTAGGCAATCTGGAGCCCTCTCTCTCTCTCTCTCTCTCT 1156  
Db 965 CTTCTCTCACTTATGTGCCACTATTTGGGCTGAAAGCTTTCTCTGGGCTTTCTCTCATAGT 906  
Qy 1157 CAGGTTCTGGAGAGCACTGGTTTGTGGGTGACACAGATGATCATCATCTCATGGA 1216  
Db 905 CAGGTTCTGGAGAGCACTGGTTTGTGGGTGACACAGATGATCATCATCTCATGGA 846  
Qy 1217 GATTGACCGAGGCGCTACCTGCTGACTGTTTCAGTAGCAGCTGACAGCACTGCAAGCT 1276  
Db 845 CATTGATCATGACCGGAACATGAGCTGGTTCACCCAGCTCCAGGCCACATGCAATGT 786  
Qy 1277 GGAGAGCTCTCTCTCAAGACTGGTTTCACTGAGACACTTAACTTCCAGATTGACACCA 1336  
Db 785 CCACAGTCTGCTCTCAATGACTGGTTTCACTGAGACACTTAACTTCCAGATTGACACCA 726  
Qy 1337 CTTCTTCCCGACCATGCGCGGACCAACTTACAGAGATCGCCCGCTGGTGAAGTCTCT 1396  
Db 725 TCTTTTCCACGATGCTTCGACACAAATACACAAAGTGGCTCCCTTGGTCACTCTCT 666

Qy 1397 ATGTGCCAGCATGGCTTGAATACAGGAGAGCCGCTACTAGGCGCCCTGTGGACAT 1456  
Db 665 GTGTGCCAAGCATGGCTTGAATACAGGAGAGCCGCTACTGTGACGCTTCCGCCGACAT 606  
Qy 1457 CATCAGGTCCCTGAGAAAGTCTGGAAAGCTGTGGCTGGAGCCCTACCTTACAAATGAAG 1516  
Db 605 CATCCACTCACTAAAGGAGTCAGGCGAGCTCTGGCTAGATGCTCTTCTTCCCAATAACA 546  
Qy 1517 CCACAGCCCGGAGACACCGTGGGGAAGGGGTGCAGG 1553  
Db 545 ACAGCCACCTTCCCGAGCTCTGGAAGAGAGGAGGAAG 509

RESULT 8  
US-10-133-937-7  
; Sequence 7, Application US/10133937  
; Publication No. US2003020728A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,  
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES  
; FILE REFERENCE: 11613.56US01  
; CURRENT APPLICATION NUMBER: US/10/133,937  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 4213  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-133-937-7

Query Match 19.1%; Score 608.2; DB 13; Length 4213;  
Best Local Similarity 66.0%; Pred. No. 7, 3e-164;  
Matches 896; Conservative 0; Mismatches 458; Indels 3; Gaps 1;

Qy 200 GGGCGAGGGGGCGCGGAGCGGAGGTGTGCTGCTGCCACCTTCAGCTGGGAGGAGATTCA 259  
Db 98 GGGCGCGAGAGCGCGGCTCAGGAGACCTTACCCCGCGCTTACCTCCTGGAGCAGGTGCG 157  
Qy 260 GAAGATAACCTTGGCAGCAGAGTGGGCTGTGCTTATGACCGCAAGGTTTACAAATCAC 319  
Db 158 CAGCGCTCAGGCTGCGAGAGCGGTGTGCTAGTATCGACCGTAAAGTGTACAAATCAG 217  
Qy 320 CAAATGGTCCATCCAGCACCCGGGGGCGAGCGGCTCATCGGCTACGCTGGAGAGA 379  
Db 218 CGAGTTTCAACCGCGGCTATCCAGGGGGCTCCCGGGTCAFCAGCCACTACCGCGGCGAG 277  
Qy 380 TGCAACGGATGCTTCCGCGCTTCCACCGCTGACCTGGAATTCGTGGGCAAGTTCCTTGA 439  
Db 278 TGCAAGATCCCTTTGTGGCTTCCACATCAAGGGCTTGTGAAGATGATATGA 337  
Qy 440 ACCCTGCTGATTTGGTGAACCTGCGCGGAGGAGCCAGCCAGGACCAAGCAAGAACTC 499  
Db 338 CTCTCTCTGATTTGGAGAACTGTCTCCAGAGCAGCCCGCTTTGAGCCCAAGAAATA 397  
Qy 500 AAAGATCACTGAGACTTCCGGGCGCTGAGGAAGAGCGCTGAGGACATGAACCTGTTC 559  
Db 398 AGAGCTGACAGATGATTTCCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGCTCATGA 457  
Qy 560 GACCAACACAGTGTCTTCT 619  
Db 458 GGCCAAACATGCT 517  
Qy 620 ATGTTTCACTGCT 679  
Db 518 CTGCTCACCTTTGGGCTCTTTGGAGCTCTTTTGGCGCTTCTCTCTCTCTCTCTCTCTCT 577

680 CTTTGCTACCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATATGGCCACTGCTGT 739  
Db |||||  
578 GCTCAGTGCAGTTTCAGGCCCAAGCTGGCTGGCTGCAACATGATATGGCCACTGCTGT 637  
Qy |||||  
740 CTACAGAAACCAAGTGGAAACCACTGTGCAAAATTCGTCATTTGGCCACTTAAAGG 799  
Db |||||  
638 CTTACAGCACTCAAGTGGAAACCACTGTGCAAAATTCGTCATTTGGCCACTTAAAGG 697  
Qy |||||  
800 TGCCTCTGCCAACTGTGGAATCATCGCACTTCCAGCACCGCAAGCCCTAAACATCTT 859  
Db |||||  
698 GGCCTCCGCGAGTTGTGGAAACCACTGTGCAAAATTCGTCATTTGGCCACTTAAAGG 757  
Qy |||||  
860 CCACAGGATCCGAGTGAACATGCTGCG---ACGTTGTTGTTCTGGCGAATGGCAGCC 916  
Db |||||  
758 CCGAAGACCCAGACATCAACATGATCCCTCTCTTTGCTTTGGGAAGATCTCTC 817  
Qy |||||  
917 CATCGAGTACGGAAGAGTGAATACCTGCTCAATCAATCAACAGCAAGATACCTT 976  
Db |||||  
818 TGTGGAGCTTGGGAACAGAAATAATATATGCGGTACCAACACAGCAAGATACCTT 877  
Qy |||||  
977 CTTCTCTGATGGCCCGCTGCTATCCCATGATATTTCCAGTACCATCATGATGAC 1036  
Db |||||  
878 CTTCTCTGATGGCCCGCTGCTATCCCATGATATTTCCAGTACCATCATGATGAC 937  
Qy |||||  
1037 CATGATCGTCCATAAGAACTGGTGGACCTGGCTGGCTGAGTACCTACATCGGTT 1096  
Db |||||  
938 TGTATCCAGGAAGAGTGGTGGACCTGGCTGGCTGATGATTAACCTTCTACGTCGCTT 997  
Qy |||||  
1097 CTTTATCACTATCACTCTTCTACGCTATCTGGAGCCCTCTTTCTTCACTTCACT 1156  
Db |||||  
998 CTTCTCTCACTATGTCGCACTATTTGGGCTGAAAGCCTTCTGGGCTTTTCTTCACT 1057  
Qy |||||  
1157 CAGTCTCTGAGAGCCACTGGTTGTTGGTGGTGCACACAGATGAATCACTCTCATGGA 1216  
Db |||||  
1058 CAGTCTCTGAGAGCCACTGGTTGTTGGTGGTGCACACAGATGAATCACTCTCATGGA 1117  
Qy |||||  
1217 GATTGACAGAGCCCTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276  
Db |||||  
1118 CATTGATCATGACCGGAACATGAGTGGTGTTCACCCAGCTCCAGCCACATGCAATGT 1177  
Qy |||||  
1277 GGAGCAGTCTCTTCTTCAAGCACTGGTTGAGTGGACACTTAACTTCCAGATTCAGACCA 1336  
Db |||||  
1178 CCACAGTCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1237  
Qy |||||  
1337 CTTCTTCCCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1396  
Db |||||  
1238 TCTTTTCCCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1297  
Qy |||||  
1397 ATGTGCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1456  
Db |||||  
1298 GTGTGCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1357  
Qy |||||  
1457 CATCAGTCTCTGAGAGTGTGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1516  
Db |||||  
1358 CATCACTCACTAAGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 1417  
Qy |||||  
1517 CCACAGCCCGGACACCTGGTGGAGAGGAGTGGAGGAGTGGAGGAGTGGAGGAG 1553  
Db |||||  
1418 ACAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454

## RESULT 9

US-10-191-513A-1

; Sequence 1, Application US/10191513A

; Publication No. US20030104596A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pardeep

; APPLICANT: Leonard, Amanda E.

; APPLICANT: Huang, Yung-Sheng

; APPLICANT: Tapas, Das

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295.US.D3

; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-1

Query Match 18.9%; Score 602.8; DB 15; Length 1335;

Best Local Similarity 66.6%; Pred. No. 1.6e-162;

Matches 878; Conservative 0; Mismatches 437; Indels 3; Gaps 1;

Qy 200 GGGGAGGGGGCCCGGAGCGGAGGTGTGGTCCCACTTTCAGCTGGGAGGAGATTCA 259  
Db 18 GGGCGCGAGACCGGGCTCAGGGACCTACCCCGGCTACTTCACTGGGAGGAGTGGC 77  
Qy 260 GAAGCATAACTGCGGACCGGACAGTGGGCTGTGATTCAGCGCAAGGTTTACAATCAC 319  
Db 78 CCAGCGCTCAGGTCGCGAGGAGCGTGGCTAGTGTGACCGGTAAAGGTGTACAACATCAG 137  
Qy 320 CAATGTCCTCATCCAGACACCGGGGGGAGCGGCTCATCGGCACTACGCTGGAGAGA 379  
Db 138 CGAGTTCACTCCCGCGGATCCAGGGGCTCCCGGCTCATCAGCCACTACGCGGGCAGGA 197  
Qy 380 TGCACCGATGCTTCCGCGCTTCCACCTGACCTGGAATTCGTGGCAAGTTCCTGAA 439  
Db 198 TGCCACCGATGCTTGGGCTTCCACATCAACAGGGGCTTGTGAAGATGATATGAA 257  
Qy 440 ACCCTGCTGATGTGTAACCTGGGAGGAGCGGAGGAGCCAGGACACGCAAGAACTC 499  
Db 258 CTCTCTCTGATGTGAGAACTGTCTCCAGAGCAGCCAGCTTTGAGCCACCAAGATAA 317  
Qy 500 AAAGATCACTGAGGACTTCCGGGCTTGAAGAGACCGGCTGAGGACATGAACCTGTTCAA 559  
Db 318 AGAGCTGACAGATGATGTTCCGGAGCTCGGGGACACAGTGGAGCGGATGGGGCTCATGAA 377  
Qy 560 GACCAACCACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619  
Db 378 GGGCAACCACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437  
Qy 620 ATGGTTCACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679  
Db 438 CTGGCTCACTCTTGGGCTTGGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 497  
Qy 680 CTTTCT 739  
Db 498 GCTCAGTCAGTTCAGGCGGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 557  
Qy 740 CTACAGAAACCCCAAGTGGAAACCACTTGTCCAAATTCGTCATTTGGCCACTTAAAGG 799  
Db 558 CTTTACAGCTCAAGTGGAAACCACTTGTCTACATCATTTTGTGATTTGGCCACTTAAAGG 617  
Qy 800 TGCCTCTGCAACTGCTGGATCATCGGCACTTCAGGACCAAGCCAGCCCAAGCTTAACTTT 859  
Db 618 GGGCCCCGCGAGTTGTTGGAAACCACTTTCAGGACCACTTCAGGACCACTTCAGGACCACTT 677  
Qy 860 CCACAGGATCCGATGTGAACATGCTGCG---ACGTTGTTGTTCTGGGCGAATGGCAGCC 916  
Db 678 CCGAAGACCCAGACATCAACATGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737  
Qy 917 CATCGAGTACGGAAGAGTGAATCACTGCGCTTACAAATCAATCAACAGCAAGATACCTT 976  
Db 738 TGTGGAGCTTGGGAACAGAAATAATATATGCGGTACCAACACAGCAAGATACCTT 797  
Qy 977 CTTCTCTGATTTGGGCGCGCTGCTCATCCCCATGATTTTCCAGTACCATCATGATGAC 1036

|      |    |   |      |
|------|----|---|------|
| 798  | DB | CTTCTTAATTGGGCCCCCAGCCCTTGCTGCTCTCTACTTCCAGTGGTATATTCTTATTT     | 957  |
| 1037 | QY | CATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGGGCCGTGAGTACTATACATCCGGTT  | 1096 |
| 858  | DB | TGTTATCCAGCGAAGAGTGGGTGGACTTGGCCCTGGATGATTACCTTCTACGTCGCGTT     | 917  |
| 1097 | QY | CTTCATCAGCTACATCCCTTTCTTAGGCATCTCTGGGAGCCCTCCITTTCTCTCAACTCAT   | 1156 |
| 918  | DB | CTTCTCTCACTATGTGCGCACTATGGGCGCTGAAGCCCTTCTGGGCGCTTTCTTCATAGT    | 977  |
| 1157 | QY | CAGGTTCTCTGGAGAGCCACTGGTTTGTGTGGGTACACAGATGAATCAATCTCATGGA      | 1216 |
| 978  | DB | CAGGTTCTCTGGAAGCAACTGGTTTGTGTGGGTGACACAGATGAACCATATTCCTCCATGCA  | 1037 |
| 1217 | QY | GATTGACCAAGGAGCCCTACCGTCACTGGTTTCAGTAGCCAGCTCAGACGCCACCTGCAACGT | 1276 |
| 1038 | DB | CATTGATCATGACCGGNAACATGACTGGGTTTCCACCCAGCTCCTGGCCACATGCAATGT    | 1097 |
| 1277 | QY | GGAGCAGTCTCTTTCAACGACTGGTTTCAGTGGACACCTTAACTTCAGAGATTGAGACCCA   | 1336 |
| 1098 | DB | CCACAAAGTCTGCGCTTCAATGACTGGTTTCAGTGGACACCTCAACTTCAGAGATTGAGACCA | 1157 |
| 1337 | QY | CGTCTTCCCCACCATGCCCCGGACAACTTACACAAGATGCCCGCGCTGGTGAAGTCTCT     | 1396 |
| 1158 | DB | TCITTTTCCACGATGCTCGACACATATTACCACAAAGTGGTCCCTCGTGGTGAAGTCCCTT   | 1217 |
| 1397 | QY | ATGTGCCAAGCATGGCAATTGAATACCAAGGAGAGACCGCTACTGAGGGCCCTGCTGGACAT  | 1456 |
| 1218 | DB | GTGTGCCAAGCGTGGCATAGATACCAAGTCCACGCCCCCTCTGTACGCGCTTCCCGACAT    | 1277 |
| 1457 | QY | CATCAGTCTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGAGCGCTTACCTTCACAAAATGA   | 1514 |
| 1278 | DB | CATCCACTCACTAAGGAGTCAAGGCGAGCTCTGGCTAGATGCGCTATCTTCACCAATAA     | 1335 |

RESULT 10

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US-91-981-876-63
; Sequence 63, Application US/09981876
; Patent No. US2002016469A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633

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| Query Match               | 17.8%; Score 565.8; DB 10; Length 1478;                                  |
|---------------------------|--|
| Best Local Similarity     | 71.2%; Pred. No. 7, 2e-152;  |
| Matches 817; Conservative | 0; Mismatches 323; Indels 8; Gaps 5;                                     |
| QY                        | 384 ACGGATGCTTCCGGCCCTTCCACCCCTGACCTGGAATTCGTGGGCAACTTCTTGAACCC 443      |
| DB                        | 16 ACGGATGCTTCCGGCCCTTCCCAATCAAGATCTCAATTTGTGCGCAAGTTCTTACAGCCC 75       |
| QY                        | 444 CTGCTGATTTGGTGAATGCGCCCGGAGAGCCAGCCAGGACCCAGCGCAAGAACTCAAAG 503      |
| DB                        | 76 CTGTTGATTTGGAGAGTGTGCTCGGAGNACCCAGCCAGGATGGACCCCTGAATGC--GC 133       |
| QY                        | 504 ATCACTGAGGACTTCGGGCCCTGAGGAAGACGGGTGAGGACATGAACCTGTTCAAGACC 563      |
| DB                        | 134 ATGGTCGAGGACTTCGAGCCCTGCACAGGAGCGGAGGACATGAAGCTGTTGATGCC 193         |
| QY                        | 564 AACACGTTGTTCTTCCTCTCTCTGCGCCACATCATCGCCCTCGAGAGCAATTCGATGG 623       |
| DB                        | 194 AGTCCACACCTTCTTTCCTTCTTCTGCGGCAATCTCGCCCATGAGGTCGTGCGCTGG 253        |
| QY                        | 624 TTCACCTGTCTTCTTACCTTTTGGCAATGGCTGGATTCCTA--CCCTCATCAGGCCCTTTGTCT 682 |
| DB                        | 254 CTCCTTATCTACCTCTGGGTCTGGGTGGTGGCCAGTGGCCCTGCGCCCTTCATCCT 313         |
| QY                        | 683 TGTACTCTTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACTCTCTGTCTA 742       |
| DB                        | 314 GGCCATCTCTCAGGCTCAGTCTGTGTGTGTGACGATGACCTGGGGCA--TGTCTCATCTT 372     |
| QY                        | 743 CAGAAACCAAGTGGAAACCACTTGTCCACAAATTCGTTCATTGGCCACTTAAAGGGTGC 802      |
| DB                        | 373 CAAGAAGCTGTGGAAACCACTGTGCCCCAGAGTTCGTGATGGGGGACGCTAAAGGGCTT 432      |
| QY                        | 803 CTCCTGCAACTGTGGAAATCATCGCCACTTCGAGCAACAAGCCAGCCTTAACTCTTCCA 862      |
| DB                        | 433 CTCGCGCACTGGTGGAACTTTCGCGCACTTCCAGCAACCCAGCCCAAGCCCAATCTTCCA 492     |
| QY                        | 863 CAGAGATCCCGATGTGAACATGTGACGCTGTGTTGTTCTGGGCGAATGGCAGCCCATCGA 922     |
| DB                        | 493 CAAAGACCCAGAGCTGACGCTGGCGCCGCTCTTCTCTTGGGGGA---GTCATCCGTGCA 549      |
| QY                        | 923 GTACGGCAAGAAGAGTGAATACCTTGCOCCTACAATCACACAGCAGAAATATCTTCTCT 982      |
| DB                        | 550 GTATGGCAAGAAGAAACGAGATACCTACCTACAACACAGCAGCACCCTGTACTTCTTCT 609      |
| QY                        | 983 GATTGGCCCGCGCTGCTCATCTCCCATGTATTTCCAGTACCAGATCATCATGACCATGAT 1042    |
| DB                        | 610 GATCGGCCCGCGCTGCTCACTCCCTGGTGAATTTGAGTGGGAAAATCTGGCGGTACATGCT 669    |
| QY                        | 1043 CGTCCATAAGAATCGGTGGACCTTGGCCCTGGGCGGTGAGTACTACATCGGTTCTTCAT 1102    |
| DB                        | 670 GGTGTGATGCATGTGGCGGATTTGTCTCTGGCGCGCAGCTTCTATGCCCGCTTCTTCTT 729      |
| QY                        | 1103 CACCTACATCCCTTTCTACGGCATCTTGGAGCGCTCTCTTTCTCTCAACTTCATCAGTT 1162    |

Db 730 ATCTACCTCCCTCTCTACGGGCTCCCTGGGTGCTGCTCTCTTTGTTGCTGTGAGGGT 789  
QY 1163 CTTGGAGAGCCACTGTTTGTGGGTACACAGATGAATCATCATCGTCATCGGATTTGA 1222  
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QY 1223 CCAGGAGGCTACCGTGACTGTTTCAAGTACAGGAGGCTGAGGAGGCTGAGGAGG 1282  
Db 850 CCAGGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 909  
QY 1283 GTCTTTCTTCAAGCACTGTTTCAAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGG 1342  
Db 910 CTCACTTTTCAAGCACTGTTTCAAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGG 969  
QY 1343 CCCACCATCCCGGACACAACTTACACAGATGCGCCCGCTGGTGAAGTCTCTATGTGC 1402  
Db 970 CCCAGGATCCCGAGACACAACTTACACAGATGCGCCCGCTGGTGAAGTCTCTATGTGC 1029  
QY 1403 CAGCATGGATTTGAATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1462  
Db 1030 CAAGCAGGCTCAGCTACAG-ATGAAGCCCTTCCCTCAGCCGCTGGTGAAGTCTCTATGTGC 1088  
QY 1463 GTCCCTGAAGAGTCTGGTGAAGTCTGGTGAAGTCTGGTGAAGTCTGGTGAAGTCT 1522  
Db 1089 GTCCCTGAAGAGTCTGGTGAAGTCTGGTGAAGTCTGGTGAAGTCTGGTGAAGTCT 1148  
QY 1523 CCCCGGGG 1530  
Db 1149 CCCAGGCG 1156

RESULT 11

US-09-148-545-63  
; Sequence 63, Application US/09148545  
; Publication No. US20030027132A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: PZ001P1  
; CURRENT APPLICATION NUMBER: US/09/148,545  
; CURRENT FILING DATE: 1998-09-04  
; EARLIER APPLICATION NUMBER: FCT/US98/04482  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,617

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; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER APPLICATION NUMBER: 60/043,674  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
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; EARLIER APPLICATION NUMBER: 60/043,315  
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; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
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; EARLIER FILING DATE: 1997-08-22



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EARLIER APPLICATION NUMBER: 60/056,845  
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EARLIER APPLICATION NUMBER: 60/056,892  
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EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 05-Sep-1997  
EARLIER APPLICATION NUMBER: 60/047,599  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER APPLICATION NUMBER: 60/056,862

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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 280  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 63  
LENGTH: 1478

Query Match 17.8%; Score 565.8; DB 11; Length 1478;  
Best Local Similarity 71.2%; Pred. No. 7.2e-152;  
Matches 817; Conservative 0; Mismatches 323; Indels 8; Gaps 5;

QY 384 ACGGATGCTTCCGCGCTTCCACCTGACCTGGAAATCGTGGCAAGTTCTTGAACCC 443  
DB 16 ACGGATGCTTCCGCTTCCATCAAGATCTCAATTTGTGCGCAAGTTCTTGAACCC 75  
QY 444 CTGCTGATTGTTGAACTGCGCCCGGAGAGCCGAGGACCCAGGACCCGCAAGAACTCAAG 503  
DB 76 CTGTTGATTGGAGAGCTGGCTCCGGAAGAACCCAGCAGGATGGACCCCTGAATGC--GC 133  
QY 504 ATCACTGAGGACTTCCGGGCGCTGAGGAAGAGCGGCTGAGGACATGAACCTGTTCAAGACC 563  
DB 134 ATGTCGAGGACTTCCGAGCCCTGCACCAGGACCCGAGGACATGAAGCTGTTGATGCC 193  
QY 564 AACACGTTGTTCT 623  
DB 194 AGTCCACCTTCTTTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 253  
QY 624 TTCCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 682  
DB 254 CTCCTTATCTAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313  
QY 683 TGCTACCTCTCAGGCCCAAGCTGGATGGCTGGAACATGATTATGGCCACCTGTCTGTCTA 742  
DB 314 GGCCATCTCTCAGGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372  
QY 743 CAGAAACCCAGTGGAAACCACTTGTCCACAAATTCCTCATTTGGCCACTTAAAGGGTGC 802  
DB 373 CAAGAGWCTGTTGGAAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432  
QY 803 CTCTGCCAACTGGTGGAAATCATTCGCCACTTCCAGCACCCAGCCAGCCTTAACATCTTCCA 862  
DB 433 CTCCGCCACTGTTGGAACTTCCGCCACTTCCAGCACCCAGCCAGCCTTAACATCTTCCA 492  
QY 863 CAGGATCCGATGTAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922  
DB 493 CAAGACCCAGACGTGACGGTGGCCCGCTTCTTCTCTCTGGGGA--GTCTCGGTGCA 549  
QY 923 GTACGGCAAGAAAGCTGAAATACCTGCCCTTACAAATCAACAGCACGAATCTTCTTCTCT 982  
DB 550 GTATGGCAAGAAAGCTGAAATACCTGCCCTTACAAATCAACAGCACGAATCTTCTTCTCT 609  
QY 983 GATTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042  
DB 610 GATCGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669  
QY 1043 CGTCCATAAGAACTGGGTGGACCTGGCCCTGAGCTACCTAGCTACCTAGCTACCTAGCT 1102  
DB 670 GGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729  
QY 1103 CAGCTACATCCCTTCTACGGCATCTGGGAGCCCTCTCTTCTTCTTCTTCTTCTTCTTCTT 1162  
DB 730 ATCTTACCTCCCTTCTACGGCATCTGGGAGCCCTCTTCTTCTTCTTCTTCTTCTTCTTCT 789  
QY 1163 CTTGGAGAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222

Db 790 CTGGAAGCCACTGCTGTTGGATCACAGATGACATCCCAAGGAGATCGG 849  
QY 1223 CCAGGAGGCTACCGTGAAGTGTTCAGTAGCAGCTGACAGCCACTGCAACGTTGGAGCA 1282  
Db 850 CCACGAGAGCAACCGGACTGGTTCAGCTCAGCTGGCAGCCACTGCAACGTTGGAGCC 909  
QY 1283 GTCTCTTTCACAGTGTGTTTCAGTGGACACCTTAACTTCAGATGAGCACCCTCTT 1342  
Db 910 CTCACTTTTCACTGTTTCAGGGGCACTCAACTTCAGATCAGACCACTCTT 969  
QY 1343 CCCCACATGCCCCGCGCAACTTACACAGATGCCCCGCTGGTGAAGTCTCTATGTGC 1402  
Db 970 CCCCAGATGCGGAGACACAACTACAGCGGTGGCCCGCTGGTCAAGTCTGTGTGC 1029  
QY 1403 CAGCATGCTATGATACCAAGGAGCGCTACTGAGGCGCTGTGACATCATCAG 1462  
Db 1030 CAGCAGCGCTCAGCTAGCA-ATGAGCCCTTCTCACCCTGGTGGACATCGTCAG 1088  
QY 1463 GTCCCTGAAGAAGTCTGGGAAGCTGTGGCTGGAGCGCTTACCTTACAAATGAAGCCACAG 1522  
Db 1089 GTCCCTGAAGAAGTCTGGTGACATCTGGCTGGAGCGCTTACCTTACATCAGTGAAGCAACA 1148  
QY 1523 CCCCCGGG 1530  
Db 1149 CCAGGCG 1156

RESULT 12  
US-09-604-287A-313  
; Sequence 313, Application US/09604287A  
; Patent No. US2002006487A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-313

Query Match 13.9%; Score 443.6; DB 9; Length 456;  
Best Local Similarity 99.1%; Pred. No. 6.1e-117;  
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGTCCTGCAACTGGTGAATCATCGCACTCCAGCACCACGCCAA 847  
Db 2 CCACCTAAAGGTCCTGCAACTGGTGAATCATCGCACTCCAGCACCACGCCAA 61  
QY 848 GCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCACTGTTCTTGGCGCA 907  
Db 62 GCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCACTGTTCTTGGCGCA 121  
QY 908 ATGGCAGCCATCGAGTACGCAAGAGAGCTGAATACCTGCTCCCTACATCACCAGCA 967  
Db 122 ATGGCAGCCATCGAGTACGCAAGAGAGCTGAATACCTGCTCCCTACATCACCAGCA 181  
QY 968 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1027  
Db 182 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 241  
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Db 242 CATCATGACATGATGTCATTAAGAACTGGTGGAGCTGGCTGGCGCTGAGCTACTA 301  
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Db 302 CATCGGTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 361  
QY 1148 CAATCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1207  
Db 362 CAATCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 421  
QY 1208 CATCATGAGATGACAGGAGGCTTACCG 1237  
Db 422 CATCATGAGATGACAGGAGGCTTACCG 451

Db 242 CATCATGACATGATGTCATTAAGAACTGGTGGAGCTGGCTGGCGCTGAGCTACTA 301  
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QY 1148 CAATCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1207  
Db 362 CAATCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 421  
QY 1208 CATCATGAGATGACAGGAGGCTTACCG 1237  
Db 422 CATCATGAGATGACAGGAGGCTTACCG 451

RESULT 13  
US-09-338-313  
; Sequence 313, Application US/0933838A  
; Patent No. US20020102602A1  
; GENERAL INFORMATION:  
; APPLICANT: Yugu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C2  
; CURRENT APPLICATION NUMBER: US/09/338,38A  
; CURRENT FILING DATE: 1999-06-23  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 313  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-338-313

Query Match 13.9%; Score 443.6; DB 10; Length 456;  
Best Local Similarity 99.1%; Pred. No. 6.1e-117;  
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTAAAGGTCCTGCAACTGGTGAATCATCGCACTCCAGCACCACGCCAA 847  
Db 2 CCACCTAAAGGTCCTGCAACTGGTGAATCATCGCACTCCAGCACCACGCCAA 61  
QY 848 GCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCACTGTTCTTGGCGCA 907  
Db 62 GCCTAACATCTTCCAAAGGATCCGATGTGAACATGCTGCACTGTTCTTGGCGCA 121  
QY 908 ATGGCAGCCATCGAGTACGCAAGAGAGCTGAATACCTGCTCCCTACATCACCAGCA 967  
Db 122 ATGGCAGCCATCGAGTACGCAAGAGAGCTGAATACCTGCTCCCTACATCACCAGCA 181  
QY 968 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1027  
Db 182 CGAATACTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 241  
QY 1028 CATCATGACATGATGTCATTAAGAACTGGTGGAGCTGGCTGGCGCTGAGCTACTA 1087  
Db 242 CATCATGACATGATGTCATTAAGAACTGGTGGAGCTGGCTGGCGCTGAGCTACTA 301  
QY 1088 CATCGGTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1147  
Db 302 CATCGGTTCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 361  
QY 1148 CAATCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 1207  
Db 362 CAATCTTCTGATTTGGCGCGCTGCTCATCCCCATGATTTCCAGTACCAGAT 421  
QY 1208 CATCATGAGATGACAGGAGGCTTACCG 1237  
Db 422 CATCATGAGATGACAGGAGGCTTACCG 451

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RESULT 14
US-09-551-621-313
; Sequence 313, Application US/09551621
; Publication No. US20030104366A1
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-621-313

Query Match      13.9%; Score 443.6; DB 11; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117; Indels 0; Gaps 0;
Matches 446; Conservative 0; Mismatches 4;

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DB 2 CCACCTTAAAGGTCCTCTGCCAACTGGTGGAAATCATCGCCACTTCGAGCACCAACGCCAA 61

QY 848 GCCTTAAACATCTTCCAAAGGATCCGATGTGAACATGCTGCACGCTGTTGTTCTGGCGGA 907
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QY 908 ATGCAGCCCATCGAGTACGCGAAGAAAGCTGAAATACCTGCGCTACAAATCACCAACGA 967
DB 122 ATGCAGCCCATCGAGTACGCGAAGAAAGCTGAAATACCTGCGCTACAAATCACCAACGA 181

QY 968 CGAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCAATGATTTCCAGTACCAAGAT 1027
DB 182 CGAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCAATGATTTCCAGTACCAAGAT 241

QY 1028 CATCATGACCAATGATCGTCCATAGAACTGGGTGGACCTGCGCTGGCGCGTACGCTACTA 1087
DB 242 CATCATGACCAATGATCGTCCATAGAACTGGGTGGACCTGCGCTGGCGCGTACGCTACTA 301

QY 1088 CATCGGTTCTTTCATCACTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCT 1147
DB 302 CATCGGTTCTTTCATCACTACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTTCT 361

QY 1148 CAATCTCATCAGGTTCTGGAGGCCATCGTTTGTGTGGGTCCACACAGATGATCATCAT 1207
DB 362 CAATCTCATCAGGTTCTGGAGGCCATCGTTTGTGTGGGTCCACACAGATGATCATCAT 421

QY 1208 CGTCATGAGATTGACCAAGGAGCGCTACCG 1237
DB 422 CGTCATGAGATTGACCAAGGAGCGCTACCG 451

RESULT 15
US-10-124-805-313
; Sequence 313, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12

```

```
; ORGANISM: Homo sapiens
US-10-007-805-313

Query Match      13.9%; Score 443.6; DB 14; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 847
DB 2 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 61

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 907
DB 62 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 121

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGTCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 967
DB 122 ATGGCAGCCCATCGAGTACGGCAAGAGTCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 181

QY 968 CGAATACCTTCTTCCCAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 1027
DB 182 CGAATACCTTCTTCCCAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 241

QY 1028 CATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCCTGGCCCTGAGTACTA 1087
DB 242 CATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCCTGAGTACTA 301

QY 1088 CATCGGTTCTTCCATACCTACCTTCTTACGGATCCTGGAGCCCTGCTTTTCT 1147
DB 302 CATCGGTTCTTCCATACCTACCTTCTTACGGATCCTGGAGCCCTGCTTTTCT 361

QY 1148 CAACCTTCATCAGGTTCCCTGGAGACCACTGGTTGTGTGGGTCCACAGATGAATCACAT 1207
DB 362 CAACCTTCATCAGGTTCCCTGGAGACCACTGGTTGTGTGGGTCCACAGATGAATCACAT 421

QY 1208 CGTCATGGAGATTGACCAAGGAGCCCTACCG 1237
DB 422 CGTCATGGAGATTGACCAAGGAGCCCTCGG 451

RESULT 18
US-09-604-287A-425
; Sequence 425, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-425

Query Match      13.9%; Score 443.4; DB 9; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 847
DB 1 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 60

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 907
DB 61 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 120

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGTCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 967
DB 121 ATGGCAGCCCATCGAGTACGGCAAGAGTCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 180

QY 968 CGAATACCTTCTTCCCAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 1027
DB 181 CGAATACCTTCTTCCCAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 240

QY 1028 CATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCCTGGCCCTGAGTACTA 1087
DB 241 CATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCCTGAGTACTA 300

; ORGANISM: Homo sapiens
US-10-076-622-313

Query Match      13.9%; Score 443.6; DB 15; Length 456;
Best Local Similarity 99.1%; Pred. No. 6.1e-117;
Matches 446; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 847
DB 2 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 61

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 907
DB 62 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 121

; ORGANISM: Homo sapiens
US-10-076-622-313

Query Match      13.9%; Score 443.4; DB 9; Length 446;
Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 847
DB 1 CCACCTTAAAGGGTGCTCTGCCAACTGGTGAATCATCCCACTTCCAGCACCAGCAA 60

QY 848 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 907
DB 61 GCCTAACATCTTCCACAAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 120

QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGTCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 967
DB 121 ATGGCAGCCCATCGAGTACGGCAAGAGTCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 180

QY 968 CGAATACCTTCTTCCCAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 1027
DB 181 CGAATACCTTCTTCCCAAGGATCCCGATGTAACATGCTGCACTGTTGTTCTGGGCGA 240

QY 1028 CATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCCTGGCCCTGAGTACTA 1087
DB 241 CATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCCTGAGTACTA 300
```

QY 1088 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTTCT 1147  
Db 301 CATCCGGTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTTCT 360  
QY 1148 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCAAT 1207  
Db 361 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCAAT 420  
QY 1208 COTCATGGAGATTGACAGGAGGCC 1232  
Db 421 COTCATGGAGATTGACAGGAGGCC 445

RESULT 19  
US-09-551-621-425  
; Sequence 425, Application US/09551621  
; Publication No. US20030104366A1  
; GENERAL INFORMATION:  
; APPLICANT: Yugu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C5  
; CURRENT FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 429  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-551-621-425

Query Match 13.9%; Score 443.4; DB 11; Length 446;  
Best Local Similarity 99.8%; Pred. No. 6.8e-117;  
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 847  
Db 1 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 60  
QY 848 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 907  
Db 61 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 120  
QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 967  
Db 121 ATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 180  
QY 968 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCCATATTTCCAGTACCAGAT 1027  
Db 181 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCCATATTTCCAGTACCAGAT 240  
QY 1028 CATCATGACCATGATCTCCATAGAACTGGGTGGAGCTGGCCCTGGGCGCTCAGTACTA 1087  
Db 241 CATCATGACCATGATCTCCATAGAACTGGGTGGAGCTGGCCCTGGGCGCTCAGTACTA 300  
QY 1088 CATCGGTTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTTCT 1147  
Db 301 CATCGGTTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTTCT 360  
QY 1148 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCAAT 1207  
Db 361 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCAAT 420  
QY 1208 COTCATGGAGATTGACAGGAGGCC 1232  
Db 421 COTCATGGAGATTGACAGGAGGCC 445

RESULT 20  
US-10-124-805-425  
; Sequence 425, Application US/10124805  
; Publication No. US20030166022A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Persing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C12  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-124-805-425

Query Match 13.9%; Score 443.4; DB 13; Length 446;  
Best Local Similarity 99.8%; Pred. No. 6.8e-117;  
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 847  
Db 1 CCACCTTAAGGGTGCCTCTGCCAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 60  
QY 848 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 907  
Db 61 GCCTAACATCTTCCACAAGGATCCGATGTTGGGAATCATCCCACTTCCAGCACACGCCAA 120  
QY 908 ATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 967  
Db 121 ATGGCAGCCCATCGAGTACGGCAAGAGAGCTGAATACCTGCCCTACAAATCACCAGCA 180  
QY 968 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCCATATTTCCAGTACCAGAT 1027  
Db 181 CGAATATCTTCTCTGATTGGGCGCGCTGCTCATCCCCATATTTCCAGTACCAGAT 240  
QY 1028 CATCATGACCATGATCTCCATAGAACTGGGTGGAGCTGGCCCTGGGCGCTCAGTACTA 1087  
Db 241 CATCATGACCATGATCTCCATAGAACTGGGTGGAGCTGGCCCTGGGCGCTCAGTACTA 300  
QY 1088 CATCGGTTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTTCT 1147  
Db 301 CATCGGTTCTTTCATCACTACATCCCTTTCTACGGCATCTGGAGCCCTCTCTTTTCT 360  
QY 1148 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCAAT 1207  
Db 361 CAATTCATCAGGTTCTGGAGAGCCACTGGTTGTGTGGGTACACAGATGAATCAAT 420  
QY 1208 COTCATGGAGATTGACAGGAGGCC 1232  
Db 421 COTCATGGAGATTGACAGGAGGCC 445

RESULT 21  
US-10-007-805-425  
; Sequence 425, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: McNeill, Patricia D.

```
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-425

Query Match
Best Local Similarity 13.9%; Score 443.4; DB 14; Length 446;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGGATCATCGCCACTTCCAGCACCGCCAA 847
Db 1 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGGATCATCGCCACTTCCAGCACCGCCAA 60
QY 848 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTTCTGGGCGA 907
Db 61 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTTCTGGGCGA 120
QY 908 ATGGCAGCCCATCGAGTACGCGCAAGAGAGTGAATACCTGCCCTACATCCAGCA 967
Db 121 ATGGCAGCCCATCGAGTACGCGCAAGAGAGTGAATACCTGCCCTACATCCAGCA 180
QY 968 CGAATACCTTCTCTGATTTGGCCGCGCTGTCTATCCCTATGTTTCCAGTACCAT 1027
Db 181 CGAATACCTTCTCTGATTTGGCCGCGCTGTCTATCCCTATGTTTCCAGTACCAT 240
QY 1028 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 1087
Db 241 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 300
QY 1088 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 1147
Db 301 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 360
QY 1148 CAATTCATCAGTCTCTGGAGGACCTGTTTGTGTTGGTTCACAGATGATACAT 1207
Db 361 CAATTCATCAGTCTCTGGAGGACCTGTTTGTGTTGGTTCACAGATGATACAT 420

RESULT 22
US-10-076-622-425
; Sequence 425, Application US/10076622
; Publication No. US2003023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C11
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-425

Query Match
Best Local Similarity 13.9%; Score 443.4; DB 15; Length 446;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 99.8%; Pred. No. 6.8e-117;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 788 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGGATCATCGCCACTTCCAGCACCGCCAA 847
Db 1 CCACCTTAAAGGGTGCCTCTGCCAACTGGTGGATCATCGCCACTTCCAGCACCGCCAA 60
QY 848 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTTCTGGGCGA 907
Db 61 GCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTTGTTTCTGGGCGA 120
QY 908 ATGGCAGCCCATCGAGTACGCGCAAGAGAGTGAATACCTGCCCTACATCCAGCA 967
Db 121 ATGGCAGCCCATCGAGTACGCGCAAGAGAGTGAATACCTGCCCTACATCCAGCA 180
QY 968 CGAATACCTTCTCTGATTTGGCCGCGCTGTCTATCCCTATGTTTCCAGTACCAT 1027
Db 181 CGAATACCTTCTCTGATTTGGCCGCGCTGTCTATCCCTATGTTTCCAGTACCAT 240
QY 1028 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 1087
Db 241 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 300
QY 1088 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 1147
Db 301 CATCATGACATGATCGTCCATAGAACCTGGTGGACCTGCTATCCCTATGTTTCCAGTACCAT 360
QY 1148 CAATTCATCAGTCTCTGGAGGACCTGTTTGTGTTGGTTCACAGATGATACAT 1207
Db 361 CAATTCATCAGTCTCTGGAGGACCTGTTTGTGTTGGTTCACAGATGATACAT 420

RESULT 23
US-10-191-513A-13
; Sequence 13, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-13

Query Match
Best Local Similarity 13.2%; Score 421.6; DB 15; Length 864;
Matches 584; Conservative 0; Mismatches 249; Indels 3; Gaps 1;

QY 682 TTGCTACTCTCAGGCCCGGATGGTGGTGAACATGATTTATGCGACCTCTCTGCT 741
Db 29 TTGCGGCGAGTTTCAGGCCCGGATGGTGGTGAACATGATTTATGCGACCTCTCTGCT 88
QY 742 ACAGAAAACCAAGTGGAAACCACTTGTCCAAATTCGTTCATTTGGCCCACTTAAGGGTG 801
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; LOCATION: (1)...(453)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29095

Query Match      12.1%; Score 384.4; DB 11; Length 453;
Best Local Similarity 95.6%; Pred. No. 6.5e-100;
Matches 394; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 89 TCAGCACCTCAAAGTGAACCACTGCTACATCACTTTTGTGATTTGGCCACCTGAAGGGG 148
DB 802 CTTCTGCCAACTGGTGGATCATCGCACTTCCAGCACCAAGCTAACTACTTCC 861
DB 149 CCCCCGCCAGTTGGTGGAAACCATGCACTTTCAGCACCACTGCGAAGCCCACTGCTCC 208
QY 862 ACAAGATCCCGATGTGAACATGCTGC---ACGTGTTTGTTCGGCGGAATGGCAGCCCA 918
DB 209 GCAAGACCCAGACATCAACATGATCCTCTCTTTTGGCTTTGGGGAAGATCTCTCTG 268
QY 919 TCAGTACGCCAAGAGAGCTGAATACCTGCTTACATCACCAGCAGCAATACTTCT 978
DB 269 TGGAGCTTGGGAAACAGAAATAATATGCGGTACCAACACACGACCAATACTTCT 328
QY 979 TCCGTGATGGCGCGCGCTCATCCCATGATTTCCAGTACCAAGATCATCATGACCA 1038
DB 329 TCCTAATGGCCCCCAGCCTTCTGCTCTCTTCTTCCAGTGGTATATTTTCTATTG 388
QY 1039 TGATGTCCTAAGAACTGGGTGGACCTGCTGCTGGCGCTCAGCTACTACATCCGGTCT 1098
DB 389 TTATCCAGCGAAAGATGGGTGGACTTGGCCCTGGATGATACCTTCTACGTCGGCTCT 448
QY 1099 TCATCACTCATCCCTTTCTAGGGCATCCTGGGAGCCCTCTTTTCTCAACTTCATCA 1158
DB 449 TCCTCACTTATGCCCACATATTGGGCTGAAGCCTTCTGGGCCCTTTCTTCATAGTCA 508
QY 1159 GGTTCCTGGAGAGCACTGTTGTGTGGTTCACAGATGAATCATCATGTCATGAGA 1218
DB 509 GGTTCCTGGAAAGCACTGTTGTGTGGTTCACAGATGAATCATTTCCCATGCA 568
QY 1219 TTGACAGGAGGCTACCGTGACTGTTTCAGTAGCAGCTGACAGCCACCTGCAAGCTGG 1278
DB 569 TTGATCATGACCGAAACATGAGCTGGTTCACCCAGCTCCAGGCCACATGCAATGTC 628
QY 1279 AGCAGTCTCTTCAACAGACTGTTTCAGTAGGACCTTAACTTCCAGATTGACACACC 1338
DB 629 ACAAGTCTGCTTCAATCACTGTTTCAGTAGGACCTTCAACTTCCAGATTGACACCATC 688
QY 1339 TCTTCCCAACATGCCCGGCACAACTTACAGAGATCGCCCGCTGGTGAAGTCTCTAT 1398
DB 689 TTTTTCACAGATGCTGACACAAATACACAAAGTGGTCCCTGCTGCTGCTGCTG 748
QY 1399 GTGCCAAGCATGGCATTTGAATACAGGAGAGCGCTACTGAGGGCCCTGCTGGACATCA 1458
DB 749 GTGCCAAGCATGGCATAGATGACAGTCCAGGCCCTGCTGTCAGCCCTTCCCGGACATCA 808
QY 1459 TCAGTCCCTGAAGAGTCTGGAGCTGTGCTGGAGCCTACTCTTCAAAATGA 1514
DB 809 TCCACTCAAGAGAGTCAAGGAGCTGCTGGCTAGATGCTTCTTCAACNATAA 864

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RESULT 24
US-09-918-995-29095
; Sequence 29095, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29095
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)...(453)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29095

Query Match      12.1%; Score 384.4; DB 11; Length 453;
Best Local Similarity 95.6%; Pred. No. 6.5e-100;
Matches 394; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 440 ACCCTCTGATTTGGTGAATGCCCCGAGGAGCCAGCCAGGACCCAGGCAAGAACTC 499
DB 42 ATCAGTACAGNGCGGNGGAATTCCTGGCTTCGAGGCCAGCCAGGACCCAGGCAAGAACTC 101
QY 500 AAGATCACTGAGGACTTCCGGGCCCTTGAGGAAGACGGCTGAGGACATGAACCTGTCAA 559
DB 102 AAGATCACTGAGGACTTCCGGGCCCTTGAGGAAGACGGCTGAGGACATGAACCTGTCAA 161
QY 560 GACCAACACGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
DB 162 GACCAACACGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 221
QY 620 ATGTTTCACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 679
DB 222 ATGTTTCACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 281
QY 680 CTTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 739
DB 282 CTTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 341
QY 740 CTACAGAAAACCCCAAGTGGAGCACTTGTCCCAAAATTTGTCATTGGCCACTTAAAGGG 799
DB 342 CTACAGAAAACCCCAAGTGGAGCACTTGTCCCAAAATTTGTCATTGGCCACTTAAAGGG 401
QY 800 TGCCTCTCCAACTGGTGGAAATCATGCGCACTTCCAGACCCAGCCAGCT 851
DB 402 TGCCTCTCCAACTGGTGGAAATCATGCGCACTTCCAGACCCAGCCAGCT 453

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RESULT 25
US-10-191-513A-35
; Sequence 35, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-35

Query Match      11.6%; Score 370.4; DB 15; Length 960;
Best Local Similarity 64.5%; Pred. No. 9.6e-96;
Matches 570; Conservative 0; Mismatches 311; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCGCGGAGCGGAGGTGTGGTGCCCACTTTCAGCTGGAGGAGATCA 259
DB 48 GGCGCGGAGAGCGGGCTCAGGACCTTACCCCGGCTACTTCACTTGGGACGAGGTGC 107

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Db 795 CTACTCCAGTGGTATATTTCTATTGTTATCCAGCAAGAGTGGTGGACTTGGC 854  
QY 1070 CTGGGCGGTCA 1080  
Db 855 CTGGATCAGCA 865

RESULT 27  
US-10-191-513A-34  
; Sequence 34, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295, US, D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-34

Query Match 11.0%; Score 351.8; DB 15; Length 990;  
Best Local Similarity 64.7%; Pred. No. 2.2e-90;  
Matches 540; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 200 GGGCGAGGGGGCCCGAGCGGAGGTCGGTGGCCACCTTCAGTGGAGGAGATTC 259  
Db 18 GGGCGGAGAGCCGCGCTCAGGAGCACTACCCCGCGCTACCTTCCCTGGAGAGGTGGC 77

QY 260 GAAGCATAACTGGGACCGACAGTGGGCTGATTCAGCGCAAGGTTTCAACATCAC 319  
Db 78 CCAGCGTCAAGGTGCGAGGAGCGGTGGCTAGTATGACCGCTAAGTGTACACATCAG 137

QY 320 CAAATGTTCCATCAGCACCCCGGGGGCCAGCGGGTCATCGGCGACTACGCTGGAGA 379  
Db 138 CGAGTTCCACCCCGCGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACCGCGGGCAGGA 197

QY 380 TGCAACGGATGCCCTTCGCGGCTTCCACCGCTGACCTGGAATTCGTGGGCAAGTTCTTGAA 439  
Db 198 TGCCACGATACCTTTTGTGGCTTCCATCATCACAGGGCTTGTGAGAGATATAGAA 257

QY 440 ACCCTCTGATTCGTTGAACTGGCCCGAGAGGCCAGCCAGGACCAAGGAGAACTC 499  
Db 258 CTCTCTCTGATTGGAGACTGTCTCCAGAGCGAGCCAGCTTTGAGCCCAAGAAATAA 317

QY 500 AAGATCACTGAGACTTCGGGCGCTTGAGAGAGCGCTGAGACATGAACCTGTTCAA 559  
Db 318 AGAGCTGACATGAGTTTCGGGAGCTTCGGGGCCACAGTGAGCGGATGGGTCTATGAA 377

QY 560 GACCAACCACTGTTTCTTCCTCCTCCTCGGCCACATCATCGCCCTGGAGAGCATGTC 619  
Db 378 GGCCAAACCATGCTTCTTCCTGCTGTACTCTCTGCAATCTTGTCTGTGATGGGTCTAG 437

QY 620 ATGGTTCACTGCTTCACTTCTGCAATGGGTGATTCCTACCTCATCAGCGCTTGT 679  
Db 438 CTGGCTACCCCTTGGGTCTTTGGAGCGTCTTTTGGCCCTTCTCTCTGTGCGGTGCT 497

QY 680 CTTCTCTACTCTCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGCGCCACCTGTCTGT 739

Db 498 GCTCAGTGGAGTTCAGGCCAGGCTGGCTGGCTGGAGCATGACTTTGGGCACCTGTGGT 557  
QY 740 CTACAGAAAACCAAGTGGAAACACCTTGTCCACAAATTCGTCATTTGGCCACTTAAGGG 799  
Db 558 CTTTCAGCACCTCAAAGTGGAAACCATCTGCTACATCATTTTGTGATTTGGCCACCTGAAGG 617  
QY 800 TGCTCTGCCAACTGGTGGAAATCATCGCCACTTCCAGCACCAGGCCAAGCCTTAACATCTT 859  
Db 618 GGCCCCCGCCAGTGTGGTGGAAACCATGTCATTTCCAGCACCATGCCAAGCCCACTGCTT 677  
QY 860 CCACAAGGATCCCGATGTGAACATGCTGC---ACGTGTTTGTTCGGGGAATGGCAGCC 916  
Db 678 CCGCAAGACCCAGACATCAACATGTCATCCCTTCTTTGCTTGGGGAAGATCCTCTC 737  
QY 917 CATCGAGTACGCAAGAGAGCTGAATACCTGCGCTCAATCAATCAGCAGCAACATCTT 976  
Db 738 TGTGGAGCTTTGGGAACAGAGAAATATATATGCGGTACCAACCAACGACCAAAATCTT 797  
QY 977 CTTCTCTGATTGGCGCGCGCTGCTCATCCCATGATTTTCCAGTACCAAGATCATC 1031  
Db 798 CTTCTCTAATTGGGCGCCCGCCAGCCTTGTGCTCTCTACTTCCAGTGGTATATTTC 852

RESULT 28  
US-09-981-876-119  
; Sequence 119, Application US/09981876  
; Patent No. US20020164669A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: P2001P1  
; CURRENT APPLICATION NUMBER: US/09/981,876  
; CURRENT FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 09/148,545  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,161  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,502  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,633  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,583  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,617  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,581



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; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 2016

Query Match
Best Local Similarity 56.5%; Pred. No. 1.3e-81;
Matches 533; Conservative 1; Mismatches 261; Indels 7; Gaps 5;

QY 361 GGCACCTACGCTGGAGAGATGCAACGGATGCGCTTCGCGCCCTTCACACCTGACCTGGGAAT 420
Db 135 GCGGAGCGCTGGGAGNCCACAGATGCGCTTCGTCCTTCATCAAGATCTCAATT 194
QY 421 TCGTGGCGAAGTCTTGAACCCCTGCTGATGGTGAACTGGCCCCGGAGAGCCAGCC 480
Db 195 TTGTGGCGAA-TTCCTACAGCCCTCTTGATTGGAGAGTGCGTCGGAAGAACCCAGCC 253
QY 481 AGGACACGCGAAGAACTCAAAGATCACTGAGGACTTCGCGGCCCTCGAGGAAGACGGCTG 540
Db 254 AKGATGACCCCTGATGC--GCATGGTCGAGACTTCGAGGCCCTGCACAGGACGCG 311
QY 541 AGGACATGAACCTGTTCAAGACCAACAGCGTTCCTCTCTCTCTCTCTCTCTCTCTCTCA 600
Db 312 AGGACATGAAGCTGTTGATGCGCAGTCCCACTTCCTTCTCTCTCTCTCTCTCTCTCTCT 371
QY 601 TCGCCCTGGAGAGCATGCAATGCTTCACTGCTCTTCTACTTTGGCAATGGCTGATTCCTA 660
Db 372 TGCGCATGGAGTGTGGCCCTGCTCTTATCTACCTCTCGGTCTCTGGCTGGTGCCCA 431
QY 661 -CCCTATACAGCGCTTTGCTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 719
Db 432 GTGCCCTGSGNCGCTTCATCTCTGGCCATCTCTCAGGCTCAGTCTCTGTGTCTCTGCA 491
QY 720 GATTATGGCCACCTGTCTGTCTACAGAAAACCAAGTGAACCACTTGTCCCAAAATTC 779
Db 492 GACCTGGGCA-TGCTCACTTCAAGAAGTCTGTGTGGAAACCAAGTGGCCCAAGTTC 550
QY 780 GTCAATTGGCCACTTAAAGGTGCTCTGCGCACTGTGTGGAACTATGCGCACTTCCAGCAC 839
Db 551 GTGATGGGCGAGCTTAAAGGGCTTCTCGCCCACTGTGTGGAACCTTCCGCCACTTCCAGCAC 610
QY 840 CACCCCAAGCCTTACATCTTCCAAAGGATCCCGATGTGAACATGTGTCACGCTGTTTGT 899
Db 611 CACGCCAAGCCCACTCTTCCAAAGACCCAGACGTCGCGGTGGCGCGGTCTTCTC 670
QY 900 CTGGGCGAATGGCGCCCATCGATACGGCAAGAGAGCTGAATACCTGCTCCCTACAT 959
Db 671 CTGGGGGA--GTCATCCGTGAGTATGNCNCAAGAAAGAACGATACCTACCCCTACAC 728
QY 960 CACGAGACGAATATCTTCTCTGATTTGGGCGCGCTGTCTATCCCACTGATTTCCAG 1019
Db 729 CAGGAGACCTGTACTTCTTCTGATCGCGCGCGCTGTCTACCCCTGGTGAACCTTGA 788
QY 1020 TACCAGATCATGACCATGATCGTCATGAAGAACTGGGTGGAGCTGGCTGGCGCGTC 1079
Db 789 GTGGAAAACTGGCGTACATGCTGTGTGTCATGCACTGGGCGGATTTGCTCTGGGCGCC 848
QY 1080 AGCTACTACATCCGGTCTTCTATCACTACATCTTCTTCTAGGCGATCCTGGAGCCCTC 1139
Db 849 AGCTCTATGCGGCTTCTTCTTATCTTATCTCTACCTCCCTCTCTACGCGCTCCTGGG 908
QY 1140 CTTTTCTCACTTCATCAGGT 1161
Db 909 CTCCTCTTTTGTCTGTGAGT 930

RESULT 29
US-09-148-545-119
; Sequence 119, Application US/09148545

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RESULT 29  
US-09-148-545-119  
; Sequence 119, Application US/09148545  
: Publication No. US20030027132A1

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 2016

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Query Match      10.1%; Score 321.8; DB 11; Length 2016;
Best Local Similarity 66.5%; Fred. No. 1.3e-81;
Matches 533; Conservative 1; Mismatches 261; Indels 7; Gaps 5;

Qy 361 GGCACCTAGCTGGAGAGATGCAAGGATGCTTCCGGCGCTTCCACCTGGAAT 420
Db 135 GCGAGGGGCTGCGGGAGNCCCAACAGGATGCTTCCGTGCTTCCATCAAGATCTCAAT 194
Qy 421 TCGTGGGCAAGTCTTGAACCCCTGCTGATGTGGAAGTGGCCCGGAGAGAGCCAGCC 480
Db 195 TTGTGGGCAAA-TTCCTACAGCCCCCTGTGATGGAGAGCTGGCTCCGAGAGACCCAGCC 253
Qy 481 AGGACCAACGGCAAGAACTCAAGATCACTGAGGACTTCCGGGCGCTTCCGAGAGAGCGCTG 540
Db 254 AKGATGGACCCCTGGAATGC--GCATGTGCGAGGACTTCCGAGCGCTTCCACAGCAGCCG 311
Qy 541 AGGACATGACCTGTTCAGACCAACACCGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 312 AGGACATGAGCTGTTTGTATGATCCAGTCCACCTTCTTGTCTTCTTCTTCTTCTTCTTCT 371

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601 TCGCCCTGAGAGCAATTGCAATGTTTCACTGTCTTCTACTTTGGCAATGGCTGGATTCTTA 660  
 Db |||||  
 372 TGGCAATGAGGTGTGGCTGGCTCTTATCTACTCTGGGTCTGGCTGGTGGCCCA 431  
 Qy |||||  
 661 -CCCTCATCAGCGCTTGTCTTCTACTCTTCACTGGCCCAAGCTGGATGGCTGCAAT 719  
 Db |||||  
 432 GTGCCCTGNGCGCCCTTCACTCTGGCCATCTCTCAGGCTCAGTCTGTGTCTGAGCAT 491  
 Qy |||||  
 720 GATTATGGCCACTGTCTCTACAGAAACCAAGTGGAAACCACTTGTCCACAAATTC 779  
 Db |||||  
 492 GACCTGGGCA -TGCTCCATCTTCAAGAGTCTCTGGTGAACCAAGTGGCCAGAGTTC 550  
 Qy |||||  
 780 GTCAATGGCCACTTAAAGGTGGCTCTGCAACTGGTGGAAATCATCGCACTTCCAGCAC 839  
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 551 GTGATGGGCACTTAAAGGCTTCTCCGCCACTGGTGGAAATTCGGCCACTTCCAGCAC 610  
 Qy |||||  
 840 CAGCCCAAGCTTAACTCTTCCACAGGATCCGATGTGAACATGTGCACGTGTTTGT 899  
 Db |||||  
 611 CAGCCCAAGCTTAACTCTTCCACAGGATCCGATGTGAACATGTGCACGTGTTTGT 899  
 Qy |||||  
 900 CTGGGCGAATGGAGCCCAATCGAGTACGAGCAAGAGCAAGTGAATACCTGCCCTACAT 959  
 Db |||||  
 671 CTGGGCGA -GTCACTCGTGAATGTGNCACAGAACCGAGATACCTACCTACCAAC 728  
 Qy |||||  
 960 CAGCAGCAAGTACCTTCTTCTGATGGCGCGCTCTCATCCCATGATTTCCAG 1019  
 Db |||||  
 729 CAGCAGCACTGTACTTCTTCTGATCGCGCGCTCTCATCCCTGTGAACTTTGA 788  
 Qy |||||  
 1020 TACCATCATCATGACCAATGATCGTCCATAGAACTGGGTGACCTGGCCCTGGCGCTC 1079  
 Db |||||  
 789 GTGGAATACTGGCGTACATCTGTGTGATGATGAGTGGCGGATTTGCTCTGGCGCGCC 848  
 Qy |||||  
 1080 AGTACTACATCGGTTCTTCTATCACTACATCCCTTCTAGGCACTCTGGAGCCCTC 1139  
 Db |||||  
 849 AGTTCTATCGCGCTTCTTCTATCTACCTCCCTTCTAGGCACTCTGGAGCCCTC 908  
 Qy |||||  
 1140 CTTTCTCACTTCATCAGGT 1161  
 Db |||||  
 909 CTCTTCTTGTGTGTCAGGT 930

RESULT 30  
 US-10-191-513A-4  
 ; Sequence 4, Application US/10191513A  
 ; Publication No. US20030104596A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pardeep  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; APPLICANT: Tapas, Das  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.D3  
 ; CURRENT APPLICATION NUMBER: US/10/191,513A  
 ; PRIORITY FILING DATE: 2002-09-25  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 304  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-191-513A-4

Query Match 9.5%; Score 302.4; DB 15; Length 304;  
 Best Local Similarity 99.7%; Pred. No. 2.1e-76;  
 Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

630 GTCTTCTACTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTCTCTTGTCTACC 689  
 Db |||||  
 1 GTCTTTTACTTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTGTCTTGTCTACC 60  
 Qy |||||  
 690 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 749  
 Db |||||  
 61 TCTCAGGCCCAAGCTGGATGGCTGCAACATGATTATGGCCACCTGTCTGTCTACAGAAA 120  
 Qy |||||  
 750 CCCAAGTGGAAACCACTTGTCCACAAATTCGTAATGGCCACTTAAAGGGTGCCTCTGCC 809  
 Db |||||  
 121 CCCAAGTGGAAACCACTTGTCCACAAATTCGTAATGGCCACTTAAAGGGTGCCTCTGCC 180  
 Qy |||||  
 810 AACCTGGTGGAAATCATCGCCACTTCCAGCACCGCCCAAGCTTAAACATCTTCCACAAGGAT 869  
 Db |||||  
 181 AACCTGGTGGAAATCATCGCCACTTCCAGCACCGCCCAAGCTTAAACATCTTCCACAAGGAT 240  
 Qy |||||  
 870 CCGCATGTGAACATGTGTGCAACGTGTTTCTGGGGAATGGCAGCCCATCGAGTACGGC 929  
 Db |||||  
 241 CCGCATGTGAACATGTGTGCAACGTGTTTCTGGGGAATGGCAGCCCATCGAGTACGGC 300  
 Qy |||||  
 930 AAGA 933  
 Db |||||  
 301 AAGA 304

RESULT 31  
 US-09-880-107-3920/c  
 ; Sequence 3920, Application US/09880107  
 ; Patent No. US20020142981A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horne, Darci T.  
 ; APPLICANT: Vockley, Joseph G.  
 ; APPLICANT: Scherf, Uwe  
 ; APPLICANT: Gene Logic, Inc.  
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
 ; FILE REFERENCE: 44921-5028-WO  
 ; CURRENT APPLICATION NUMBER: US/09/880,107  
 ; CURRENT FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/211,379  
 ; PRIOR FILING DATE: 2000-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/237,054  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 3950  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3920  
 ; LENGTH: 292  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z40715  
 US-09-880-107-3920

Query Match 9.2%; Score 292; DB 10; Length 292;  
 Best Local Similarity 100.0%; Pred. No. 2e-73;  
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2882 CTGAGCTGCTGTGAGTCAATCAACCTCAATCACTTCTAGATTTCAGGGAAGGCGCAGC 2941  
 Db 292 CTGAGCTGCTGTGAGTCAATCAACCTCAATCACTTCTAGATTTCAGGGAAGGCGCAGC 233  
 Qy 2942 ACCAACAACCTCAGAAATGGGGCTTTTCGGGGAAGGCGCTAGTCCCTCCAGCTCTAAGCAG 3001  
 Db 232 ACCAACAACCTCAGAAATGGGGCTTTTCGGGGAAGGCGCTAGTCCCTCCAGCTCTAAGCAG 173  
 Qy 3002 CCAGGAGGACCTGCATCTAAGCATCTGGGTTCATGGCAATGGCATGCCCTCCAGCTA 3061  
 Db 172 CCAGGAGGACCTGCATCTAAGCATCTGGGTTCATGGCAATGGCATGCCCTCCAGCTA 113  
 Qy 3062 CTGTATGCCCGGACCCCGCAGAGGAGAAATGAACCATAGGAGCTGATCGTAATGTT 3121  
 Db 112 CTGTATGCCCGGACCCCGCAGAGGAGAAATGAACCATAGGAGCTGATCGTAATGTT 53  
 Qy 3122 TATCATGTACTTCTCCCGCCCTTCTTGTGAAATAAATAAGGAATTTT 3173

Db 52 TATCATGTTACTTCCCCACCCCTACATTTTGTGAATAAATAAGGAATTTT 1

RESULT 32  
US-09-873-319-740/c  
; Sequence 740, Application US/09873319A  
; Publication No. US20030134324A1  
; GENERAL INFORMATION:  
; APPLICANT: Munges, William E.  
; APPLICANT: Kulkarni, Prakash  
; APPLICANT: Getzenberg, Robert H.  
; APPLICANT: Waga, Iwao  
; APPLICANT: Yamamoto, Jun  
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic  
; FILE REFERENCE: 44921-5029-US  
; CURRENT APPLICATION NUMBER: US/09/873.319A  
; EARLIER FILING DATE: 2001-06-05  
; EARLIER APPLICATION NUMBER: US 60/223,323  
; EARLIER FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 755  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 740  
; LENGTH: 292  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 Z40715  
US-09-873-319-740

Query Match 9.2%; Score 292; DB 13; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2e-73;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2882 CTGAGCTGCTGTGAGTCTACCCACTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 2941  
DB 292 CTGAGCTGCTGTGAGTCTACCCACTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 233  
QY 2942 ACCAACAACTCAGATGAGGGGCTTTTCGGGAGGGGCGCTAGTCCCGCCAGCTCTAAGCAG 3001  
DB 232 ACCAACAACTCAGATGAGGGGCTTTTCGGGAGGGGCGCTAGTCCCGCCAGCTCTAAGCAG 173  
QY 3002 CCAGGAGGAGCTGCATCTAAGCAATCTGGGTTGCCATGGCAATGGCATGCCCGCCAGCTA 3061  
DB 172 CCAGGAGGAGCTGCATCTAAGCAATCTGGGTTGCCATGGCAATGGCATGCCCGCCAGCTA 113  
QY 3062 CTGTATGCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 3121  
DB 112 CTGTATGCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 53  
QY 3122 TATCATGTTACTTCCCGCCCTACATTTTGTGAATAAATAAGGAATTTT 3173  
DB 52 TATCATGTTACTTCCCGCCCTACATTTTGTGAATAAATAAGGAATTTT 1

RESULT 33  
US-09-960-706-1117/c  
; Sequence 1117, Application US/09960706  
; Publication No. US20030134280A1  
; GENERAL INFORMATION:  
; APPLICANT: Munges, William E.  
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas  
; FILE REFERENCE: 44921-5029-01US  
; CURRENT APPLICATION NUMBER: US/09/960,706  
; EARLIER FILING DATE: 2001-09-24  
; EARLIER APPLICATION NUMBER: 60/223,323  
; EARLIER FILING DATE: 2000-08-07  
; EARLIER APPLICATION NUMBER: 09/873,319  
; EARLIER FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: PatentIn Ver. 2.1

Query Match 8.0%; Score 253.8; DB 15; Length 473;  
Best Local Similarity 71.8%; Pred. No. 2.5e-62;  
Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAAGCTGGGTGGACCTGGCGCTGAGTACTACATCGGTCTTCTATCAGCTAC 1109  
DB 9 AAGAAGTGGGTGGACCTGGCGCTGAGTACTACCTTCTAGCTCGCTTCTTCTCTAT 68  
QY 1110 ATCCCTTCTACGGCATCTCGGAGGCCCTCTTCTCACTCATCAGGTTCCTGGAG 1169  
DB 69 GTGCCACTATTGGGGCTGAAGCCCTCTCTGGGCTTTTCTTCTATAGTCTAGTTCTGGAA 128

; SEQ ID NO 1117  
; LENGTH: 292  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 Z40715  
US-09-960-706-1117

Query Match 9.2%; Score 292; DB 13; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2e-73;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2882 CTGAGCTGCTGTGAGTCTAACCACCTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 2941  
DB 292 CTGAGCTGCTGTGAGTCTAACCACCTAATCAGTCTTTAGATTGAGGGGAGGGCAGGC 233  
QY 2942 ACCAACAACTCAGATGAGGGGCTTTTCGGGAGGGGCGCTAGTCCCGCCAGCTCTAAGCAG 3001  
DB 232 ACCAACAACTCAGATGAGGGGCTTTTCGGGAGGGGCGCTAGTCCCGCCAGCTCTAAGCAG 173  
QY 3002 CCAGGAGGAGCTGCATCTAAGCAATCTGGGTTGCCATGGCAATGGCATGCCCGCCAGCTA 3061  
DB 172 CCAGGAGGAGCTGCATCTAAGCAATCTGGGTTGCCATGGCAATGGCATGCCCGCCAGCTA 113  
QY 3062 CTGTATGCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 3121  
DB 112 CTGTATGCCCCGACCCCGCAGAGGAGCAATGAACCCATAGGAGCTGATCGTAATGTT 53  
QY 3122 TATCATGTTACTTCCCGCCCTACATTTTGTGAATAAATAAGGAATTTT 3173  
DB 52 TATCATGTTACTTCCCGCCCTACATTTTGTGAATAAATAAGGAATTTT 1

RESULT 34  
US-10-191-513A-36  
; Sequence 36, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295,US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 473  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-36

Query Match 8.0%; Score 253.8; DB 15; Length 473;  
Best Local Similarity 71.8%; Pred. No. 2.5e-62;  
Matches 333; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1050 AAGAAGCTGGGTGGACCTGGCGCTGAGTACTACATCGGTCTTCTATCAGCTAC 1109  
DB 9 AAGAAGTGGGTGGACCTGGCGCTGAGTACTACCTTCTAGCTCGCTTCTTCTCTAT 68  
QY 1110 ATCCCTTCTACGGCATCTCGGAGGCCCTCTTCTCACTCATCAGGTTCCTGGAG 1169  
DB 69 GTGCCACTATTGGGGCTGAAGCCCTCTCTGGGCTTTTCTTCTATAGTCTAGTTCTGGAA 128





RESULT 37  
US-10-191-513A-37  
; Sequence 37, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 449  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: k = g or t/u at position 5  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (6)...(6)  
; OTHER INFORMATION: m = a or c at position 6  
US-10-191-513A-37

Query Match 7.1%; Score 226.8; DB 15; Length 449;  
Best Local Similarity 71.0%; Pred. No. 1.4e-54;  
Matches 314; Conservative 0; Mismatches 127; Indels 1; Gaps 1;  
QY 1078 TCAGTACTATACATCGGTTCTTCATCACTACATCCCTTTCTACGGCATCTCGGGAGCCC 1137  
Db 7 TTACCTTTAGCTCGGCTCTTCTCCTACTATGCGCACTATTGGGCT-GAAGCTTC 65  
QY 1138 TCCTTTTCTCACTCATCTAGTTCTCGGAGAGCCACTGTTTGTGTGGTCAACAGA 1197  
Db 66 TGGGCTTTTCTTCATAGTCAAGTTCTCGGAAAGCACTGTTTGTGTGGTCAACAGA 125  
QY 1198 TGAATCACATGCTCATGGAGATTGACAGGAGGCTACCGTACTGTTTCACTAGCCAGC 1257  
Db 126 TGAACCATATTCCCATGACATTGATCATGACCGGAAACATGACTGGGTTTCCACCCAGC 185  
QY 1258 TGACAGCCACTGCAACGTTGGAGCAGTCTTCTTCAACAGCTGTTTCACTGAGTGGACCTTA 1317  
Db 186 TCCAGGCCACATGCAATGTCACAAAGTGTCTTCAATGACTGTTTCACTGAGTGGACCTCA 245  
QY 1318 ACTTCAGATTGAGCAGCACCCTTCTCCACCATCCCGGACAACTTACACAAGATCG 1377  
Db 245 ACTTCAGATTGAGCAGCACCCTTCTTCCACCATCCCGGACAACTTACACAAGTGG 305  
QY 1378 CCCCCTGTGTGAAGTCTCTATGTGCCAAGCATGGCATTGAATACACAGAGAGCGGTAC 1437  
Db 306 CTCCTCTGTGTGAGTCTTGTGTGCCAAGCATGGCATTGAATACACAGAGAGCGGTAC 365  
QY 1438 TGAGGCCCTGTGGACATCATCAGTCTCCCTCAAGAGTCTCGGAAGCTGTGGTGGAGC 1497  
Db 366 TGTACGCTTGGCCGACATCATCCTCAATGAAGTCAAGGAGTCTGTGGTGGAGC 425  
QY 1498 CCTACCTTCAACAATGAAGCCA 1519  
Db 426 CCTATCTTCAACAATGAAGCA 447

RESULT 38  
US-09-783-590-5518  
; Sequence 5518, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16.2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/420,856  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5518  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (40)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (52)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (67)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (69)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (92)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (101)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (139)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (162)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (184)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (227)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (247)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (252)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (280)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (298)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (302)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (311)







Db 1 VFYFGNGWIPITLITAFVLATSOAQAQWLGQHDYGHLSVYRKPKWNLVHKFVIGHLKGASA 60  
QY 211 NWNHRRHFQHHAKPNI FHKDPDNNLVHVFVLGEWQPIEYGGKKLYLPYNHQBHEVFFLIG 270  
Db 61 NWNHRRHFQHHAKPNI FHKDPDNNLVHVFVLGEWQPIEYGGKKLYLPYNHQBHEVFFLIG 120  
QY 271 PELLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFITY:PFYGIIGALLFLNFIRFLE 330  
Db 121 PELLIPMYFOYQIIMTMVHKWVDLAWAVSYIRFFIT-IPFYGIIGALLFLNFIRFLE 179  
QY 331 SHWFVWVTQMMHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSGLHNFQIEHHLPPT 390  
Db 180 SHWFVWVTQMMHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSGLHNFQIEHHLPPT 239  
QY 391 MPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 444  
Db 240 MPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 293

## RESULT 4

US-10-102-806-650  
; Sequence 650, Application US/10102806  
; Publication No. US20030054421A1  
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P4103P1C1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 650  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-102-806-650

Query Match 65.4%; Score 1594; DB 15; Length 286;  
Best Local Similarity 100.0%; Pred. No. 1.1e-154;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 IPTLITAFVLATSOAQAQWLGQHDYGHLSVYRKPKWNLVHKFVIGHLKGASANWNRHF 219  
Db 1 IPTLITAFVLATSOAQAQWLGQHDYGHLSVYRKPKWNLVHKFVIGHLKGASANWNRHF 60  
QY 219 QHHAKPNI FHKDPDNNLVHVFVLGEWQPIEYGGKKLYLPYNHQBHEVFFLIGPPLIPMY 278  
Db 61 QHHAKPNI FHKDPDNNLVHVFVLGEWQPIEYGGKKLYLPYNHQBHEVFFLIGPPLIPMY 120  
QY 279 FOYQIIMTMVHKWVDLAWAVSYIRFFITY:PFYGIIGALLFLNFIRFLESFWVVT 339  
Db 121 FOYQIIMTMVHKWVDLAWAVSYIRFFITY:PFYGIIGALLFLNFIRFLESFWVVT 180  
QY 339 QMMHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSGLHNFQIEHHLPPTMPRNLHK 398  
Db 181 QMMHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSGLHNFQIEHHLPPTMPRNLHK 240  
QY 399 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 444  
Db 241 IAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSKGKMLDAYLHK 286

## RESULT 5

US-10-262-617-1  
; Sequence 1, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 09/048,888  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CDI  
US-10-262-617-1

Query Match 64.0%; Score 1560.5; DB 15; Length 445;  
Best Local Similarity 62.3%; Pred. No. 5.4e-151;  
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

QY 1 MGKGGNQ--EGAAEREVSVPFSHEEIQKHLNRDTSGLVIDRKVYNITKNSIQHPGGOR 58  
Db 1 MGVGEGPGRGPAQPGAFPTFCMEQIRAHQPGDKWLVIRRVYDISRWAQRHPGGSR 60  
QY 59 VIGHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEEPQDQHGKSKITEDFRALRK 118  
Db 61 LIGHGAEADATDAFRAHQDLNFKLQPLLIGELAPEEPQDQGLNAQLVEDFRALHQ 120  
QY 119 TADNMNLFKTNHVFLLLAHIALESIAWFTVFVFGNGWITLITAFVLATSOAQAQWLG 178  
Db 121 AAEADMKLFDASPTFFAFLGHILAKELVLAWLIIYLLGPGWVPSALAAFTLAISQAQSWCL 180  
QY 179 QHDYGHLSVYRKPKWNLVHKFVIGHLKGASANWNRHFQHHAKPNI FHKDPDNNLVH 238  
Db 181 QHDLGHASIFKSKWNNHVAQKFWMGOLKGFSAHWNFRHFQHHAKPNI FHKDPDNNLVH 240  
QY 239 FVLGEWQPIEYGGKKLYLPYNHQBHEVFFLIGPPLIPMYFOYQIIMTMVHKWVDLAW 298  
Db 241 FLIGE--SSVEYGGKKRYLPYNQOHLFFLIGPPLITLVNFEVENLAYMLVCWQWADLLW 299  
QY 299 AVSYIRFFITY:PFYGIIGALLFLNFIRFLESFWVVTQMMHIVMEIDQAYRDWFS 358  
Db 300 AASFYARFFLSLFFYGVGVLLFFVAVRVLESFWVVTQMMHIVMEIDQAYRDWFS 359  
QY 359 QLTATCNVEQSFNDWFSGLHNFQIEHHLPPTMPRNLHKAIPLVKSLCAKHGIEYQEK 418  
Db 360 QLAATCNVEPSLFTNWFSGHLNFQIEHHLPMPRPNYSRVAPLVKSLCAKHGLSYEVPK 419  
QY 419 LLRALDIIIRSLKSKGKMLDAYLHK 444  
Db 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445

## RESULT 6

US-10-262-617-3  
; Sequence 3, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 09/048,888  
; PRIOR FILING DATE: 1998-03-26

```

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Inbyte ID No. US20030077747A1 2056310CD1
; US-10-262-617-3

Query Match
Best Local Similarity 62.0%; Score 1515; DB 15; Length 444;
Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKHNLRDTSGLVIDRKYVNIITKWSIOHPGQGVIGHYAGED 67
DB 7 AETAAGGTPRYFTWDEVAQRSGGCEERWLVIDRKYVNIISFTRRHPPGGRVISHYAGQD 66

QY 68 ATDAFRAFPDLEFVCKFLKPLLIIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNMLFK 127
DB 67 ATDPFVAFHINKGLVKYNNLSLIGELSPQSFPTKKNELTDFRELRATVERMGLMK 126

QY 128 TNHVFLLLIHIALESIAFWTFVFGNGWPTLTITAFVLATSOAQAGWLQHDYGHLSV 187
DB 127 ANHVFFLLYLLHLLDGAWLTLWVGTSFLPFLCAVLLSAVOAQAGWLQHDYGHLSV 186

QY 188 YRKPKNHLVHKFVIHGLKGASANNWNNHRRHQHAKPNIFHXDPDNNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLLHFFVIGHLKGAPASWNNHMHFQHHAKPNCFRKDPDINN-HPFFALGKIL 245

QY 246 PIYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHGHYFFLIGPPLIPMYFOYQIIMTVHKNWVDLAWAVSYIR 305

QY 306 FFITYPFYIGLALLFLNFIRESHFWVWVTQNMHIWVEIDQAYRDFWFSQLTATCN 365
DB 306 FFLTYVPLLGKAFGLGFFIVRLESNFWVWVTQNMHIWVEIDQAYRDFWFSQLTATCN 365

QY 366 VEGSFNDWFSGHNFQIEHLLPFTWPRNHLKIAPLVKSCLAKHGIEYQEKPLLRALLD 425
DB 366 VHSKAFNDWFSGHNFQIEHLLPFTWPRNHLKIAPLVKSCLAKHGIEYQEKPLLRALLD 425

QY 426 IIRSLKSGKMLDAYLHK 444
DB 426 IIRSLKSGKMLDAYLHK 444

RESULT 7
US-10-191-513A-12
; Sequence 12, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa = Unknown or other at position 444
; US-10-191-513A-42

Query Match
61.3%; Score 1493.5; DB 15; Length 444;

```



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Best Local Similarity 61.5%; Pred. No. 3.9e-144;
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

QY 11 AAREVSVPT--PSWEEIOKHLNRTDGLVIDRKVNIITKSGIOHPGGORVIGHYAGED 67
Db 7 AAEATAAGTTPRYFTWDEVAQRSGCEERWLVIDRKVNIISFTTRRHPGGSRVISHYAGD 66
QY 68 ATDAFAFHPDLEFVGKFLKPLLIGELAPEPSODHGKNSKITEDFRALKTKTADNNLKF 127
Db 67 ATDPPFAFHINKGLVKYNNLSLIGELSPSPQSPPTKNKELTDEPE-LRATVERMGLMK 125
QY 128 TNHVFLLALLAHIIAIESIAWFTVYFGNGWIPITLITAFVLATSAQAAGLQHDYGHLSV 187
Db 126 ANHVFLLYLLHILLDGAAMLTLWVFGTSELPFLCAVLLSAVQAAGLQHDYGHLSV 185
QY 188 YRKPKNHLVHKFVIGHLKGASANNHHRFQHAKPNIIFHKDPDVNMLH--VFVLGEWQ 245
Db 186 PSTSKWNHLLHFFVIGHLKGAPASNNHMHFQHAKPNCFRKDPDINN-HPPFFALGKIL 244
QY 246 PIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMVHKNNWVDLAWAVSYIR 305
Db 245 SVELGKQKKYMPYNNHGHYFFLIGPPLIPMYFOYQIIMTMVHKNNWVDLAWAVSYIR 304
QY 306 FFITYIPYIGLALLFNIRFLESHWVWVVTQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 305 FFLIVPPLGLKAFGLFFIVRFLSNWVWVVTQNNHIVMEIDQAYRDWFSQLTATCN 364
QY 366 VEQSFENDWFSGLNFOIEHLHFTPMRHNHKTAPLAKSIKAKHGIEYOKPLLRALLD 425
Db 365 VHKSAFNWFSGLNFOIEHLHFTPMRHNHKTAPLAKSIKAKHGIEYOKPLLRALLD 424
QY 426 IIRSLKSGKWLMDAYLHK 444
Db 425 IIRSLKSGKWLMDAYLHK 443

RESULT 9
US-10-191-513A-39
; Sequence 39, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10191513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-39

Query Match 46.3%; Score 1128; DB 15; Length 360;
Best Local Similarity 57.2%; Pred. No. 8e-107;
Matches 203; Conservative 56; Mismatches 90; Indels 6; Gaps 3;

QY 11 AAREVSVPT--FSWEEIOKHLNRTDGLVIDRKVNIITKSGIOHPGGORVIGHYAGED 67
Db 7 AAEATAAGTTPRYFTWDEVAQRSGCEERWLVIDRKVNIISFTTRRHPGGSRVISHYAGD 66
QY 68 ATDAFAFHPDLEFVGKFLKPLLIGELAPEPSODHGKNSKITEDFRALKTKTADNNLKF 127

us-09-719-601-5.rapb
Best Local Similarity 61.5%; Pred. No. 3.9e-144;
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

QY 67 ATDPPFAFHINKGLVKYNNLSLIGELSPSPQSPPTKNKELTDEPELRATVERMGLMK 126
QY 128 TNHVFLLALLAHIIAIESIAWFTVYFGNGWIPITLITAFVLATSAQAAGLQHDYGHLSV 187
Db 127 ANHVFLLYLLHILLDGAAMLTLWVFGTSELPFLCAVLLSAVQAAGLQHDYGHLSV 186
QY 188 YRKPKNHLVHKFVIGHLKGASANNHHRFQHAKPNIIFHKDPDVNMLH--VFVLGEWQ 245
Db 187 PSTSKWNHLLHFFVIGHLKGAPASNNHMHFQHAKPNCFRKDPDINN-HPPFFALGKIL 245
QY 246 PIEYGGKKLKYLPYNHGHYFFLIGPPLIPMYFOYQIIMTMVHKNNWVDLAWAVSYIR 305
Db 245 SVELGKQKKYMPYNNHGHYFFLIGPPLIPMYFOYQIIMTMVHKNNWVDLAWAVSYIR 305
QY 306 FFITYIPYIGLALLFNIRFLESHWVWVVTQNNHIVMEIDQAYRDWFSQLTATCN 360
Db 305 FFLIVPPLGLKAFGLFFIVRFLSNWVWVVTQNNHIVMEIDQAYRDWFSQLTATCN 360

RESULT 10
US-10-191-513A-14
; Sequence 14, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10191513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-14

Query Match 45.2%; Score 1103; DB 15; Length 287;
Best Local Similarity 66.9%; Pred. No. 2.1e-104;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GMTPTLITAFVLATSAQAAGLQHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNHHR 216
Db 8 GGIPAV-----QAQAAGLQHDYGHLSVSTKNNHLLHFFVIGHLKGAPASANNHHR 58
QY 217 HFQHAKPNIIFHKDPDVNMLH--VFVLGEWQIEYGGKKLKYLPYNHGHYFFLIGPPL 274
Db 59 HFQHAKPNCFRKDPDINN-HPPFFALGKILSVELGKQKKYMPYNNHGHYFFLIGPPL 117
QY 275 IPMYFOYQIIMTMVHKNNWVDLAWAVSYIRPITYIPYIGLALLFNIRFLESHW 334
Db 118 LPLYFQWYIFVFIQKRWVDLAWMITFYRFLSNWVWVVTQNNHIVMEIDQAYRDWFS 177
QY 335 VWTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFENDWFSGLNFOIEHLHFTPMR 394
Db 178 VWTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFENDWFSGLNFOIEHLHFTPMR 337
QY 395 NLHKIAPLVKSLCAKGIYQEKPLRALDIIRSLKSGKWLMDAYLHK 444
Db 238 NYHKVAPLVQSLCAKGIYQEKPLRALDIIRSLKSGKWLMDAYLHK 287
```

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RESULT 11
US-10-191-513A-15
; Sequence 15, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (288)...(288)
; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-10-191-513A-15

Query Match
Best Local Similarity 45.2%; Score 1103; DB 15; Length 288;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAAGWLQHDYGHLSVYRKPNHNLVKFVIGHLKGASANNWNR 216
DB 8 GGIPAV-----QAAGWLQHDYGHLSVYRKPNHNLVKFVIGHLKGASANNWNR 58
QY 217 HFQHHAKPNIFHKDPDVMNLH--VFVLGEMQPIEVGKKLKYLPYNHGHYFFLLGPPLL 274
DB 59 HFQHHAKPNIFHKDPDVMNLH--VFVLGEMQPIEVGKKLKYLPYNHGHYFFLLGPPLL 117
QY 275 IPMYFQVQIMTMVHKNWDLAWAVSYIRFFITYIPFYIGLGLALLFNIRPLESHWF 334
DB 118 LPYFQWYIFVYIQRKQWDLAWMITFVYRFFLTVPPLGLKAFGLGFFIVRFLSNWF 177
QY 335 VWTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSCHLNFOIEHHLFPTMPRH 394
DB 178 VWTQNNHIVMEIDQAYRDWFSQLTATCNVEQSFNDWFSCHLNFOIEHHLFPTMPRH 237
QY 395 NLHKAIPVKSCLKAGHIEQKPLLRALLDIRSLKSGKMLDAYLHK 444
DB 238 NYHKVAPVQSLCAKHGIEQKPLLRALLDIRSLKSGKMLDAYLHK 287

RESULT 12
US-10-191-513A-40
; Sequence 40, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-19

Query Match
Best Local Similarity 37.3%; Score 909.5; DB 15; Length 347;
Matches 167; Conservative 43; Mismatches 68; Indels 7; Gaps 4;

QY 19 PT---ESWEEIQKHNLRTDGLVIDRKVYNIITKWSIQHPGQGVIGHYAGEDATDAFRAP 75
DB 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNIITKWSIQHPGQGVIGHYAGEDATDAFRAP 62
QY 76 HPDLEFVGKFLKPLLLIGELAPEPSODHGKNSKITEDFALRKTAEMLFKTNHVFLL 135
DB 63 HINKGLVKKYMSLLIGELAPEPSODHGKNSKITEDFALRKTAEMLFKTNHVFLL 122
QY 136 LLAAHIIALESIAWFTVFYFGNGWIPITLITAFVLATSAQAAGWLQHDYGHLSVYRKPNH 195
DB 123 YLLHILLDDGAALTLWVFGTSPFLLCVALLSAVQAAGWLQHD--GHLSVFSTSKWNH 181
QY 196 LVHKFVIGHLKGASANNWNRHHRHFOHAKNIPHKDPDVMNLH--VFVLGEMQPIEVGKK 253
DB 182 LLHFFVIGHLKGASANNWNRHHRHFOHAKNIPHKDPDVMNLH--VFVLGEMQPIEVGKK 240
QY 254 LKYLPNYHQRHYEYFFLIGPPLIIPMYFYQYQIIMTMVHKNWDLAW 298
DB 241 KKYMPYHQRHYEYFFLIGPPLIIPMYFYQYQIIMTMVHKNWDLAW 285

RESULT 13
US-10-191-513A-19
; Sequence 19, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-513A-19
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Query Match 32.2%; Score 784; DB 15; Length 219;
Best Local Similarity 61.7%; Pred. No. 6.9e-72;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;

QY 157 GWITPILATVATSAQAAGLQHDYGHLSVYRKPKNNHLVHKFVIGHLKGASAKNNHR 216
DB 8 GGIPAV-----QAQAAGLQHDYGHLSVYRKPKNNHLVHKFVIGHLKGASAKNNHR 58

QY 217 HFQGHAKPNIFFHKDPDNNMLH--VFVLGEQPIEYGGKLLKYLPPYNNHQHEYFELIGPEPLL 274
DB 59 HFQGHAKPNCFRKDPDNNM-HPFFALGKLSVELGKQKKYNNHQHYFFLIGPPAL 117

QY 275 IPMYFOYIIMTVMVHQNVDLAWVSYYIRFTITVIFVYILGALLFNFIPLSHWP 334
DB 118 LPLFYQYIFVFIQKQKVDLAWMITFYRFFLTVPVLLGKAFGLGFIIVRFLSNWF 177

QY 335 VVYQNNHIVMEIDOBAYRDFSSQLTATCNVQSRENDFWS 376
DB 178 VVYQNNHIVMEIDOBAYRDFSSQLTATCNVKSAPDNDFS 219

RESULT 14
US-10-191-513A-20
; Sequence 20, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.B3
; CURRENT APPLICATION NUMBER: US/10191.513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (128)...(128)
; OTHER INFORMATION: Xaa = Unknown or other at position 128
US-10-191-513A-20

Query Match 24.1%; Score 587.5; DB 15; Length 182;
Best Local Similarity 62.3%; Pred. No. 7.1e-52;
Matches 101; Conservative 22; Mismatches 36; Indels 3; Gaps 2;

QY 139 HIIAIESIAFWTVFYFGNGWIPTLITAFVLTSAQAAGLQHDYGHLSVYRKPKNNHLVH 198
DB 2 HILLDGAWLTLWVFGTSFLPFLLCVLLSAGVQAAGLQHDYGHLSVYRKPKNNHLH 61

QY 199 KPVIGHLKGASANNHRRHFQHAKPNIFFHKDPDNNMLH--VFVLGEQPIEYGGKLLKY 256
DB 62 HFVIGHLKGASANNHRRHFQHAKPNCFRKDPDNNM-HPFFALGKLSVELGKQKKY 120

QY 257 LPPYNNHQHEYFELIGPEPLLIPMYFOYIIMTVMVHQNVDLAW 298
DB 121 MPYNNHQHYFFLIGPEPLLIPLYFOYIIMTVMVHQNVDLAW 162

RESULT 15
US-09-967-477B-8
; Sequence 8, Application US/09967477B
```

```
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiac Qiu
; APPLICANT: Haiping Hong
; TITLE OF INVENTION: FAD4, FAD5, FADS-2, AND FADS6, NOVEL
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: BN2-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
US-09-967-477B-8

Query Match 20.4%; Score 497; DB 10; Length 459;
Best Local Similarity 27.7%; Pred. No. 4.7e-42;
Matches 132; Conservative 79; Mismatches 176; Indels 90; Gaps 16;

QY 22 SWERTQKNIKRTDGLVIDRKVYNIITKWSIOHPGQORVIGHYAGEDATDAFRAHPDLEF 81
DB 13 SWKEIREHATPATAVIVHVKVYDISKWD-SHPGGS-VMLTQAGEDATDAFVHPSSAL 70

QY 82 VGKFLKPLLIGEL-----APEEPSQD--HGKSKITE---DPRALKRDAEDNNLPTKN 129
DB 71 --KLEQFYVGVDVDETSKAEIEGEPASDEERARRERINEFTIAYRRLRVKYGKGLYDAS 128

QY 130 HVFFELLAHIIALESIAFWTVFYFGNGWIPTLITAFVLTSAQAAGLQHDYGHLSVYR 189
DB 129 ALTYAWKLVSTFGIAVLSMAICFPF-NSFAMVWAGVINGLYFOQSGWLADFLHNQVCE 187

QY 190 KPKNNHLVHKFVIGHLKGASANNHRRHFQHAKPNI-----FHKDPDNNMLHVFVLG 242
DB 188 NRTGLNGLICLVGNAWQGFVSQWKKNNKLNHLHSAKDEGFIGDIDTM-----241

QY 243 EQQPIEYGGKLLKYLPPYNNHQHEYF-----FLIGPELLIPMY-----FOYQI 283
DB 242 ---PILLAWSKENARKAFSAHGPFFIRNOAFLYFELLALLARLSWLAQSFYVTFEFSFI 298

QY 284 I-----MTMIVHKNVVDLAWAVSY-----IRFFITYIPFYIGLALLFNLF 325
DB 299 FDKVEFDGPEKAGLVHYIWI---QLAIFYFCNMSLFEVAYFLMQASCGLLALVF---352

QY 326 IRFLESHWVFWTQNNHIVMEI-DOEAYRDNWFSQLTATCNVQSRENDFWSGHLNFOIE 384
DB 353 -----SIGHNGMSVYERETKPDQWQLQVTTIRASVFMDFWFGGNNYQID 399

QY 385 HHLFPTMPRNLHKLAPLVKSLCAKHGIEYQKPLLRALLDIIIRSLKSKGKLWLDAY 441
DB 400 HHLFPLVPRNLKPNVNLKSLCKEFDIPFHETGWEVGVVDHLDADISKEFITEF 456

RESULT 16
US-09-769-863-14
; Sequence 14, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
```

```
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-09-769-863-14

Query Match      20.0%; Score 487.5; DB 12; Length 453;
Best Local Similarity 27.9%; Pred. No. 4.3e-41;
Matches 133; Conservative 92; Mismatches 164; Indels 87; Gaps 19;

QY 7 QGGAAREVSVPTFSWEEIQKHLRTDGLVDRKYNITKWSIQHPGQORVIGHAGE 66
Db 3 QGQKAEK-----ISWATIREHNRQDNAMIVIHKKYVDISAFE-DHPGGV-VNFTQAGE 53

QY 67 DATDAFRAPHPDLRFVGGKFLKPLLIGEL-----APEPSSQDHGKNSK--ITEPFRALRKT 119
Db 54 DATDAFAVHFSSAL--KLEQYVGVDDQSTAAVDTISDEVKKSQSDFIASVKLRLE 111

QY 120 AEDMNLFTKNHVFLLLAHIIALESIAFTVFVFGNGWIPTLITAFVLATSOAQAGWLQ 179
Db 112 VKRLGLYDSSKLYLYKCASTLSIALVSAACILHF-DSTAMYMVAAVILGLFYQCCGWL 170

QY 180 HDYGHLSYVRKPKNHLVHKFV---IGHL-KGASANWNHHRHFOHAKPNI-----FH 228
Db 171 HDFLHQVFE---NHLFGDLGVNMGVNLQWGFQVQWKNKXNTHAIPNLHATPEIAFH 226

QY 229 KDPDYNMLHFVFLGEPQIEYGGKKLKYLPYNHGHYEYFFLIGPPLLIYMYQYQIIMTI 288
Db 227 GPDIDITPILA--W-----SLKWA---CHAVDSPVG--LFFMYQAYLYPIL 268

QY 289 VHKNWVDLAWAYSIVIRFITVIP-----FYGILGALLFLNFIREFL 329
Db 269 L---FARISWVIOQAWYAFYNNVPGGTDKVOYPLERAGLLLYGWNGLGVYAANMSLL 325

QY 330 ESHWFVWVTQ-----MNHVMEI-DQEAIRDWFSSQLPATCNVQSFNDWFS 376
Db 326 QAAAFLFVQASCGFLFAMVFSVGHNGMEVFDKSKDPFKLQVLSTRNVTSSLWIDWFM 385

QY 377 GHNLFOIEHLFPTRHNLHKAIPVKSCLAKHGIEYQEKPLLRALLDIIRSLKK 432
Db 386 GGLNYQIDHHLFPMVPRHNLPALNVLSLCKQYDIPYHETGFIAGMAEVVHLE 441

RESULT 18
US-10-431-952-14
; Sequence 14; Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/10/431,952
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match      20.0%; Score 487.5; DB 12; Length 453;
Best Local Similarity 27.9%; Pred. No. 4.3e-41;
Matches 133; Conservative 92; Mismatches 164; Indels 87; Gaps 19;

QY 7 QGGAAREVSVPTFSWEEIQKHLRTDGLVDRKYNITKWSIQHPGQORVIGHAGE 66
Db 3 QGQKAEK-----ISWATIREHNRQDNAMIVIHKKYVDISAFE-DHPGGV-VNFTQAGE 53

QY 67 DATDAFRAPHPDLRFVGGKFLKPLLIGEL-----APEPSSQDHGKNSK--ITEPFRALRKT 119
Db 54 DATDAFAVHFSSAL--KLEQYVGVDDQSTAAVDTISDEVKKSQSDFIASVKLRLE 111

QY 120 AEDMNLFTKNHVFLLLAHIIALESIAFTVFVFGNGWIPTLITAFVLATSOAQAGWLQ 179
Db 112 VKRLGLYDSSKLYLYKCASTLSIALVSAACILHF-DSTAMYMVAAVILGLFYQCCGWL 170

QY 180 HDYGHLSYVRKPKNHLVHKFV---IGHL-KGASANWNHHRHFOHAKPNI-----FH 228
Db 171 HDFLHQVFE---NHLFGDLGVNMGVNLQWGFQVQWKNKXNTHAIPNLHATPEIAFH 226

QY 229 KDPDYNMLHFVFLGEPQIEYGGKKLKYLPYNHGHYEYFFLIGPPLLIYMYQYQIIMTI 288
Db 227 GPDIDITPILA--W-----SLKWA---CHAVDSPVG--LFFMYQAYLYPIL 268

QY 289 VHKNWVDLAWAYSIVIRFITVIP-----FYGILGALLFLNFIREFL 329
Db 269 L---FARISWVIOQAWYAFYNNVPGGTDKVOYPLERAGLLLYGWNGLGVYAANMSLL 325

QY 330 ESHWFVWVTQ-----MNHVMEI-DQEAIRDWFSSQLPATCNVQSFNDWFS 376
Db 326 QAAAFLFVQASCGFLFAMVFSVGHNGMEVFDKSKDPFKLQVLSTRNVTSSLWIDWFM 385

QY 377 GHNLFOIEHLFPTRHNLHKAIPVKSCLAKHGIEYQEKPLLRALLDIIRSLKK 432
Db 386 GGLNYQIDHHLFPMVPRHNLPALNVLSLCKQYDIPYHETGFIAGMAEVVHLE 441

RESULT 17
US-10-054-534B-14
; Sequence 14; Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.P1
; CURRENT APPLICATION NUMBER: US/10/054,534B
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-054-534B-14

Query Match      20.0%; Score 487.5; DB 12; Length 453;
Best Local Similarity 27.9%; Pred. No. 4.3e-41;
Matches 133; Conservative 92; Mismatches 164; Indels 87; Gaps 19;
```

Db 112 VKRLGLDYSSKLYLYKCASTLSIALVSAACILHP-DSTAMYVAAVILGLFYQCCGWL 170  
Qy 180 HDYCHLSVYKPKWHLVHPV---ICHL-KGASANWNRHHRHAKENI-----FH 228  
Db 171 HDFLHQVFE---NHLFGDLGVGVNLMWQGSVQWKKRNTHTAIPLNLTATPIAPH 226  
Qy 229 KDPDNNMLHVFVLGEMQPIBYGKKKLYLPYNHCHYEYFFLIGPPLIPMYFYQIIMTI 288  
Db 227 GDDIDTMPILA--W-----SLQWA---QHAVDSPV---LFFMYQAYLVFPIL 268  
Qy 289 VHKWVDLAVNAVSYIRFFITYP-----FYGLGALLFLNIREL 329  
Db 269 L---FARISVIOAMVAFYVNGVGGTFDKVQVPLLERAGLLIYGNLGLVFAANWLL 325  
Qy 330 ESHFVWVWTO-----MMHIVMEI-DOEAYRDNFSSOLTATCNVEQSFNDWFS 376  
Db 326 QAAAFVSVQASGLFLAMVFSVGHNGMEYFDKSKDFKQLVLSRNVTSLLWIDWFM 385  
Qy 377 GHLNFQIEHLFPMPRHNHLKIAPLVKSICAKHGIEYQKPLRALLDIIRSLKK 432  
Db 386 GGLNYQIDHLLFPMVPRHNLPALNVLSKLCQYDIPYHETGFIAGNAEYVVHLE 441

RESULT 19  
US-10-278-391-4  
; Sequence 4, Application US/10278391  
; Publication No. US20030159164A1  
; GENERAL INFORMATION:  
; APPLICANT: KOPCHIK, JOHN J.  
; KELDER, BRUCE  
; HUANG, YUNG-SHENG  
; KIRCHNER, STEPHEN J.  
; MUKERJI, PRADIP  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM  
; PRODUCTS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/278,391  
; FILING DATE: 23-Oct-2002  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,578  
; FILING DATE: 29-MAY-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-03348  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. US20030159164A1 Relevant  
; TOPOLOGY: No. US20030159164A1 Relevant  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-278-391-4

Query Match. 18.8%; Score 459; DB 12; Length 457;  
Best Local Similarity 24.9%; Pred. No. 3.6e-38;  
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;  
Qy 17 SVTPFSWEEI-----QKNLRTDSGLVTRKVVYNTKWSIQHQPQGVIGHVAGEDA 68  
Db 6 SVRTFTRAEVNAEALNEGKDAEAPFLMIIDNKYDVRREVPDPHGGSVILTH-VGKGG 64  
Qy 69 TDAFRAPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEOMNLPKT 128  
Db 65 TDVPTDTHP--EAAWETLANFVVDI--DESDRDI-KNDDFAAEVRKLRITLFSILGYVDS 119  
Qy 129 NHVFFLLLAHIALLESIAWTFVYFG-NGWIPILITAFVLATSAQAQAGMLQHDYGHLSV 187  
Db 120 SKAYTAFKVSFNLCTWGLSTVIVAKGQTSITLANVLSAALLGLFWQCCGWLHDFLHHQV 179  
Qy 188 YRKPKNHLVHKFVIGHLKGASANWNRHHRHAKENIPIHKDPDNNMLHVFVLGEMQPI 247  
Db 180 FQDRFWGLDFGAFLGVCQGFSSSWKDKKNTHTAAAPNVHGEDPDIDTHPLTWSE---- 235  
Qy 248 EYGKKKLYLPYNHCHYEYFFLIGPPLIPMYFYQIIMTIHVKWV-----VDLAWA 299  
Db 236 -----HALENFSDVPDEBETRMWSRF-----MVLNQTFWYFPIILSFARLSWC 277  
Qy 300 VSYIRFFITYPIFYGILGALLFLNFIR--FLESHWFVW----- 336  
Db 278 LQ-SILFVLPGQAKPGSARVPISLVEQLSLAMEN-TWYLATMELFIKDPNNMLVYFLV 335  
Qy 337 -----VTQNNHIVMEI---DQEAYRDNFSSOLTATCNVEQSFNDWFSGLHNFQ 382  
Db 336 SQAVCGNLLAIIVFSLNHNMPVISKEEAVDMDFFTKQITIGRDVHPGLFANWFTGLNYQ 395  
Qy 383 IEHLFPMPRHNHLKIAPLVKSICAKHGIEYQKPLRALLDIIRSLKKSGK 435  
Db 396 IEHLFPMPRHNHLKIAPLVKSICAKHGIEYQKPLRALLDIIRSLKKSGK 448

RESULT 20  
US-10-191-513A-11  
; Sequence 11, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (458)...(458)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-10-191-513A-11

Query Match. 18.8%; Score 459; DB 15; Length 458;  
Best Local Similarity 24.9%; Pred. No. 3.6e-38;  
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;

|    |   |     |  |     |
|----|---|-----|--|-----|
| QY |   | 17  | SVPFSEBEEI-----QXHNRTDSGLVIDRKVNNITKWSIQHGGQRVICHYAGEDA      | 68  |
|    | : | :   | :  | :   |
| Db |   | 6   | SVRFTTAEVLNAEALNEGKKDAEPPLMTIDNKVDVFEBFDHPDGGSVILTH-VGXDG    | 64  |
|    | : | :   | :  | :   |
| QY |   | 69  | TDAFRAFHDLEFVGFKLPLLGLAPEPSSODHGKNSKITEDFAEKTAEDNMNLFKT      | 128 |
|    | : | :   | :  | :   |
| Db |   | 65  | TDVCTFHP--EAWEFLANFYVGDI---DSDDRDI-KNDDFAAEVFKLTLEFQSUGYYDS  | 119 |
|    | : | :   | :  | :   |
| QY |   | 129 | NHVFFLLLAHHIALESIANFTVFPYG-NGWIPTLITAFVLATSQAQAGWLQHDYCHLSV  | 187 |
|    | : | :   | :  | :   |
| Db |   | 120 | SKAYYAFKVSPNLICWGLSTVIIVAKWGOTSTLANVLSAALLGLFWCQCGLAHDELHQV  | 179 |
|    | : | :   | :  | :   |
| QY |   | 188 | YRKPKNHLVHKPFYIGHLKASANNWNHRHFQHUAENPHFKDDPDVNMLHVFVLEWQPI   | 247 |
|    | : | :   | :  | :   |
| Db |   | 180 | FQDRFGWDLFOAFJGGVCQGFSWKDKKNTHAAPNVRGEDPIDTHPLTWGE----       | 235 |
|    | : | :   | :  | :   |
| QY |   | 248 | EYGKKKIKYLPYNHQBHEFFYLGPPLLIIMFYOYQIINTMIVHKNW-----VDLAWA    | 299 |
|    | : | :   | :  | :   |
| Db |   | 236 | -----HALEMFSDVPEELTRMSRF----MVLNQTWFYPFILSFAELSWC            | 277 |
|    | : | :   | :  | :   |
| QY |   | 300 | VSYVIRPITIYPYGILGALLFNIFR--FLSSHFWV-----                     | 336 |
|    | : | :   | :  | :   |
| Db |   | 278 | LQ-SILFVLPNGQAHKPSGARVPISLVEQLSLAMHW-TWYLATMFLFKDPYNNMLVPLYV | 335 |
|    | : | :   | :  | :   |
| QY |   | 337 | -----VTOMNHIMEI---DOEAYRDVSSFOLTATCNVEOSPFENDWFSGHNFQ        | 382 |
|    | : | :   | :  | :   |
| Db |   | 336 | SOAVCGNLLAIVPSLNHNHNPVISKEBAVMDFFTQIITGRDVBHCLPANWFTUGLNIQ   | 395 |
|    | : | :   | :  | :   |
| QY |   | 383 | IEHLLFTMPMRNNLHKIAPLVKSLCAKHGIEYOEKPLLRALLDIIRSLKKSGK        | 435 |
|    | : | :   | :  | :   |
| Db |   | 396 | IEHLLFTSMPRHNFSKIQPAVEILCKRYNNRVHTTGMIETGAERTSRNLNEVSK       | 448 |
|    | : | :   | :  | :   |

```

RESULT 21
US-10-191-513A-41
; Sequence 41, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US96/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

```

```

69 QY TDAPRAEPDLEFVGKFLKPLTIGELAPEPEPQDGHGKSKITEDPRALRKTAEDMNFLEKT 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 Db TDVPTDTHP--EAAWETLANFYVGDI--DESDDI-KXDDFAAEVRKLRTLFQSLGYVDS 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 QY NHVEFLLLAHIALESIANFVYFVG-NGWPTLITAPVLATSOAQAGWLOCHDYGHLSV 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 Db SKATYAKVSNFCINGLSVTIVAKWGQTSITUANVLSAALLGLFWOCCGWLHADFLLHQV 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
198 QY YRKPKMNLHVKEVIGHLKGASANNMNRHFOHAKPNI FHKDPDVNMLHVFLVGEWQPI 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
180 Db FQDRFWGDLFGAFLGGVCGCGSSWWKDXNTHAA PNVHGSDPDIDTHPLLTWSE---- 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
248 QY EYGKKLKYLPYNHQHEHYFLIGPPLIDMYFOYQIIMTIVHKNW-----VDLAWA 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
236 Db -----HALENFSDPDELTAKWSRF-----MVLNQTWFFPILSPARJUSWC 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 QY VSVYIRFFITYIPFYGILGALLFLNPIR--FLESHFWV----- 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
278 Db LQ-SILEVLPNGQAHKPSGARVPISVEQLSAMHW-TWYLATWFLFKDPVNNLVYFLV 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
337 QY -----VTCMHNIWEI-----DOEAYRWFSOQTATCNVEQSFENDWFGSHLNFQ 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
336 Db SOAVCGNLLAIVFSLNHNGKPIXSEAEVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQ 395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
383 QY IEHLFPTMPRNLHKAIPVLSLCAKHGIEYOEKPLLRALLIDIRSLKSGK 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
396 Db IEHLFSPMRHNFNSKIQPAVETLCKYNNRVHTTGMIEGTAEVFSRLNEVSK 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 22
US-10-340-779A-11
; Sequence 11, Application US/10340779A
; Publication No. US20030152963A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobatt, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Helianthus annuus
US-10-340-779A-11

```

|     |  |     |
|-----|--|-----|
| 78  | -DIEFVGKFLKPLLIGELAPESQDHGKNSKITEDPRAKRTAEDNMNLEKTNHVFPLLL | 136 |
| QY  |  |     |
| 82  | LDKLFYGHLYKQV-----SDISRDYRKELASEFAKAGMEPKKGHGVIYS          | 126 |
| DB  |  |     |
| 137 | LAHIIALESAMPVTFYFGNGHPIITIAFVLATLSQAQWLQDHYGHLVSRYRKPKNHL  | 196 |
| QY  |  |     |
| 127 | LCFVSLILSACVGVLYSGSEWI-HMLSGAILGLAWMOIAYGLHDAGHYOMATRGKNKF | 195 |
| DB  |  |     |

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QY 197 VHKFVIGHLKASANNWNRHFOHAKNPINPHKDPDVNMLHVF-----VLGEWQPIBYGK 251
DB 186 AGIFIGNCITGISIAWKKWTNAHIAACNSLDYDPLQHLPLMVAASKLNSITSFYG- 244
QY 252 KKLKXLP-----YHQHEFFELIGPPLIPMYFOYQIIMTMIVHKWVLDLAWAVSYIRF 306
DB 245 RQLAFDPLARFFVSQVHYLYPIMCVARNVLYL--QILLISKRK----- 288
QY 307 FITYIPFYG--ILGALLFLNFIRESHWFW-----VTOMNHVMEIDQ--- 349
DB 289 ----IPDRGLNLGLTFTWTFPLVLSRLPNPBRVAFVLVSFCVTGICHIQITLNFSG 344
QY 350 EAY-----RDWFSSQLTATCNVEOSPFNDWFSGHLNFOIEHHLFPTMPRHNLHKIAPLV 403
DB 345 DVIYVPPKGDWFEKQTRGTIDACSSWMDNFFGGLQFQLEHHLFPLPCHLRSISPIC 404
QY 404 KSLCAKHGIEYOEKPLLRALLDIIRSLK 431
DB 405 RELCKXNLPYVSLSYFDYANVTTLKTLR 432

RESULT 23
US-10-340-779A-13
; Sequence 13, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Borago officinalis
US-10-340-779A-13

Query Match 17.9%; Score 436.5; DB 12; Length 448;
Best Local Similarity 29.0%; Pred. No. 7,1e-36;
Matches 130; Conservative 63; Mismatches 182; Indels 73; Gaps 16;

QY 24 BEIQKHLRTDSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGEDATDAFRAHP----- 77
DB 12 DELKNDKPGDLWISIQKAYDVSDWKDPHGGSPFLKSLAQGEVTDFAVAFHPASTWKN 71
QY 78 -DLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEADNLP-KTNHVFLL 135
DB 72 LDKFFTGYLKYDSV-----SEVSKDYRLKLVFEFSKGLYDKKGHIMP-A 115
QY 136 LLAHIIALESIAWFTVYFGNGWIPITLITAFVLSQAQGLQHDYGLSHLYRKPKNH 195
DB 116 TLFCLFAMLFAMSVYGVLFCEGVVHLFSGCLMGFLWISQGMIGHDAGHVMVSDRLNK 174
QY 196 LVHKFVIGHLKASANNWNRHFOHAKNPINPHKDPDVNMLHVFVL-----GEWPIBYG 250
DB 175 FMGIFAANCLSGISIGWKNWNNHAIACNSLEYDPLQYIPPLVSSKFFGSLTSHFYE 234
QY 251 KK-----KLKYLPHNHOHEFFELIGPPLIPMYFOYQIIMTMIVHKWVLDLAWAVSYIRF 306
DB 235 KRLTFDSLSPFFVSQYQHTFYPIMCAARLNMVQ-SLIM-LITKN-----VSRYA--- 283

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QY 307 FITYIPFYGILGALLFLNFIRES-----FW-----VVTOMNHVMEID--QEA 351
DB 284 -----HELLCCLVFSIWPVLVCLNPNWGRINMFVTSASLVTKNQVQVSLNHFSSV 336
QY 352 Y-----RDWFSSQLTATCNVEOSPFNDWFSGHLNFOIEHHLFPTMPRHNLHKIAPLV 405
DB 337 YVGPKNWFEKQTRGTIDISCPWMDWFGGLQFQIEHHLFPPKPRCNLKRKISPYVIE 396
QY 406 LCAKHGIEYOEKPLLRALLDIIRSLK 433
DB 397 LCKKNLPPYASFSKANEMTUTLRT 424

RESULT 24
US-10-029-756-5
; Sequence 5, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-029-756-5

Query Match 17.6%; Score 429.5; DB 14; Length 448;
Best Local Similarity 28.8%; Pred. No. 3.7e-35;
Matches 129; Conservative 63; Mismatches 183; Indels 73; Gaps 16;

QY 24 BEIQKHLRTDSGLVIDRKVYNTKWSIQHPGQQRVIGHYAGEDATDAFRAHP----- 77
DB 12 DELKNDKPGDLWISIQKAYDVSDWKDPHGGSPFLKSLAQGEVTDFAVAFHPASTWKN 71
QY 78 -DLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEADNLP-KTNHVFLL 135
DB 72 LDKFFTGYLKYDSV-----SEVSKDYRLKLVFEFSKGLYDKKGHIMP-A 115
QY 136 LLAHIIALESIAWFTVYFGNGWIPITLITAFVLSQAQGLQHDYGLSHLYRKPKNH 195
DB 116 TLFCLFAMLFAMSVYGVLFCEGVVHLFSGCLMGFLWISQGMIGHDAGHVMVSDRLNK 174

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QY 196 LVHKEVIGHLKGSANWNNHRRFHQHAKEPNI FHKDPDNNMLHVFVL-----GEMQPIEYG 250  
 DB 175 FMGIFAANCLSGISIGWKNWNAHHAACNSLEYDDPDLOXIPFLVSSKFFGSLTSHFYE 234  
 QY 251 KK-----KLKYLPHNHOHEYFFLIGPPLLIPMYFOYQIIMTWIHHKNWVDLAWAVSYIRF 306  
 DB 235 KRLFDLSLRSFVSQHWTFPIWCAARLNNYQ-SLIM-LLTKRN-----VSYZAQ- 284  
 QY 307 FITYIPFYGIIGALLFLNFIRES---HW-----FV-----WVTOMNHVMEID---OEA 351  
 DB 285 -----ELGCLVFSWYPLLVSCLPNWGERIMFVIASLVTGMOQVQFSLHFSSV 336  
 QY 352 Y-----RDWSSQLTATCNVQSFDFSGHLNFOIEHLLFPTMPRHNLHKAIPLVKS 405  
 DB 337 YGKPKGNWFEKQDGLDLSCPWMDWFGGSGQFQIEHLLFPMPRCNLRKISPIVIE 396  
 QY 406 LCAKHGIBYQEKPLRLALLDIIRSLKS 433  
 DB 397 LCKKHLPYNYASFPSKANEMTLRLNT 424  
 RESULT 25  
 US-10-029-756-27  
 ; Sequence 27, Application US/10029756  
 ; Publication No. US20020108147A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thomas, Terry L.  
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/10/029,756  
 ; FILING DATE: 21-Dec-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/934,254  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Presser, Leopold  
 ; REGISTRATION NUMBER: 19,827  
 ; REFERENCE/DOCKET NUMBER: 9383ZYXWVU  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 27:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 452 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
 US-10-029-756-27  
 Query Match 16.9%; Score 411.5; DB 14; Length 452;  
 Best Local Similarity 25.6%; Pred. No. 2.6e-33;  
 Matches 115; Conservative 80; Mismatches 168; Indels 87; Gaps 16;  
 QY 9 EGAEREVSVPTFSWIEIOKHNLTDSGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDA 68

DB 2 EGEAKKYITA-----EDLRRHNKSGDLWISIQGVYDCSRWABHPGGEVPLLSLAGQDV 56  
 QY 69 TDAFPAFPDLEFVCKFLKPLILIGELAPEBSQDHGKSKITEDFRALRKTAEADNMLF-- 126  
 DB 57 TDAFAYHPGTAW--RHLDPLFTGYIYKDK-----FEVSEISKYVRLNENMSGPIPEK 109  
 QY 127 KTNHVEFFLL-----LLAHIIALESIAWFTVYFQNGWIPITLITAFVIAATSOAQAGW 177  
 DB 110 KGHIMWTFVGVAVVMAAIVYGVLASVSG-----VHMLCAGLLGLLWIAAY 157  
 QY 178 LOHDYGHISVYKPKWNLHVKFVIGHLKGSANWNNHRRFHQHAKEPNI FHKDPDNNMLH 237  
 DB 158 VGHDSGHVQVMPTRGNRITQIAGNITLIGSIAWKTWTHNAHLACNSLDYDPLQHIP 217  
 QY 238 VF-----VLGEQPIEYGGKKLKY-----LPYNHQBHEYPFLIGPPLLI--PMYFQYQI 283  
 DB 218 VFAVSTRLENSITSVFYG-RVLKPDVARFLVSYQHWTYV-----PVMIFGVNLFITQ 270  
 QY 284 IMTMVHKWVDLA-----WAVSYVIREFTIYIPYVIGLIGALLFNFIRESHWF 334  
 DB 271 FLLLTTRDVPDRALNLMGIAVFWT---WFFLVVSCLPNHPERFGFVLISFA----- 319  
 QY 335 VVYTMNHVMEIDQ---EAY-----RDWSSQLTATCNVQSFDFSGHLNFOIEH 385  
 DB 320 --VTAICHVQFTLNHPSGDTYVGPKNWPEKQTKGTIDITCPPWMDWFFGGLQFQLEH 377  
 QY 386 HLPFTMPRHNLHKAIPLVKS LCAKHGIBYQ 415  
 DB 378 HLPFLPRGQLRKIAPLARDLCKKHGMPYR 407  
 RESULT 26  
 US-10-054-534B-35  
 ; Sequence 35, Application US/10054534B  
 ; Publication No. US20030167525A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Huang, Yung-Sheng  
 ; APPLICANT: Das, Tapas  
 ; APPLICANT: Thurmond, Jennifer M.  
 ; APPLICANT: Pereira, Suzette L.  
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
 ; FILE REFERENCE: 6763.US.P1  
 ; CURRENT APPLICATION NUMBER: US/10/054,534B  
 ; PRIOR FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: US 09/769,863  
 ; PRIOR FILING DATE: 2001-01-25  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 35  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Isochrysis galbana  
 US-10-054-534B-35  
 Query Match 16.3%; Score 398.5; DB 12; Length 442;  
 Best Local Similarity 27.9%; Pred. No. 5.4e-32;  
 Matches 116; Conservative 73; Mismatches 174; Indels 53; Gaps 13;  
 QY 25 EIQKHNLRTDSGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATDAFRAHPDLEFVGK 84  
 DB 35 DVTVSSIDAEMKEMINGRVYDVSFVKHFGGS-VIKFQLGADASDAVNNFVRSKKADK 93  
 QY 85 FLKPLIGELAPEEPSQDHGKSKITEDFRALRKTAEADNMLFKN--HVFF--LILLIAHI 140  
 DB 94 MLXSL-----PSRPAEAGYAQDDISRDFEKLRLKEEGYFEENLVHVSRYCDEVILAMY 147  
 QY 141 IALLESIAWFTVYFGNGWIPITLITAFVLATSOAGMLQHDYHLSVYRKPKNHVLVHKF 200  
 DB 148 WAGVQLIWSGVWFLG-----AIVAGIAQGCGLWQHEGGHYSLTGNKIKIDRHILQMA 198  
 QY 201 VIGHLKGSANWNNHRRFHQHAKEPNI FHKDPDNNMLHVFVLGEWQPIEYGGKKLKYLPYN 260

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Db 199 IYGLGCMSCYWRNQHKNHATPOKLGTDPLQTMPLVAFKHVCAKARGKAWLAW- 257
Qy 261 HQHEYFLGPPILLIMYFOYQIIM- - - - - TMIVHKWVDLAWAVSYIRFFIT- - - - - 309
Db 258 -QAPLFF- -GGIICSLVSFGQVFLPHNHALRVH-NHLELAYMGLRYVLWHLAFHGLGL 313
Qy 310 - - - - - YIPFYGILGALLFLNFIREFLSHFWVWVTQNNHIVMEIDOEAYRDWSSQLTATC 364
Db 314 SSLRLAFYVAVGTVFTNF-AVSHTHKDV-VPTKHI- - - - - SWALYSANHTT 361
Qy 365 NVQSPFNDFSHLAFQIEHHLFPTMPRNLHKAIPVKSICAKHIEYQOEKPL 420
Db 362 NCSDSPFVNMWMLNFQIEHLLFPSPQYNHHPKAPRVLRALFEKHGVYDVRPYL 417

RESULT 27
US-09-769-863-29
; Sequence 29, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium aureum
US-09-769-863-29

Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;

Qy 1 MGKGNQGEAAAREVSVPTFSWBEIQKHNLRDLSGLVIDRKVYNITKWSIQHPGQORVI 60
Db 1 MGRGEGQVNSA- - - - - QVAQGGAGTRKTILIEGEVDVT--NFRHPGGS-II 45
Qy 61 GHYAGE- - - - - DATDAFRAFPDLEFVGKFLKPL-LIGELAPEE- - - - - PSQDHGKNSKITE 111
Db 46 KFLTTDGTAEVDATNAPREFHCRSGKAEKYLKSLPKLG- - - - - APSQKFDKAEQARRDAITR 103
Qy 112 DFRALRKTAEADNMLFKTNHVFLLLAHIIALESIAWFTVYFGNGWIPTLITAFVLATS 171
Db 104 DYVKLRERWVAEGLFKPAPLHIVVPFAELALFAASFLPSMRGNVF-ATLAAIavgGIA 162
Qy 172 QAQAGWLQHDYGHLSVYRKPKNHVLHVFVGHUKGASANNWNRHFOHAKPNI FHKDP 231
Db 163 QGRGWLMECHGCHFSMTGYIPLDVRLOELVYGVGCSMSASWRYOHNKHAATPOKLKHV 222
Qy 232 DVNMLHVFVLGE- - - - - WQPIEYGGKKLKLPLYNHQBHYEFLIG- - - - - PPLLIPIMYF 279
Db 223 DDTLPLVAFNEKIAAKVRPSFQAKWLSAQAYIFAPVSCFLVGLFWTLFLHPRHMPRTS 282
Qy 280 QYQIIMTIVH-KNWVDLAWAVSY-IRFFITYIPFYGILGALLFLNFIREFLSHFWVW 337
Db 283 HFAEMAARVAVRVGVAALMHSGSDSFGLYMATFGCTYIFTN- - - - - FAVSHTHLDV 339
Qy 338 TQNNHIVMEIDOEAYRDWSSQLTATCNV-BQSFPNDWFSGLHAFQIEHHLFPTMPRNL 396
Db 340 T- - - - - EPDEFHWEVAALHTTNVSDNSWFTWMSYLNFOIEHHLFSPSLPOLNA 390
Qy 397 HKIAPLVKSLCAKHGIEYQOEKPLLRALLDIIRSLKSKG 435
Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429

RESULT 28
US-10-054-534B-29
; Sequence 29, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.P1
; CURRENT APPLICATION NUMBER: US/10/054,534B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium aureum
US-10-054-534B-29

Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;

Qy 1 MGKGNQGEAAAREVSVPTFSWBEIQKHNLRDLSGLVIDRKVYNITKWSIQHPGQORVI 60
Db 1 MGRGEGQVNSA- - - - - QVAQGGAGTRKTILIEGEVDVT--NFRHPGGS-II 45
Qy 61 GHYAGE- - - - - DATDAFRAFPDLEFVGKFLKPL-LIGELAPEE- - - - - PSQDHGKNSKITE 111
Db 46 KFLTTDGTAEVDATNAPREFHCRSGKAEKYLKSLPKLG- - - - - APSQKFDKAEQARRDAITR 103
Qy 112 DFRALRKTAEADNMLFKTNHVFLLLAHIIALESIAWFTVYFGNGWIPTLITAFVLATS 171
Db 104 DYVKLRERWVAEGLFKPAPLHIVVPFAELALFAASFLPSMRGNVF-ATLAAIavgGIA 162
Qy 172 QAQAGWLQHDYGHLSVYRKPKNHVLHVFVGHUKGASANNWNRHFOHAKPNI FHKDP 231
Db 163 QGRGWLMECHGCHFSMTGYIPLDVRLOELVYGVGCSMSASWRYOHNKHAATPOKLKHV 222
Qy 232 DVNMLHVFVLGE- - - - - WQPIEYGGKKLKLPLYNHQBHYEFLIG- - - - - PPLLIPIMYF 279
Db 223 DDTLPLVAFNEKIAAKVRPSFQAKWLSAQAYIFAPVSCFLVGLFWTLFLHPRHMPRTS 282
Qy 280 QYQIIMTIVH-KNWVDLAWAVSY-IRFFITYIPFYGILGALLFLNFIREFLSHFWVW 337
Db 283 HFAEMAARVAVRVGVAALMHSGSDSFGLYMATFGCTYIFTN- - - - - FAVSHTHLDV 339
Qy 338 TQNNHIVMEIDOEAYRDWSSQLTATCNV-BQSFPNDWFSGLHAFQIEHHLFPTMPRNL 396
Db 340 T- - - - - EPDEFHWEVAALHTTNVSDNSWFTWMSYLNFOIEHHLFSPSLPOLNA 390
Qy 397 HKIAPLVKSLCAKHGIEYQOEKPLLRALLDIIRSLKSKG 435
Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429

RESULT 29
US-10-431-952-29
; Sequence 29, Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
```

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Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429

RESULT 28
US-10-054-534B-29
; Sequence 29, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.P1
; CURRENT APPLICATION NUMBER: US/10/054,534B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium aureum
US-10-054-534B-29

Query Match 16.3%; Score 398; DB 12; Length 439;
Best Local Similarity 28.1%; Pred. No. 6.1e-32;
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;

Qy 1 MGKGNQGEAAAREVSVPTFSWBEIQKHNLRDLSGLVIDRKVYNITKWSIQHPGQORVI 60
Db 1 MGRGEGQVNSA- - - - - QVAQGGAGTRKTILIEGEVDVT--NFRHPGGS-II 45
Qy 61 GHYAGE- - - - - DATDAFRAFPDLEFVGKFLKPL-LIGELAPEE- - - - - PSQDHGKNSKITE 111
Db 46 KFLTTDGTAEVDATNAPREFHCRSGKAEKYLKSLPKLG- - - - - APSQKFDKAEQARRDAITR 103
Qy 112 DFRALRKTAEADNMLFKTNHVFLLLAHIIALESIAWFTVYFGNGWIPTLITAFVLATS 171
Db 104 DYVKLRERWVAEGLFKPAPLHIVVPFAELALFAASFLPSMRGNVF-ATLAAIavgGIA 162
Qy 172 QAQAGWLQHDYGHLSVYRKPKNHVLHVFVGHUKGASANNWNRHFOHAKPNI FHKDP 231
Db 163 QGRGWLMECHGCHFSMTGYIPLDVRLOELVYGVGCSMSASWRYOHNKHAATPOKLKHV 222
Qy 232 DVNMLHVFVLGE- - - - - WQPIEYGGKKLKLPLYNHQBHYEFLIG- - - - - PPLLIPIMYF 279
Db 223 DDTLPLVAFNEKIAAKVRPSFQAKWLSAQAYIFAPVSCFLVGLFWTLFLHPRHMPRTS 282
Qy 280 QYQIIMTIVH-KNWVDLAWAVSY-IRFFITYIPFYGILGALLFLNFIREFLSHFWVW 337
Db 283 HFAEMAARVAVRVGVAALMHSGSDSFGLYMATFGCTYIFTN- - - - - FAVSHTHLDV 339
Qy 338 TQNNHIVMEIDOEAYRDWSSQLTATCNV-BQSFPNDWFSGLHAFQIEHHLFPTMPRNL 396
Db 340 T- - - - - EPDEFHWEVAALHTTNVSDNSWFTWMSYLNFOIEHHLFSPSLPOLNA 390
Qy 397 HKIAPLVKSLCAKHGIEYQOEKPLLRALLDIIRSLKSKG 435
Db 391 PRVAPRVRALFEKHGMAYDERPYLTALGDTFANLHAVGQ 429

RESULT 29
US-10-431-952-29
; Sequence 29, Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
```

APPLICANT: Das, Tapas  
APPLICANT: Thurmond, Jennifer  
APPLICANT: Pereira, Suzette L.  
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
FILE REFERENCE: 6763.US.01  
CURRENT APPLICATION NUMBER: US/10/431,952  
PRIOR FILING DATE: 2003-05-08  
PRIOR APPLICATION NUMBER: US/09/769,863  
PRIOR FILING DATE: 2001-01-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 29  
LENGTH: 439  
TYPE: PRT  
ORGANISM: Thraustochytrium aureum  
US-10-431-952-29

Query Match 16.3%; Score 398; DB 12; Length 439;  
Best Local Similarity 28.1%; Pred. No. 6.1e-32;  
Matches 129; Conservative 74; Mismatches 202; Indels 54; Gaps 15;

QY 1 MGKGGNCGEAGAEVSVPTFSWEEIQKHNLRTDSGLVIDRKVYNITKWSIQHPGGQVVI 60  
Db 1 MGRGEGQUNSA-----QVAGGAGTRKTIIEGEVYDVT--NFRHPGGS-II 45  
QY 61 GHYAGE-----DATDAFRAHFDLEFGVKFLKPL-LIGELAPEE---PSQDHGKNSKITE 111  
Db 46 KELTDTGTEAVDATNAFREFHCRSGKAEKYLKSLPLG--APSKMKFPAKQARRDAITR 103  
QY 112 DFRALKRTAEDNLFKTNHVPFLLLAHIALESIAFWTFVFGNGMPTIITAFVLATS 171  
Db 104 DTVKUREEMVAEGLFKPADLHVIFAFIAALFAASFVLFVSGNVF-ATLAAAVAGGIA 162  
QY 172 QAAQAGHLOHDYGHLSYVRKPKNHLVHKFVI GHLKGASANNWNHHRFOHAKNPIFKHP 231  
Db 163 QCRGWLMECHGFSMTGYIPLDVLQELVYGVGSGMSASWVQHNKHATPQKLKHDV 222  
QY 232 DVNMLHVFVLGE-----WQPIEVGKKLKLKLYPNHQHEVFFLIG-----PPLLIPMYF 279  
Db 223 DTDITLFLVAFNFKIAKVRFGSQAKWLSAQAYIFAPVSCFLVGLFWTLFLHPRHPTS 282  
QY 280 QYQIIMTIVH-KNNVVDLAWAVSY-IRFFITYIPYGLGALLFLNFIRESHFWVW 337  
Db 283 HFAEMAARVVRVGVMAALMHSFGYSGSDSGLYMATFGCTYIFTN---FAVSHTHLDV 339  
QY 338 TQNHVIMEDQAEYRDWFSSQLTATCNV-EOSFFNDWFSGLHNFQIEHLLPPTPRENL 396  
Db 340 T-----EPDEFUHWVEYAAALHTNVNSDWSFITWMSYLNFIQIEHLLPPTPRENL 390  
QY 397 HKIAPLVKSLCAKHGIEYOEKPLLRALLDIIRSLKXSGK 435  
Db 391 PRVAPVRALFEKGGWAYDERPVLTAIGDTFANLHVGQ 429

RESULT 30  
US-10-340-779A-20  
Sequence 20, Application US/10340779A  
Patent No. US20030152983A1  
GENERAL INFORMATION:  
APPLICANT: Napier, Johnathan A.  
APPLICANT: Michaelson, Louise  
APPLICANT: Stobart, Keith  
TITLE OF INVENTION: Desaturase  
FILE REFERENCE: 005407.00004  
CURRENT APPLICATION NUMBER: US/10/340,779A  
CURRENT FILING DATE: 2003-03-24  
PRIOR APPLICATION NUMBER: US 09/582,034  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: FCT/GB98/03895  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: UK 9814034.6  
PRIOR FILING DATE: 1998-06-29  
PRIOR APPLICATION NUMBER: UK 9727256.1

PRIOR FILING DATE: 1997-12-23  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 443  
TYPE: PRT  
ORGANISM: C. elegans  
US-10-340-779A-20

Query Match 16.2%; Score 395.5; DB 12; Length 443;  
Best Local Similarity 28.0%; Pred. No. 1.1e-31;  
Matches 122; Conservative 62; Mismatches 174; Indels 77; Gaps 18;

QY 37 LVDRKVNIT-----KWSI-----QHPGQORVIGHYAGEDATDAFRAHP----- 77  
Db 1 MYVDKNASGLRMKVDGKMLYSEELVKKHPGG-AVIEQYKNSDATHIFAPHEGSSQAYK 59  
QY 78 --DL-----EFVGKFL-KPLLIGELAPEEPPSQDHGKNSKITEFRALKRTAEDNLF 126  
Db 60 QLDLLKKHGEHDEFFLEKLEKLDKVDINVSAYDVSAQEKWVESFEKLRQKLDHDDGLM 119  
QY 127 KTNHVEFLLLAHIALESIAFWTFVFGNGMPTIITAFVLATSQAQAGHLOHDYGHLS 186  
Db 120 KANETVFLFAISTLSINAFAYQLY-----GWYIT--SACLLALAWQOFGWLTHEFCQQ 174  
QY 187 VVRKPKNHLVHKFVI GHLKGASANNWNHHRFOHAKNPIFKHPDPVNM--LRHVFVLGEW 244  
Db 175 PFKNRRLNTISLFGNFGLOGFSRDKWKDKNTHAATNVIDHGDIDLAPLFAPIPGDL 234  
QY 245 --QPIBYGKKKLYLPYNHQHEVFFLIGPPL-----LIPMYFQYQIIMTIVHKN--W 293  
Db 235 CKYKASFEKAILKIVPY--CHLYFTAMLEPLRFSWTGQSVQVWFENQMEYKYQYQENAFW 292  
QY 294 VDLA-----NAVSVYIRFFITYIPF---YGIL-----GALLFLNFIRESHFWVWVQNMH 342  
Db 293 EQATVGHWAQVYQFLPTPLVAVYFIISOMGGILLIAHVVF-----NH 340  
QY 343 IVME---IDQAEYRDWFSSQLTATCNVEOSFFNDWFSGLHNFQIEHLLPPTPRENLHKKI 399  
Db 341 NSVDKYPANSRIINFAALQILTRNTPTSPFIDMLWGLNFIQIEHLLPPTPRENLNAC 400  
QY 400 APLVKSCLCAKHGIEY 414  
Db 401 VKYVKEWCKENNLUPY 415

RESULT 31  
US-09-967-477B-6  
Sequence 6, Application US/09967477B  
Patent No. US20020156254A1  
GENERAL INFORMATION:  
APPLICANT: Xiao Qiu  
APPLICANT: Haiping Hong  
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL  
FILE REFERENCE: ENZ-001  
CURRENT APPLICATION NUMBER: US/09/967,477B  
CURRENT FILING DATE: 2002-04-16  
PRIOR APPLICATION NUMBER: 60/236,303  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 60/297,562  
PRIOR FILING DATE: 2001-06-12  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 456  
TYPE: PRT  
ORGANISM: Thraustochytrium sp.  
US-09-967-477B-6

Query Match 15.2%; Score 369.5; DB 10; Length 456;  
Best Local Similarity 24.3%; Pred. No. 5.3e-28;  
Matches 118; Conservative 86; Mismatches 179; Indels 103; Gaps 21;

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QY 21 FSEBIOKHLNRTDGLVDRKYNITKSIQHPGQORVIGHVAGEDATDAFAHEPDLE 80
Db 9 FTQWEVAKENTAKSAWIIIRGEVIDTEWADKHPGGSSELIVLHSGRECTDTFYSHPPSN 68
QY 81 FVGKFLKPLLIGELAP--BEP--SODHGKNSKITEDFRALRKTAEADNLFKTNHVFLL 136
Db 69 RADKILAKYKIGLVGGYEPFVKPDGSGFYKECSE-----RVAE---YFTNNLDPKAA 119
QY 137 LAHIIALESIAWTFVFGNGNITPTL-ITAFVLATSOAQAGW-----LQHD 181
Db 120 FAGL-----WRWVFVFAVALAYMGWNLIPGNVYQAVAMGVFGVQALPLLVHMD 172
QY 182 YGHLVSVYRKPKNHVKFVIGHLKAS-ANWNNHRHFQHKAPNIFHKDPDVNMLHVEV 240
Db 173 SSHAACSSPAMQIIIGRVMDWFAGASMYSLNQHVVGGHIVTNVAGADPDL----- 225
QY 241 LGWQPIEYK-----KKUKYLP-YNHQHEYFLGPPL--LIPMYFQYQIIMTVH- 290
Db 226 -----PVDFSDVRRIVHRQVLLPIYKFQHIYL-----PPLYGLVKFRIQDVFETVSL 276
QY 291 -----XWVDLAWAVSYIRFFITYIP-----FYGILGALLFLNFI 328
Db 277 TNGVRVNPVPSDWQOMIFAKAFW-TFYRIYIPLAWLKITPSTFWGV-----FLAE 328
QY 329 LESHWFV-WYTMNHVMEID-----QRAYRDNFSSQLTATCN-VEQSFNDWFSGH 378
Db 329 FTTGWYLAFFQVSHVSTECYPCGDAPSAEVDGSAISQVKSVDYAHGSPLAALFGA 388
QY 379 LNFOIEHLRPTMPRNLHKLAPLVKSLCAKHGEYQCEK-LLRALLDIIRSLKSGKLM 437
Db 389 LNYQVTHLYPGISQYHPALAPIIIDVCKYNIKYTVLFTFTEALLAHFKLKNWGLG 448
QY 438 LDAYLH 443
Db 449 KPVEIH 454

RESULT 32
US-10-340-779A-4
; Sequence 4, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340.779A
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 448
; TYPE: PRT
; ORGANISM: C. elegans
US-10-340-779A-4

Query Match 14.9%; Score 363; DB 12; Length 448;
Best Local Similarity 26.5%; Pred. No. 2.4e-28;
Matches 109; Conservative 66; Mismatches 164; Indels 72; Gaps 13;

QY 53 HPGQORVIGHVAGEDATDAFAFHDPDLFVGVKFLKPLLIGELAPEEP----- 99
Db 30 HPGGS-ALITYKNMATTVFHTFHTGSKAEQVWLTEKLKCECTQEPPIKDQPIKGI 88
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QY 100 -----SODHGKNSKITEDFRALRKTAEADNLFKTNHVFLLLIIAHIIALSIAWFTV 151
Db 89 DDVNMGTNISEKESAOINKSFTDLRVRVAEGLMGDSPFYIRKI-----LETI--FTI 141
QY 152 ---FY--FGNWIPTLITAFVLATSOAQAGWLOHDYGHLSVYRKPKNHVLVHKEVIGHLK 206
Db 142 LFAYFLOVHTYLP---SAILMGVAMQOLGWLIIHEFAHQFLKRNRYNDLASFYVGNFLQ 198
QY 207 GASANWNNHRHFQHKAPNIFHKDPDVNMLHVFVLGEWQPIEYGGKLLKYLPLYNHQHEYF 266
Db 199 GFSSGGKWEQNVHHAATNVVGRDGLDLYPFYATVAEHLNNTYSQDSWMTLFEWQHVH 258
QY 267 FLIOPPLLIPMYFQYQIM-----TMVHKNWVDLAWAVS-----YIIRFIT 309
Db 259 TFMPLPFLALSLLOSIIFVSMQPHYDYVENTAIYEQVGLSEHAWWSLGOYFLPDWMT 318
QY 310 YIPEX---GIIGALLFLNFIRFLESHWVWVYTMNHVME---IDQAYRDNFSSQLTAT 363
Db 319 RIMFVLVSHLVGG-----FLLSH---VVTNHYSVKEFALSSNIMSNVACLQIMTT 366
QY 364 CNVEQSFNDWFSGHLNFQIEHHLFPTMPRNLHKLAPLVKSLCAKHGEY 414
Db 367 RMRSGREIDWLGGLNVOIEHHLFPTMPRNLHKLAPLVKSLCAKHGEY 417

RESULT 33
US-10-054-534B-31
; Sequence 31, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.PI
; CURRENT APPLICATION NUMBER: US/10/054.534B
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium aureum
US-10-054-534B-31

Query Match 14.8%; Score 360.5; DB 12; Length 439;
Best Local Similarity 24.8%; Pred. No. 4.2e-28;
Matches 114; Conservative 89; Mismatches 200; Indels 57; Gaps 17;

QY 1 MCKGNGQEGGAAREVSVPTFSWEIQHNLTDSGLVIDRKYVNTKWSIQHPGQORVI 60
Db 1 MCRGA-QGEPQATBELKSSPSEQKV-----LLIDGQLYDAT--NFRHPGGS-II 46
QY 61 GHVAGE-----DATDAFAFHDPDLFVGVKFLK--PLLIGELAPEEFSQDHGKNSKITEDF 113
Db 47 KYLCTDGKEVDATAYKFEHCRSSKAVKYNLSLPKIDGPIKYKYDAKEQARHDKLTREY 106
QY 114 RALRKTAEADNLFKTNHVFLLLIIAHIIALESIAWTFVFGNGNITPTLITAFVL-ATSO 172
Db 107 VALREQLVKGEYDFSPLEHIIYRCALAMFALFYLSFKGN--VMATIAIVIGGCVCQ 164
QY 173 AQAGWLOHDYGHLSVYRKPKNHVLHVKFVIGHLKASANWNNHRHFQHKAPNIFHKDPD 232
Db 165 GRCGWLHMHAGHYSMTGNIPVLRQEQFLYIGCGSGAWWSQHNKHAATQKLKHDVD 224
QY 233 VNMLHVFVLGE--WQPIEYGGKLLKYLPLYNHQHEYFFLIGPPLIPMYF----- 279
Db 233 VNMLHVFVLGE--WQPIEYGGKLLKYLPLYNHQHEYFFLIGPPLIPMYF----- 279
```

```

Db 225 LDTPLVANNKEIARRVKGSGFQAKWL---HLQGYIFAPVSCLLVGLFWLYLHPHMIR 281
Qy 280 ---QYIIMTMIVHKNNWVDLAWAVSYVIRPFI-TYIPFYGLGALLFNIRFLESHWV 335
Db 282 TKRNFELFSVALRVVCPMLLSMGYTVGESLGYVLTFTG-LGCTYI--FTHFAVSH--- 335
Qy 336 WVTQNNHIVMEIDQEAVERDFSSQLTATCNVE-QSFFNDWFSGLHNFQIEHHLFPPTMPRH 394
Db 336 -----THLPVS-EDEYLUHWVEYAAALHTTNVAIDSVVVTWLMMSVNFQIEHHFPCCPQF 389
Qy 395 NLHKIAPLVKSLCAKHGIEQEKPLLRALLDIIRSLKSG 434
Db 390 RHPALSSRVKXLFEDNGLVYDARSVQALKOTFGNLHEVG 429

RESULT 34
US-09-967-477B-4
; Sequence 4, Application US/09967477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haiping Hong
; TITLE OF INVENTION: FAD4, FAD5, FADS-2, AND FAD6, NOVEL
; TITLE OF INVENTION: FATY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: ENZ-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; PRIOR APPLICATION NUMBER: 2002-04-16
; PRIOR FILING DATE: 2002-04-16
; PRIOR FILING DATE: 2000-09-28
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
US-09-967-477B-4

Query Match 14.6%; Score 355; DB 10; Length 439;
Best Local Similarity 25.3%; Pred. No. 1.5e-27;
Matches 120; Conservative 85; Mismatches 182; Indels 88; Gaps 18;

Qy 1 MGKGGNGCGEAGAEAREVSVPTFSWEEIQKHLNRDTSGLVIDRKVNITKWSIQHPGQQRVI 60
Db 1 MGK-GSEGR3AA-RENTA-----EANGDKRKT---ILLEGVLYDAT--NFKHPGGS-II 46
Qy 61 GHY-----AGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEE---PSQDHGKNSKITEDF 113
Db 47 NFLTEGAGVDATQAYREFHQSGKADKYLKSLPLKLDASKVSRFSKAQEARRDAMTRDY 106
Qy 114 RALRKTAEADNNLFTKTNHVPFLLLLAHIIALESIAFTVFYFGNGWIPFTLIITAFVL-ATS 171
Db 107 AAFREELVARGYDPSLPHMIYRVEIVAFALFALS-----FWLMSKASFTSLVGVVWGIA 162
Qy 172 QAQAGMTLQHDYGHLSVYRKPKNNHLVHKFVIGHLKASANNWNRHFQHAKPNIFHKDPD 231
Db 163 QGRCGVWMEHWGSGSFTGVITLDDRMCEFPYGVGCGMSGHYKNNQHSKHAAPNRLHEDV 222
Qy 232 DVNMLHVVFGEWQPIEGYKKLKLPLYNHQQHEYFFLIGPPLIIPWFOYQIIIMTMIVHK 291
Db 223 DLNLFPLVARN-----BRVRKVK-----PGSLALWLRVQAVLPAFVSC 262
Qy 292 NWVDLAWAVSYIRF-----FITYIPFYGILGAL-----LFL----- 323
Db 263 LLIGLWTLVYHPYMLRTRKHMBFVMI FARYIGWPSLMGALGYSPTGSMYLCFGLG 322
Qy 324 ---NFIRFLESHWFWVWVQNNHIVMEIDQEARDFSSQLTATCNVE-QSFFNDWFSGLH 379
Db 323 CIYIFLQFAVSGHTLHPVT-----NPDQLWLEAYADHTVNIISTKSLWLVWMSNL 373
Qy 380 NFQIEHHLFPPTMPRHNLHKIAPLVKSLCAKHGIEQEKPLLRALLDIIRSLKSG 434

```

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Db 374 NFQIEHHLFPPTAPQFRFKEISIRVFEALFKRNLPHYDLPYTSVSTTFANLYSVG 428

RESULT 35
US-09-769-863-20
; Sequence 20, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Tung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-09-769-863-20

Query Match 14.3%; Score 348; DB 12; Length 470;
Best Local Similarity 24.9%; Pred. No. 8.8e-27;
Matches 123; Conservative 91; Mismatches 183; Indels 96; Gaps 24;

Qy 11 AABREYSV---PTFSWEEIQKHLNRDTSGLVIDRKVNITKWSIQHPGQQRVIGHYAGED 67
Db 12 AAVAETPVAGKAKFTWQEAQNTASAMIIIRGKYVDVTENANKPGGGRMVLHAGRE 71
Qy 68 ATDAFRAHPDLEFVGKFLKPLLIG-----ELAPEPSQDHGKNSKITEDFALRKTA 121
Db 72 ATDTFDSYHPFSDKASILNKYBIGTFTGPFPTFKPD-----TFYKRECKRVG 122
Qy 122 DMNLFKTNHVF-----FLLLAHIIALESIAFTVFYFGNGWIPFTLIITAFVLATSQA-Q 174
Db 123 E--YFKQNNLHPQDGPGLWRMMVFAVAGLALYGM-HFTIPALQAAAAFGVCCALP 179
Qy 175 AGMLQHDYGHLSVYRKPKNNHLVHKFVIGHLKAS-ANNWNRHFQHAKPNIFHKDPD- 232
Db 180 LLHWHDSSHASTNNPFFHYVYVGRFAMDFAGGSMVSLNQHNVGHYITNVAGSDPDL 239
Qy 233 -VNN-----LHVFLGELGQPIEVGKKLKLPLYNHQQHEYFFLIGPPL--LIIPWFO 280
Db 240 PVNMDGDIRIVNRQVF-----QPM-----YAFQHIYL-----PPLYGVGLKPR 279
Qy 281 YQ-IIMTMIVHKN-----WVDLAWAVSYIRPFTIIPFYGILG-----AL 320
Db 280 IQDFTDTFGSHNGPIRVNPHALSTWAMISSKSFV-AFYRVYLPL-AVLQMPKITYLAI 337
Qy 321 LFLAFIFLSEHFWVWVQNNHIVMEID-----QEAVERD-WFSSOL-TATCNVEQSFF 371
Db 338 FFL--AFVTCWYLAFFQVSHVSTEGYPCGDEAKMALQDEWAVSQVTSVDYAHGSM 395
Qy 372 NDWFSGLHNFQIEHHLFPPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSL 430
Db 396 TTFLAGALNYQVWHLLFPFSVQHYPAIPIIVDVCKEYNIKAYILPDFTAAPFAVHLKHL 455
Qy 431 KKSGLMLDALYH 443
Db 456 RNMQQGGIAATH 468

RESULT 36
US-10-054-534B-20
; Sequence 20, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories

```

APPLICANT: Mukerji, Pradip  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Das, Tapas  
APPLICANT: Thurmond, Jennifer M.  
APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
FILE REFERENCE: 6763.US.P1

CURRENT APPLICATION NUMBER: US/10/054.534B

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 09/769,863

PRIOR FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20

LENGTH: 470

TYPE: PRT

ORGANISM: Saprolegnia diclina

US-10-054-534B-20

Query Match 14.3%; Score 348; DB 12; Length 470;

Best Local Similarity 24.9%; Pred. No. 8.8e-27;  
Matches 123; Conservative 91; Mismatches 183; Indels 96; Gaps 24;

```
QY 11 AAAREVSV---PTFSWEEIQKHNLRDTSGLVIDRKNVNIKWSIQHOGQGVGHVAGED 67
DB 12 AAVATPVAGKKAFTWQEVQAHNTAASAWIIRGVYDVTEWANKHGGREMLHAGRE 71
QY 68 ATDAFRAPHPDLEFVGKFLKPLLIG-----ELAPEESQDHGKNSKITEDFRALKRTAE 121
DB 72 ATDTFDSYHPFSDKAESILNKYEIGTFTGPSEFFTFKPD-----TGFYKECKRVG 122
QY 122 DMNLFKTNHVF-----FLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSOA-Q 174
DB 123 E--YFKONLHPQDGFPGGLWRMMVVFVAVAGLALYGM-HFSTIFALQLAAALFGVCOALP 179
QY 175 AGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKGAS-ANWNNHRHFQHHAKNIFHKDPD- 232
DB 180 LLHVMDSDSHASYTNMPPHYVVGFRFAMDWPFAGGSMVSLNQHVGHYITNVAGSDPDL 239
QY 233 -VNM-----LHVFLGEMQPIEYGGKKLKVLPYNHQHIEYFFLIGPPL--LIPMYFQ 280
DB 240 PVNMGDTRIRIVNRQVF-----QPM-----YAFQHIYL-----PPLYGVGLKFR 279
QY 281 YQ-IIMTMIVHKN-----WDLAWAVSYIIRFFITYIPFYGILG-----AL 320
DB 280 IQDFTDTGSHNGIRVNPALSTWAMISKSFV-AFYRVYLP-ALVQMPIKTYLAI 337
QY 321 LFLNFIRESHFWVVTQMHVMEID-----QEAYRD-WFSSQL-TATCNVEQSF 371
DB 338 FFL--AEFTVGYLAFNQVSHVTECGYPCGDEAKMALQDEWAVSQVKTSDVYAHGSMW 395
QY 372 NDFSGHLNFQIEHLLFPTMPRHNLHKIAPLKSICAKHGIEYQEKP-LLRALLDIIRSL 430
DB 396 TTFLAGALNYQVWHLPFSVQYHYPAPAIPIVDVCKEYNIKYAILPDFTAAFAVHLKHL 455
QY 431 KKSGLMLDAYLH 443
DB 456 RNMGQGGIAATH 468
```

RESULT 37

US-10-431-952-20

Sequence 20, Application US/10431952

Publication No. US20030190733A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas

APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF

FILE REFERENCE: 6763.US.O1

CURRENT APPLICATION NUMBER: US/10/431.952

CURRENT FILING DATE: 2003-05-08

PRIOR APPLICATION NUMBER: US/09/769,863

PRIOR FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20

LENGTH: 470

TYPE: PRT

ORGANISM: Saprolegnia diclina

US-10-431-952-20

Query Match 14.3%; Score 348; DB 12; Length 470;

Best Local Similarity 24.9%; Pred. No. 8.8e-27;

Matches 123; Conservative 91; Mismatches 183; Indels 96; Gaps 24;

```
QY 11 AAAREVSV---PTFSWEEIQKHNLRDTSGLVIDRKNVNIKWSIQHOGQGVGHVAGED 67
DB 12 AAVATPVAGKKAFTWQEVQAHNTAASAWIIRGVYDVTEWANKHGGREMLHAGRE 71
QY 68 ATDAFRAPHPDLEFVGKFLKPLLIG-----ELAPEESQDHGKNSKITEDFRALKRTAE 121
DB 72 ATDTFDSYHPFSDKAESILNKYEIGTFTGPSEFFTFKPD-----TGFYKECKRVG 122
QY 122 DMNLFKTNHVF-----FLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSOA-Q 174
DB 123 E--YFKONLHPQDGFPGGLWRMMVVFVAVAGLALYGM-HFSTIFALQLAAALFGVCOALP 179
QY 175 AGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKGAS-ANWNNHRHFQHHAKNIFHKDPD- 232
DB 180 LLHVMDSDSHASYTNMPPHYVVGFRFAMDWPFAGGSMVSLNQHVGHYITNVAGSDPDL 239
QY 233 -VNM-----LHVFLGEMQPIEYGGKKLKVLPYNHQHIEYFFLIGPPL--LIPMYFQ 280
DB 240 PVNMGDTRIRIVNRQVF-----QPM-----YAFQHIYL-----PPLYGVGLKFR 279
QY 281 YQ-IIMTMIVHKN-----WDLAWAVSYIIRFFITYIPFYGILG-----AL 320
DB 280 IQDFTDTGSHNGIRVNPALSTWAMISKSFV-AFYRVYLP-ALVQMPIKTYLAI 337
QY 321 LFLNFIRESHFWVVTQMHVMEID-----QEAYRD-WFSSQL-TATCNVEQSF 371
DB 338 FFL--AEFTVGYLAFNQVSHVTECGYPCGDEAKMALQDEWAVSQVKTSDVYAHGSMW 395
QY 372 NDFSGHLNFQIEHLLFPTMPRHNLHKIAPLKSICAKHGIEYQEKP-LLRALLDIIRSL 430
DB 396 TTFLAGALNYQVWHLPFSVQYHYPAPAIPIVDVCKEYNIKYAILPDFTAAFAVHLKHL 455
QY 431 KKSGLMLDAYLH 443
DB 456 RNMGQGGIAATH 468
```

RESULT 38

US-10-029-386-29651

Sequence 29651, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: AEMICA-X-2

EXPRESSION ANALYSIS TWO

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annonax Sequence Listing Engine vers. 1.1

SEQ ID NO 29651

LENGTH: 76

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHRL1.1  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.4  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.3  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.9  
 US-10-029-386-29651

Query Match 14.2%; Score 347; DB 12; Length 76;  
 Best Local Similarity 94.4%; Pred. No. 9.2e-28;  
 Matches 67; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 104 GNSKITEDFRALRKTADNMFLKTNHVFLLLAHIALESIAWFTVFYFGNGWIPTLI 163  
 DB 4 GQSKITEDFRALRKTADNMFLKTNHVFLLLAHIALESIAWFTVFYFGNGWIPTLI 63  
 QY 164 TAFVLATSOAQ 174  
 DB 64 TAFVLATSOVR 74

RESULT 39  
 US-09-903-456-30  
 Sequence 30, Application US/09903456  
 Patent No. US20020138874A1

GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Mukerji, Pradip  
 APPLICANT: Leonard, Amanda Eun-Yeong  
 APPLICANT: Huang, Yung-Sheng  
 APPLICANT: Pereira, Suzette L.  
 TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF  
 FILE REFERENCE: 6407.US.P3  
 CURRENT APPLICATION NUMBER: US/09/903,456  
 CURRENT FILING DATE: 2001-07-11  
 PRIOR APPLICATION NUMBER: US 09/624,670  
 PRIOR FILING DATE: 2000-07-24  
 PRIOR APPLICATION NUMBER: US 09/379,095  
 PRIOR FILING DATE: 1999-08-23  
 PRIOR APPLICATION NUMBER: US 09/145,828  
 PRIOR FILING DATE: 1998-09-02  
 NUMBER OF SEQ ID NOS: 116  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 30  
 LENGTH: 446  
 TYPE: PRT  
 ORGANISM: Mortierella alpina

US-09-903-456-30  
 Query Match 14.0%; Score 342.5; DB 10; Length 446;  
 Best Local Similarity 26.0%; Pred. No. 3e-26;  
 Matches 121; Conservative 64; Mismatches 184; Indels 97; Gaps 22;  
 QY 4 GGNQGEAAREVSVPTFSWEERIKXNLTDSGLVDRKVNITKWSIQHPGQGVIGHY 63  
 DB 2 GTDQCK-----TFTWEELAAHNTKDDLLAIRGRVYDVKFLSRHPGQGVTLILG 51  
 QY 64 AGEDATDAFRAFPDLEFVGKFLKPIILIGELAPE-----EPSQHGKNSKITEDFRALR 117  
 DB 52 AGRDVTPVPMYHA-FGAADAIKMYVGTLSNELPIPEPTVFH-----KTIK 100  
 QY 118 KTAE-----DMVLKTNHV-----FFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLA 169  
 DB 101 TRYEGVFTDRNIDPKRNPETGWRYALIFGSLIASYVAQVLFVFFVVERTWL-QVFAILING 159  
 QY 170 TSOAQAGWLQ-HDYGHLSVVRKEK-WNHL--VHKFVIGHLKGSANWNHRE-FOHAKP 224  
 DB 160 FACAQVGLNPLHDASHFVSVTHNTVWKILGATHDF----FNGASYLVVMYQEMLGHPT 215  
 QY 225 NIFHKDPDVM-----LHVFLGSEWQPIEYCKKXKLYLPYNHQHE 264

DB 216 NIAGADPDVSTSEBDDVRRIKQKQWVFNHINQNFV-----PFLYGLLAFKVRQDINIL 270  
 QY 265 YFFLLGPELLIPMYFQYQIIMTIVHKWVDLAWAVSYIRFFTYIPFYGILGALLFLN 324  
 DB 271 YFVKINDAIRVNPISHTWTFM-----WGGKAPFVWYRLIVPLQYLP-----LGKVVLLF 320  
 QY 325 FIR-FLESHWFVWVQMHVMEI-----DOEA--YRDPSSQLTATCNVQSPFND--- 373  
 DB 321 TVADMVSSYIWLALTFOAHNVVEVQWPLPDENGILQKDMAAQVETT-----QDYAHDHSL 376  
 QY 374 WFS--GHLNFQIEHRLFTMPRNLHKTAPLVKSLCAKHGIEYOEK 417  
 DB 377 WTSITGSLNYQAVHHLFNVSOHYPDILAIKNTCTSEYKVPYLK 422

RESULT 40

US-10-278-391-2  
 Sequence 2, Application US/10278391  
 Publication No. US20030159164A1

GENERAL INFORMATION:  
 APPLICANT: KOPCHIK, JOHN J.  
 KELDER, BRUCE  
 HUANG, YUNG-SHENG  
 KIRCHNER, STEPHEN J.  
 MUKERJI, PRADIP

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM  
 PRODUCTS

NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MEDLEN & CARROLL, LLP  
 STREET: 220 MONTGOMERY STREET, SUITE 2200  
 CITY: SAN FRANCISCO  
 STATE: CALIFORNIA  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 94104

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/278,391  
 FILING DATE: 23-Oct-2002  
 CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/087,578  
 FILING DATE: 29-MAY-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837  
 REFERENCE/DOCKET NUMBER: OHU-03348  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 446 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: No. US20030159164A1 Relevant  
 TOPOLOGY: No. US20030159164A1 Relevant  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-278-391-2

Query Match 14.0%; Score 342.5; DB 12; Length 446;  
 Best Local Similarity 26.0%; Pred. No. 3e-26;  
 Matches 121; Conservative 64; Mismatches 184; Indels 97; Gaps 22;  
 QY 4 GGNQGEAAREVSVPTFSWEERIKXNLTDSGLVDRKVNITKWSIQHPGQGVIGHY 63  
 DB 2 GTDQCK-----TFTWEELAAHNTKDDLLAIRGRVYDVKFLSRHPGQGVTLILG 51





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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 10, 2003, 19:33:52 ; Search time 330 Seconds

(without alignments)  
4471.752 Million cell updates/sec

US-09-719-601-5

Title: 2438

Sequence: 1 MGRGNGQGEAARREVSPT.....DIIRSLKSGKLMDAYLHK 444

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09719601/runat\_09122003\_094910\_21283/app\_query.fasta\_1.583  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cgi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09719601@cgn\_1\_164@runat\_09122003\_094910\_21283  
-NCPU=6 -ICPU=3 -NO WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
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15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
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17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Query | Score | Match | Length | ID | Description |
|------------|-------|-------|-------|--------|----|-------------|
| -----      |       |       |       |        |    |             |

## ALIGNMENTS

### RESULT 1

US-10-191-513A-8  
; Sequence 8, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Faridip  
; APPLICANT: Leonard, Ananda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; PRIOR FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2257

Sequence 8, Appli  
Sequence 7, Appli  
Sequence 232, App  
Sequence 2, Appli  
Sequence 455, App  
Sequence 7, Appli  
Sequence 4, Appli  
Sequence 1, Appli  
Sequence 63, Appli  
Sequence 6, Appli  
Sequence 119, App  
Sequence 119, App  
Sequence 13, Appli  
Sequence 34, Appli  
Sequence 35, Appli  
Sequence 5, Appli  
Sequence 425, App  
Sequence 425, App  
Sequence 313, App  
Sequence 313, App  
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Sequence 23095, A  
Sequence 36, Appli  
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Sequence 37, Appli  
Sequence 3, Appli  
Sequence 3070, Ap  
Sequence 7, Appli  
Sequence 13, Appli  
Sequence 13, Appli  
Sequence 13, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 6399, Ap  
Sequence 558, App  
Sequence 595, App  
Sequence 5518, Ap  
Sequence 25, Appli

1 1935 79.4 2257 15 US-10-191-513A-8  
2 1646 67.5 1843 15 US-10-191-513A-7  
3 1894 65.4 1474 15 US-10-102-806-232  
4 1560.5 64.0 1717 15 US-10-262-617-2  
5 1516 62.2 1972 9 US-09-822-849A-485  
6 1516 62.2 4213 13 US-10-133-937-7  
7 1515 62.1 1928 15 US-10-262-617-4  
8 1508 61.9 1335 15 US-10-191-513A-1  
9 1348 55.3 1686 15 US-10-191-513A-6  
10 1300 53.3 1478 11 US-09-981-876-63  
11 1300 53.3 1478 11 US-09-148-545-63  
12 1162 47.7 2016 10 US-09-981-876-119  
13 1162 47.7 2016 11 US-09-148-545-119  
14 1103 45.2 864 15 US-10-191-513A-13  
15 960 39.4 990 15 US-10-191-513A-34  
16 933 38.3 960 15 US-10-191-513A-35  
17 923 37.9 918 15 US-10-191-513A-5  
18 834 34.2 446 9 US-09-604-287A-425  
19 834 34.2 446 11 US-09-551-621-425  
20 834 34.2 446 13 US-10-124-805-425  
21 834 34.2 446 14 US-10-007-805-425  
22 834 34.2 446 15 US-10-076-622-425  
23 834 34.2 456 9 US-09-604-287A-313  
24 834 34.2 456 10 US-09-339-338-313  
25 834 34.2 456 11 US-09-551-621-313  
26 834 34.2 456 13 US-10-124-805-313  
27 834 34.2 456 14 US-10-007-805-313  
28 834 34.2 456 15 US-10-076-622-313  
29 705 28.9 453 11 US-09-918-995-29095  
30 620 25.4 473 15 US-10-191-513A-36  
31 585 24.0 304 15 US-10-191-513A-4  
32 566 23.2 449 15 US-10-191-513A-37  
33 566 23.2 449 15 US-10-191-513A-3  
34 499 20.5 567 13 US-10-029-386-3070  
35 497 20.4 1380 10 US-09-967-477B-7  
36 487.5 22.0 1362 13 US-09-769-863-13  
37 487.5 20.0 1362 13 US-10-054-534B-13  
38 487.5 20.0 1362 13 US-10-431-952-13  
39 459 18.8 1374 13 US-10-278-391-3  
40 435.5 17.9 1685 14 US-10-029-756-4  
41 434 17.8 475 9 US-09-864-761-6399  
42 426.5 17.5 1350 10 US-09-938-842A-558  
43 424.5 17.4 493 10 US-09-728-445-595  
44 420 17.2 315 10 US-09-783-590-5518  
45 411.5 16.9 1702 14 US-10-029-756-26

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-8

Alignment Scores:
Pred. No.: 3,266-216 Length: 2257
Score: 1935.00 Matches: 352
Percent Similarity: 88.84% Conservative: 30
Best Local Similarity: 81.86% Mismatches: 44
Query Match: 79.37% Indels: 4
DB: 15 Gaps: 2

US-09-719-601-5 (1-444) x US-10-191-513A-8 (1-2257)
QY 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35
DB 7 CTTACCCCGCGTACTTTCACCTGGACGAGGCGGCGGCGCTCAGGTCGCGAGAGCGG 66
QY 36 GlyLeuValIleAspArgLysValTrpAsnIleThrLysTrpSerIleGlnHisProGly 55
DB 67 TGGCTAGTGCATGACCGTAAGGTGTACCAACATCAGCAGGTTTCCACCCGCGCATCCAGG 126
QY 56 GlyGlnArgValIleGlyHisTrpAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75
DB 127 GGTCTCCCGGTCATCAGCCATCAGCCGCGGCGAGGATGCCAGATCCCTTTGTGCGCTTC 186
QY 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAla 95
DB 187 CACATCAACAGGCGCTTGTGAAGAAGTATATGAATCTCTCTCTGATTGGAGAACTGTCT 246
QY 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAla 115
DB 247 CAGAGCAGCCCGCTTTGAGCCCGCCACCAAGATTAAGAGCTGACAGATGAGTTCCGGAG 306
QY 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeu 135
DB 307 CTGCGGCGCACAGTGAGCGGATGGGCTCATGAAGGCCAACCATGTCTTCTTCTGCTG 366
QY 136 LeuLeuAlaHisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGly 155
DB 367 TACCTCTGCATCATCTGTGTCGATGGTGAGCGCTGCTGAGCGCTGCTGAGCGCTTGGG 426
QY 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeu---AlaThrSerGlnAlaGln 174
DB 427 ACGTCCTTTTGGCTTCTCTCTCTGTCGGTGCTGCTCAGTGCGAGTTCCAGCGCCCAA 486
QY 175 AlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerValTrpArgLysProLysTrpAsn 194
DB 487 GCTGGATGGTGCACATGATTATGGCCACCTGTCTGTCTACAGAAACCCCAAGTGGAA 546
QY 195 HisLeuValHisLysPheValIleGlyHisLeuLysGlyValAsnSerAlaAsnTrpTrpAsn 214
DB 547 CACCTTGTCCAAATTCGTCATTGGCCACTTAAGGGTGCCTTGCCTGCAACTGGTGAAT 606
QY 215 HisArgHisPheGlnHisAlaLysProAsnIlePheHisLysAspProAspValAsn 234
DB 607 CATCGCACCTTCAGCACACCGCCCAAGCCTTAACATCTTCCCAAGAGATCCCGATGGAAC 666
QY 235 MetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTrpGlyLysLysLysLeu 254
DB 667 ATGCTGCACGTGTTGTTCTGGCGGATGGCAGCCCATCGAGTCGCGCAAGAAGAGCTG 726
QY 255 LysTrpLeuProTrpAsnHisGlnHisGluTrpPhePheLeuIleGlyProProLeuLeu 274
DB 727 AAATACCTGCGCTTACCAATCACCAGCAGCAATATCTTCTGATTGGCGCGCGCTGCTC 786
QY 275 IleProMetTrpPheGlnTrpGlnIleIleMetThrMetIleValHisLysAsnTrpVal 294
DB 787 ATCCCCATGATTTCCAGTACCAAGATCATCATCATCATCATCATCATCATCATCATCAT 846
QY 295 AspLeuAlaTrpAlaValSerTrpTrpIleArgPhePheIleThrTrpIleProPheTrp 314
DB 847 GACCTGGCCCTGGGCGGTACGACTACTATCCGGTTCCTTCTATCATCATCATCATCATCAT 906
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QY 315 GlyIleLeuGlyAlaIleLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPhe 334
DB 907 GGCACTCTGGAGGCGCTCTCTTTTCTCACTTCATCAGGTTCCTGGAGAGCCACTGGTTT 966
QY 335 ValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGluAlaTrpArgAsp 354
DB 967 GTGTGGTCCACACAGATGAATCAGATCGTCATGGAGATTGACAGAGGCGCTTACCGTGC 1026
QY 355 TrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrp 374
DB 1027 TGGTTCAGTAGCAGCTGACGCCACTGCAACCTGGAGCAGTCTCTTCTTCAACGACTGG 1086
QY 375 PheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHis 394
DB 1087 TTCACTGGACACCTTAACCTTCAGATTGAGCACCACTCTTCCCCACCATGCCCCGGCAC 1146
QY 395 AsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTrp 414
DB 1147 AACTTACAAAGATCCCGCGCTGGTGAAGTCTCTATGTGCCAGCATGGCAATTGAATAC 1206
QY 415 GlnGlyLysProLeuLeuArgAlaLeuAspIleIleArgSerLeuLysLysSerGly 434
DB 1207 CAGGAGAGCGGCTACTGAGGCGCTGCTGGACATCATCAGGTCCCTGAAGAAGTCTGGG 1266
QY 435 LysLeuTrpLeuAspAlaTrpLeuHisLys 444
DB 1267 AAGCTGTGGTGGACGCGCTTACCTTCACAAA 1296

RESULT 2
US-10-191-513A-7
; Sequence 7, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-7

Alignment Scores:
Pred. No.: 1,966-182 Length: 1843
Score: 1646.00 Matches: 294
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.51% Indels: 0
DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-191-513A-7 (1-1843)
QY 151 ValPheTrpPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
DB 1 GTCCTTTTACITGGCAATGGCTGATTCCTTACCTCATCAGCGCTTTGTCTTGTCTACC 60
QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTrpGlyHisLeuSerValTrpArgLys 190
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Db 61 TCTCAGGCCCAAGCTGGTGGTGTGCTCAACATGATTATGGCCACCTGTGTCTCAGACAAA 120  
QY 191 ProLysTrpAsnHisLeuValHisPheValIleGlyHisLeuLysGlyAlaSerAla 210  
Db 121 CCCAGTGGAAACCACTTGTTCACAAATTCCTCATTTGGCCACTTAAAGGGTGCCTCTGCC 180  
QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230  
Db 181 AACTGGTGGATCATCGCCACTTCAGCACCAAGCCCAAGCCCTAAACATCTTCCACAGGAT 240  
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250  
Db 241 CCGGATGTAACATGCTCAGCTGTGTTTCTGGCGAATGGCAGCCCATCGAGTACGGC 300  
QY 251 LysLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuIleGly 270  
Db 301 AAGAAGAGCTGAAATACCTGCCCTACAAATCACCAGCACGAATACTTCTTCTGATTGGG 360  
QY 271 ProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIleValHis 290  
Db 361 CCGCGCTGCTCATCCCATGATTTTCAGTACCAGATCATCATGACCATGATCGTCCAT 420  
QY 291 LysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIleThrTyr 310  
Db 421 AAGAACTGGTGGACCTGGCTGGCGCTCAGCTACTACATCCGGTCTTTCATCACTAC 480  
QY 311 IleProPheTyrGlyIleGluGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330  
Db 481 ATCCCTTTCTACGGCATCCTGGGAGCCCTCTTTCTCTCAACTTCATCAGGTTCTCTGGAG 540  
QY 331 SerHisTrpPheValTrpValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350  
Db 541 AGCCACTGGTTGTGGGTACACAGATGATACATCGTCTGATGGAGATGACCAAGAG 600  
QY 351 AlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370  
Db 601 GCCTACCGTACTGTTTCTAGTACGAGCTGACAGCCACTCGCAACCTGAGGAGCAGTCTTC 660  
QY 371 PheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThr 390  
Db 661 TTCACAGTCTGGTTCAGTGGACACCTTAACCTTCAGATTCAGACCACTCTTCCCAACC 720  
QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410  
Db 721 ATGCCCGCGCAAACTTACACAAAGATCGCCCGCTGGTGAAGTCTCTATGTGCAAGCAT 780  
QY 411 GlyIleGluTyrGlnGlyLysProLeuArgAlaLeuLeuAspIleIleArgSerLeu 430  
Db 781 GCATGTAATACAGGAGAGCCGCTACTGAGGCGCTGCTGGACATCATCAGTCCCTG 840  
QY 431 LysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444  
Db 841 AAGAAGTCTGGGAAGCTGTGGCTGGACGCTACCTTCACAAA 882

## RESULT 3

US-10-102-806-232  
; Sequence 232, Application US/10102806  
; Publication No. US20030054421A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103PLC1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1993-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 232

; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1337)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1359)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1377)  
; OTHER INFORMATION: n equals a,t,g, or c  
; US-10-102-806-232  
Alignment Scores:  
Pred. No.: 1-73e-176 Length: 1474  
Score: 1594.00 Matches: 286  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.38% Indels: 0  
DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-102-806-232 (1-1474)

QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178  
Db 3 ATTCTTACCTCATCAGGCCCTTTGTCTGTCTCTCAGGCCCAAGCTGGATGGCTG 62  
QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198  
Db 63 CAACATGATTATGGCCACCTGTCTGTCTACAGAAAACCAAGCTGGACCCACCTTGTCCAC 122  
QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218  
Db 123 AAATTCTGTCATTTGGCCACTTAAAGGGTGCCTCTGCCAACTGGTGGAAATCATGCCACTTC 182  
QY 219 GlnHisHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisVal 238  
Db 183 CAGCACCAAGCCCTAAACATCTTCCACAGGATCCCGATGTGAACATGTGTCACGCTG 242  
QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuPro 258  
Db 243 TTTGTTCTGGGGAAATGGCAGCCCATCGAGTACGCGCAAGAAAGTGAATACCTGCC 302  
QY 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyr 278  
Db 303 TACATACACGACGACGATPACTTCTCTGANTGGCCGCCCTGCTCATCCCCATGAT 362  
QY 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298  
Db 363 TTCAGTACAGATCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCCTGG 422  
QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGly 318  
Db 423 GCGTTCAGTACTACATCCGGTCTTTCATCACTACATCCCTTCTACGGCATCTCTGGGA 482  
QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338  
Db 483 GCCTCTCTTCTCAACTTCATCAGTTCCTGGAGAGCCACTGGTTTGTGGGTGCACA 542  
QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSer 358  
Db 543 CAGATGAATCAGATCATCGTTCATGAGATTGACAGGAGGCTACCGGTACCTGGTTCAGTAGC 602  
QY 359 GlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHis 378  
Db 603 CAGCTGACAGCCACCTGCAACCTGGAGCAGTCTCTTCTTCAACGACTGGTTTCAGTGGACAC 662  
QY 379 LeuAsnPheGlnIleGluHisIleLeuPheProThrMetProArgHisAsnLeuHisLys 398  
Db 663 CTTAACTTCCAGATTGAGCACCACTCTTCTCCCACTGTCCTCCCGGCACAACTTACACAAAG 722

QY 399 IleAlaProLeuValIysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418  
 DB 723 ATCGCCCGCTGGTGAAGTCTATGTGCAAGCAGTGGCATGGAATACAGGAGAGCGG 782  
 QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeu 438  
 DB 783 CTACTGAGGCGCTGCTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGCTG 842  
 QY 439 AspAlaTyrLeuHisLys 444  
 DB 843 GACGCTACCTTCACAAA 860

## RESULT 4

US-10-262-617-2  
 ; Sequence 2: Application US/10262617  
 ; Publication No. US2003007747A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Shah, Purvi  
 ; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
 ; FILE REFERENCE: PP-0494-1 DIV  
 ; CURRENT APPLICATION NUMBER: US/10/262,617  
 ; PRIOR FILING DATE: 2002-09-30  
 ; PRIOR APPLICATION NUMBER: 09/048,888  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 2  
 ; LENGTH: 1717  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CB1  
 US-10-262-617-2

## Alignment Scores:

Pred. No.: 1.9e-172 Length: 1717  
 Score: 1560.50 Matches: 278  
 Percent Similarity: 76.23% Conservative: 62  
 Best Local Similarity: 62.33% Mismatches: 103  
 Query Match: 64.01% Indels: 3  
 DB: 15 Gaps: 2

US-09-719-601-5 (1-444) x US-10-262-617-2 (1-1717)

QY 1 MetGlyLysGlyGlyAsnGlnGly-----GluGlyAlaAlaGluArgGluValSerVal 18  
 DB 75 ATGGCGCGCTCGGGAGCGCGGACCGCGGAGGGACCGCGGACCGCGGCGCGGCGCGCTG 134  
 QY 19 ProThrPheSerTrpGluGluIleGlnLysHisAsnLeuArgThrAspSerGlyLeuVal 38  
 DB 135 CCACCTTCCTGCTGGGAGAGATCCGCGCGCACAGACCGCGCGCGCGCGACAGTGGCTGGTGC 194  
 QY 39 IleAspArgLysValTyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyGlnArg 58  
 DB 195 ATGAGCGCGCGTCTACGACATCAGCGCGTGGCGACAGCGGCGCACCGCGGCGCGCGCG 254  
 QY 59 ValIleGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPheHisProAsp 78  
 DB 255 CTCATCGCGCACCGCGGTGAGGACCGCACCGATGCCGTCCGTCCCTTCATCAAGAT 314  
 QY 79 LeuGluPheValGlyLysPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluGlu 98  
 DB 315 CTCATTTTGGCCCAAGTTCCTACAGCCCTGTGTGATTGAGAGCTGGCTCCGGAAGAA 374  
 QY 99 ProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLys 118  
 DB 375 CCCAGCAGGATGGACCCCTGAATCGCGCAGCTGGTCGAGGACTCCGAGCCCTGCACCG 434  
 QY 119 ThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAla 138

DB 435 GCAGCCGAGGACATGAAGCTGTTGTGATGCCAGTCCACACCTTCTTTGCTTCTTACTGGGC 494  
 QY 139 HisIleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyrPheGlyAsnGlyTrp 158  
 DB 495 CACATCTCGCCATGAGGTGCTGGCTGCTCTTATCTATCTCTGCTGGTCTCTGGCTGG 554  
 QY 159 IleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeu 178  
 DB 555 GTGCCAGTGGCTGGCGGCTTCATCTTGGCCATCTCTCAGGCTCAGTCTGGTGTCTG 614  
 QY 179 GlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHis 198  
 DB 615 CAGCATGACCTGGGCCATGCTCCATCTTCAAGAAGTCTCTGGTGGAAACACGCGGCCAG 674  
 QY 199 LysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPhe 218  
 DB 675 AAGTTCGTGATGGGCGAGCTTCTCGGCCACTGGTGGAACTTCGCGCACTTC 734  
 QY 219 GlnHisAlaLysProLysPheHisLysAspProAspValAsnMetLeuHisVal 238  
 DB 735 CAGCACCGCCCAAGCCCAACATCTTCCAAAGACCCAGACGTGACGTGGCGGCCGTC 794  
 QY 239 PheValLeuGlyGluTrpGlnProIleGluTyrGlyLysLysLysLysLysLysLys 258  
 DB 795 TTCTCTCTGGGGAG---TCATCGTGGAGTATGGCAAGAGAAACGACATACCTACCC 851  
 QY 259 TyrAsnHisGlnHisGluTyrPhePheLeuIleGlyProLeuLeuLeuLeuProMetTyr 278  
 DB 852 TACAACCGACGACGACCTGTACTTCTTCTGATCGGCCCGCGCTGCTACCCCTGGTGAAC 911  
 QY 279 PheGlnTyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrp 298  
 DB 912 TTGAAGTGGAAATCTGGCGGTACTGTGTGTGATGTCAGTGGCGGATTTGCTCTGG 971  
 QY 299 AlaValSerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyLysLeuGly 318  
 DB 972 GCGCGCAGCTTCTATGCGCGCTTCTTCTTATCTCTGATCGGCCCGCGCTGCTACCGCGTGGG 1031  
 QY 319 AlaLeuLeuPheLeuAsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThr 338  
 DB 1032 GTGCTGCTCTTCTTTGTGTGTGTCAGGGTCTCTGGAAGCCACTGTTCTGTGTGATCACA 1091  
 QY 339 GlnMetAsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSer 358  
 DB 1092 CAGATGAACCAATCCCAAGGAGATCGGCGCACGAGAAGCACCGGAGCTGGTCTCT 1151  
 QY 359 GlnLeuThrAlaThrCysAsnValGluLysSerPhePheAsnAspTrpPheSerGlyHis 378  
 DB 1152 CAGTGGCGGCGACCTGCAACGTCGAGCCCTCACTTTTCCAACTGTTTACGCGGCGAC 1211  
 QY 379 LeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLys 398  
 DB 1212 CTCAACTCCAGATCGAGCACCACTCTTCCCGAGGATGCCAGACACAACTACAGCGCG 1271  
 QY 399 IleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysPro 418  
 DB 1272 GTGCGCGCGTGGTCAAGTGGCTGTGTGCCAAGCACCGCTCAGCTACAGTCAAGTCAAGCC 1331  
 QY 419 LeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeu 438  
 DB 1332 TTCCTCAGCGCGCTGGTGGACATGTCAGGTCCCTGAAGAAGTCTGCTGATCATCTGGCTG 1391  
 QY 439 AspAlaTyrLeuHisLys 444  
 DB 1392 GACGCTACCTCCATCAG 1409

## RESULT 5

US-09-822-849A-485/c  
 ; Sequence 485: Application US/09822849A  
 ; Patent No. US20020045170A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary  
 ; APPLICANT: Fechtel, Kim  
 ; APPLICANT: Agostino, Michael J.  
 ; APPLICANT: Howes, Steven H.  
 ; APPLICANT: Resnick, Richard J.  
 ; APPLICANT: Gulukota, Kamalakara  
 ; APPLICANT: Graham, James R.  
 ; APPLICANT: Genetics Institute, Inc.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
 ; FILE REFERENCE: GIN 6403  
 ; CURRENT APPLICATION NUMBER: US/09/822.849A  
 ; CURRENT FILING DATE: 2001-09-04  
 ; PRIOR APPLICATION NUMBER: 60/195,582  
 ; PRIOR FILING DATE: 2000-04-06  
 ; NUMBER OF SEQ ID NOS: 598  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 485  
 ; LENGTH: 1972  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-822-849A-485

Alignment Scores:  
 Pred. No.: 3,97e-167 Length: 1972  
 Score: 1516.00 Matches: 272  
 Percent Similarity: 76.08% Conservative: 62  
 Best Local Similarity: 61.96% Mismatches: 99  
 Query Match: 62.18% Indels: 6  
 Gaps: 3

US-09-719-601-5 (1-444) x US-09-822-849A-485 (1-1972)

|    |      |  |      |
|----|------|--|------|
| QY | 11   | AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln     | 27   |
| DB | 1864 | CGCGCGGAGACCGCGGCTCAGGAGCTACCCGCGCTACTTCACTGGGAGCGAGTGGCC    | 1805 |
| QY | 28   | LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr | 47   |
| DB | 1804 | CAGCGCTCAGGCTGCGAGCGGCTGCTAGTGTGACCTGACCTGAGGTTGACATCAGC     | 1745 |
| QY | 48   | LysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp    | 67   |
| DB | 1744 | GAGTTACCCGCGCATCCAGGGGCTCCCGGCTCATCAGCCACTACGCGGCGGCGAGAT    | 1685 |
| QY | 68   | AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys | 87   |
| DB | 1684 | GCCACGGATCCCTTTGTGGCTTCACATCAACAAGGCGCTTGTGAAGAAGTATATGAAC   | 1625 |
| QY | 88   | ProLeuLeuIleGlyGluLeuAlaProGluLuproSerGlnAspHisGlyLysAsnSer  | 107  |
| DB | 1624 | TCTCTCTGATTGGAGACTGTCTCCAGCAGCGCCAGCTTTGAGCCCAAGAAATAA       | 1565 |
| QY | 108  | LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys | 127  |
| DB | 1564 | GAGCTGACAGATAGTTCCCGGAGCTCGGCGCCACAGTGGAGCGGATGGGCTCATGAAG   | 1505 |
| QY | 128  | ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla    | 147  |
| DB | 1504 | GCCACCAAGTCTTCTCTGCTGTACTGTGACATCTTGTCTGGATGGTGGCGCC         | 1445 |
| QY | 148  | TrpPheThrValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal | 167  |
| DB | 1444 | TGGCTCAACCTTGGGCTTTGGGAGCGTCTTTTGGCCCTTCTCTCTGTCGCGTGTG      | 1385 |
| QY | 168  | LeuAlaThrSerGlnAlaGluAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal | 187  |
| DB | 1384 | CTCAGTGAGTTTCAGCCAGCTGGCTGGCTGACATGACTTTGGGCACCTGTCCGTC      | 1325 |
| QY | 188  | TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly | 207  |
| DB | 1324 | TTACGACCTCAAGTGAACCATCTGCTACATCATTTTGTGATTGGCCACTGAAGGG      | 1265 |
| QY | 208  | AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe | 227  |

|    |      |  |      |
|----|------|--|------|
| DB | 1264 | GCCCCCGCGAGTGTGGAAACCAATGTCATCTCCAGCACCATGCCAGCCCACTGCTTC    | 1205 |
| QY | 228  | HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyLeuTrpGln  | 245  |
| DB | 1204 | CGCAAAGACCCAGACATCAACATG---CATCCCTTCTTCTTGTGCTGGGAAGATCCTC   | 1148 |
| QY | 246  | ProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGluTyr       | 265  |
| DB | 1147 | TTCTGGAGCTTGGGAACAGAAATAATATATGCGGTACACACACAGACACATAC        | 1088 |
| QY | 266  | PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleLeuMet | 285  |
| DB | 1087 | TTCTTCTTAATTGGGCGCCAGCTTGTGCTCTCTACTTCCAGGTATATTTCTAT        | 1028 |
| QY | 286  | ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg | 305  |
| DB | 1027 | TTTGTATTACGCGAAAGAGTGGGTGGCTTGGCTGGATGATTACTTTCACCTCCGC      | 968  |
| QY | 306  | PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe | 325  |
| DB | 967  | TTCTTCTCTCATTTATGTGCTACTATTGGGCTGAAAGCTTCTCTGGGCTTTCTTCTCAT  | 908  |
| QY | 326  | IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet | 345  |
| DB | 907  | GTGAGTTCTCGAAAGCAACTGGTTGTGTGGTGACACAGATGAACCATATTTCCCATG    | 848  |
| QY | 346  | GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn | 365  |
| DB | 847  | CACATTGATCATGACCGGAACATGAGTGGTGTTCACCCAGCTCCAGGCCACATGCAAT   | 788  |
| QY | 366  | ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleLysHis | 385  |
| DB | 787  | GTCCCAAGCTGCGCTTCAATGACTGGTTCAGTGACACCTCACTTCAGATTGAGCAC     | 728  |
| QY | 386  | HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer | 405  |
| DB | 727  | CATCTTTTCCACGATGCTCGACACATATACACAAAGTGGCTCCCTGTGGAGTCC       | 668  |
| QY | 406  | LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp | 425  |
| DB | 667  | TTGTGTGCCAAGCATGGCATAGTACCAGTCCAAAGCCCTCTCTGTCAGCTTCGCCGAC   | 608  |
| QY | 426  | IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys    | 444  |
| DB | 607  | ATCATCCACTCAATAAGGAGTCAGGCGAGCTCTGGCTAGATGCTTCTTCCACCA       | 551  |

RESULT 6  
 US-10-133-937-7  
 ; Sequence 7, Application US/10133937  
 ; Publication No. US20030207278A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Khan, Javed  
 ; APPLICANT: Ringner, Markus  
 ; APPLICANT: Peterson, Carsten  
 ; APPLICANT: Meltzer, Paul  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,  
 ; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
 ; TITLE OF INVENTION: OTHER BIOLOGICAL STATES  
 ; FILE REFERENCE: 11613.56US01  
 ; CURRENT APPLICATION NUMBER: US/10/133,937  
 ; CURRENT FILING DATE: 2002-11-04  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: Patent In version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 4213  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-133-937-7

Alignment Scores:  
 Pred. No.: 1.36e-166 Length: 4213  
 Score: 1516.00 Matches: 272

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Percent Similarity: 76.08% Conservativity: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.18% Indels: 6
Db: 13 Gaps: 3

US-09-719-601-5 (1-444) x US-10-133-937-7 (1-4213)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 99 GCCCGGAGACCGCGGCTCAGGACCTACCCGGGCTACTTCCAGTGGGACGAGGTGCC 158
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIleThr 47
Db 159 CAGCGCTCAGGTGGCGAGCGGTGGGTAGTACCGACCGTAAAGGTGTAAACATCAGC 218
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGluAsp 67
Db 219 GAGTTACCCCGCGGCATCCAGGGGCTCCCGGGTTCATCAGCCACTACCGCGGCGAGAT 278
QY 69 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 279 GCCCGGATCCCTTTTGTGGCTTCCACATCAACAAGGGCTTGTGAAGATATATGAAC 338
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 339 TCTCTCTGATTGGAGACTGCTCCAGAGCGCCAGCTTTGAGCCACCACCAAGATATAA 398
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 399 GAGCTACAGATGAGTTCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGCTCATGAAG 458
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleAlaLeuGluSerIleAla 147
Db 459 GCCACCACTGCTTCTCTGCTGCTACCTGCTGCACATCTTCTCTGCTGGTGCAGCC 518
QY 148 TrpPheThrValPheTyRheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167
Db 519 TGGCTACCGCTTGGGTCTTGGAGCTCTTTTGGCTTCTCTCTCTCTCTCTCTCTCTCT 578
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyRlyHisLeuSerVal 187
Db 579 CTGAGTGCACTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTGGGCACTTCGCTC 638
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 639 TTCAGCACCTCAAGTGAACCATCTGCTACATCATTTTGTGATGGCCACCTGAAGGG 698
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
Db 699 GCCCGCGCCAGTTGGTGGAAACCATGCACTTCCAGCACCATGCCAAGCCCACTGCTTC 758
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 759 CGCAAGACCCACACATCAACATG---CATCCCTTCTTCTTCTTCTTCTTCTTCTTCT 815
QY 246 ProIleGluTyRglyLysLysLysLeuLysTyLeuProTyAsnHisGlnHisGluTyR 265
Db 816 TCTGTGAGCTTGGGAAACAGAAATAATATGCGGTACACCAACCACCAAGCAACATAC 875
QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyRheGlnTyRLeuIleMet 285
Db 876 TTCTTCTAATTTGGGCCCCCAGCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 935
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyIleArg 305
Db 936 TTTGTTATCCAGCGAAAGAGTGGGTGGACTTGGCTGGATGATTACCTTCTACGTCGCG 995
QY 306 PhePheLeuThrTyIleProPheTyRglyLysLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 996 TTTCTCTCTATGTCACACTATTGGGCTGAAAGCCCTTCTGGGCTTTTCTTCATA 1055
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValTrpGlnMetAsnHisIleValMet 345
Db 326 ILeArgPheLeuGluSerHisTrpPheValTrpValTrpGlnMetAsnHisIleValMet 345

1056 GTCAGGTTCTCTGGAAAGCAACTGGTTTGTGGTGGTGACACAGATGAACCATATTCCCATG 1115
346 GluIleAspGlnGluAlaTyRArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
1116 CACATTGATCATGACCGGAACATGACTGGGTTTCCACCCAGCTCCAGGCCACATGCAAT 1175
366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
1176 GTCCCAAGCTGCGCTTCAATGACTGGTTCAGTGACGACCTCACTTCAGATTGAGCAC 1235
386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
1236 CATCTTTTCCACGATGCTCGACACATTAACCAAAAGTGGCTCCCTGGTGAGTCC 1295
406 LeuCysAlaLysHisGlyIleGlyTrpGlnGlyLysProLeuLeuArgAlaLeuLeuAsp 425
1296 TTGTGTGCAAGCATGGCATGAGTACCAAGTCCAAAGCCCTCTGTGACGCTTCCCGGAC 1355
426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyRLeuHisLys 444
1356 ATCATCTCACTCAATAAGGAGTCAGGGCAGCTCTGGCTAGATGCCTATCTTCAACCA 1412

RESULT 7
US-10-262-617-4
; Sequence 4, Application US/10262617
; Publication No. US2003007747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PP-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; PRIORITY FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CB1
US-10-262-617-4

Alignment Scores:
Pred. No.: 5,01e-167 Length: 1928
Score: 1515.00 Matches: 272
Percent Similarity: 76.08% Conservativity: 62
Best Local Similarity: 61.96% Mismatches: 99
Query Match: 62.14% Indels: 6
Db: 15 Gaps: 3

US-09-719-601-5 (1-444) x US-10-262-617-4 (1-1928)
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 102 GCCCGGAGACCGCGGCTCAGGACCTACCCGGGCTACTTCCAGTGGGACGAGGTGCC 161
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIleThr 47
Db 162 CAGCGCTCAGGTGGCGAGGCGGTGGCTAGTGTATGATCAACCGTAAGGTGTACACATCAGC 221
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGluAsp 67
Db 222 GAGTTCACCCCGCGCATCCAGGGGCTCCCGGCTCATCAGCCACTACCGCGGCGAGAT 281
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 282 GCCACGGATCCCTTTGTGGCTTCCACATCAACAAGGGCTTGTGAAGATATATGAAC 341
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QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 342 TCTCTCTGATTGAGAACGTCCTCAGAGCAGCCCGCTTGGAGCCACCAAGATATAA 401
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 402 GAGCTGACAGATGAGTTCGGGAGCTGCGGCCACAGTGCAGCGGATGGGGCTCATGAAG 461
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 462 GCCAACCATGCTCTCTCTGCTGTCCTGCTGCATCTTGTGCTGGATGGTGCAGCC 521
QY 148 TrpPheThrValPheThrPheGlyAsnGlyTrpIleProThrLeuLeuThrAlaPheVal 167
Db 522 TGGCTCACCTTTGGGTCCTTGGAGCGCTCTTTTGGCCCTTCTCTGCTGCGGTGCTG 581
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspPheGlyHisLeuSerVal 187
Db 582 CTCAGTCAGTTGAGGCCCGAGCTGGCTGGCTGCAGCATGACTTTGGGCACCTGTGCGTC 641
QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 642 TTCAGCACCTCAAGTGGAAACCATCTGTACATCATTTTGTGATTGGCCACCTGAAGGG 701
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisIleAlaLysProAsnIlePhe 227
Db 702 GCCCCCGCCAGTTGGTGGAAACCATGTCACATCTCCAGCACCATGCCAAGGCCAATCTCTC 761
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 762 CGCAAGACCCAGCACATCAACATG---CATCCCTTCTCTCTTGGCTTGGGAGATCCTC 818
QY 246 ProIleGluTyrGlyLysLysLysLeuLysLysLeuProTyrAsnHisGlnHisGluTyr 265
Db 819 TCTGTGAGCTTGGGAAACAGAAATAATATATGCGGTACCAACCCAGCACCAATATC 878
QY 266 PhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285
Db 879 TTCTTCTTAATTGGGCCCCCAGCTTCTGCTGCTCTACTTCCAGTGGATATTTCTAT 938
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrpIleArg 305
Db 939 TTTGTTATCCAGCGAAAGAGAGTGGGTGAGCTTGGCTTGGATGATTACTTCTACGTCCGC 998
QY 306 PhePheIleThrTrpIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 999 TTCTTCTCATTAATGTCACATAATGGGCGCTGAAGCCCTTCTGGGCTTTCTTCATA 1058
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValTrpGlnMetAsnHisIleValMet 345
Db 1059 GTCAGGTTCTCTGGAAGCAACTGGTTTGTGTGGGTGACACAGATGAACCATATTCCCATG 1118
QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1119 CACATTGATCATGACCGGAACATGGACTGGGTTTCCACCAGCTCCAGGCCACATGCAAT 1178
QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1179 GTCCACAGTCTGCTTCAATGACTGGTTGAGTGACACACTCACTTCCAGATTGAGCAC 1238
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1239 CATCTTTTCCCGATGCTCTGACACAAATATACCAAAAGTGGCTCCCTCGGTGAGTCC 1298
QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1299 TTGTGTCCAGCATGGCATAGATGACAGTCCAGGCCCTGCTGTGCTGAGCTTCGCCGAC 1358
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1359 ATCATCTCACTCAATAAGAGTCAAGGCGAGCTGCTGCTAGATGCTTCTTCCCAA 1415
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RESULT 8
US-10-191-513A-1
; Sequence 1, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-1
Alignment Scores:
Pred. No.: 1,83e-166 Length: 1335
Score: 1508.00 Matches: 271
Percent Similarity: 75.85% Conservative: 62
Best Local Similarity: 61.73% Mismatches: 100
Query Match: 61.85% Indels: 6
DB: 15 Gaps: 3
US-09-719-601-5 (1-444) x US-10-191-513A-1 (1-1335)
QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluIleGln 27
Db 19 GCCGCCGAGAGCGCGGCTCAGGACCTACCCCGCGCTACTTCACTCGGACGAGTGCC 78
QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThr 47
Db 79 CAGCGCTCAGGCGTGCAGGAGCGGTGCTAGTATCGACCCGTAAGGTGTACAACATCAGC 138
QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAsp 67
Db 139 GAGTTTACCCCGCGCATCCAGGGGCTCCCGGTTCATCAGCCACTACCGCGGCGAGAT 198
QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 199 GCCACGGATCCCTTTGTGGCTTCCACATCAACAGGCGCTTGTGAAGAAGTATATGAAC 258
QY 88 ProLeuLeuIleGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 259 TCTCTCTGATGGAGAACTGTCTCCAGAGCAGCCAGCTTGGAGCCACCAAGATATAA 318
QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 319 GAGCTGACAGATGAGTTCGGGAGCTGCGGCCACAGTGGAGCGATGGGGCTCATGAAG 378
QY 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147
Db 379 GCCAACCATGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
QY 148 TrpPheThrValPheThrPheGlyAsnGlyTrpIleProThrLeuLeuThrAlaPheVal 167
Db 439 TGGCTCACCTTTGGGTCCTTGGGAGCGCTCTTTTGGCCCTTCTCTGCTGCGGTGCTG 498
QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 499 CTCAGTGCAGTTCAAGGCCCGAGCTGGCTGGCTGCAGCATGACTTTGGGCACCTGTGCGTC 558
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QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207
Db 559 TTCAGCACTCAAAGTGAACCATCTGCTCATCATATTGTGATTGGCCACCTGAAGGG 618
QY 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLysProAsnIlePhe 227
Db 619 GCGCCGGCCGATGGTGGAAACCAATGATGCTTCAGCACCACCAAGCCCACTGCTTC 678
QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 679 CGCAAGACCCAGACATCAATG---CATCCCTTCCTTCCTTGGGGAAGATCCTC 735
QY 246 ProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 265
Db 736 TCTGTGGAGCTTGGGAACCAAGAAATATATGCGGTACAAACCAACCAATATAC 795
QY 266 PhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIleMet 285
Db 796 TCTTCTCTCAATGCGCCCGCCAGCTTGTCTGCTCTCTCTCTCTCTCTCTCTCTCT 855
QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArg 305
Db 856 TTTGTATCCAGCGAAAGAGTGGGTGGACTGGCTGGATGATACCTTACGTCGCG 915
QY 306 PhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhe 325
Db 916 TTTCTTCTCACTTATGTGCCACTATTTGGGCTGAAGCCTTCTTGGGCTTTTCTCAT 975
QY 326 IleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIleValMet 345
Db 976 GTCCAGTCTCTGGAAGCAACTGGTTGTGTGGGTGACACAGATGAACCATATTCCTCAT 1035
QY 346 GluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1036 CACATTGATCATGACCGAATGAGTGGTGTGTGGGTGACACAGATGAACCATATTCCTCAT 1095
QY 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1096 GTCCACAGCTGCTGCTTCAATGACTGGTTTCACTGGGACACCTCACTTCCAGATTGAGCAC 1155
QY 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1156 CATCTTTTTCACGATGCTGCTGACCAATACCAATGAGTGGTTCCTTGGTGGAGTCC 1215
QY 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1216 TTGTGTGCCAAGCGTGGCATAGATACAGTACAGTCCAGCCCTGCTGACGCTTCCCGCAC 1275
QY 426 IleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHisLys 444
Db 1276 ATCATCCACTCACTAAAGAGTCCAGGCGAGCTCTGCTGATGCTTATCTTCCACCA 1332

RESULT 9
US-10-191-513A-6
; Sequence 6, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US.D3
; CURRENT APPLICATION NUMBER: US/10191,513A
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-6

Alignment Scores:
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Score: 1348.00 Matches: 241
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.23% Indels: 0
DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-191-513A-6 (1-1686)
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223
Db 3 CACTTAAAGGTTGCTCTGCACTTGGTGAATCATCGCACTTCCAGCACCCACGCAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTTAAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTGTTTGTCTGGCGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLysLys 263
Db 123 TGGCAGCCCATCGAGTACGGCAAGAGTGAATACCTGCTGCTTACAATCACCAGCAC 182
QY 264 GluTyrPhePheLeuIleGlyProPheLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATATCTTCTTCTGATTTGGGCGCGCTGCTCATCTCCCATGTTATTTCCAGTACGATC 242
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTrp 303
Db 243 ATCATGACCATGATCTCCATAAGACTGGGTGGACCTGGCTGGGCCCTGAGTACTAC 302
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGGTCTTTCATCATCTACCTACATCCCTTCTACGGCATCTGGGAGCCCTCTTTTCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACTTATCATGAGTCTCTGGAGAGCCACTGGTTGTGGGTCCACACAGATGAATCACATC 422
QY 344 ValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThr 363
Db 423 GTCATGGAGATTGACCAGGAGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
QY 364 CysAsnValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIle 383
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QY 384 GluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuVal 403
Db 543 GAGCACCACTCTTCCCAACCATGCGCCGCGCACAACTTACACAGATCGCCCGCTGGTG 602
QY 404 LysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeu 423
Db 603 AAGTCTCTATGTGCCAAGCATGGCATTAATACAGGAGGAGCGCTGCTGCTGCTGCTGCT 662
QY 424 LeuAspIleIleArgSerLeuLysLysSerGlyLysLeuTrpLeuAspAlaTyrLeuHis 443
Db 663 CTGGACATCATCAGTCCCTGGAAGAGTCTGGGAAGCTGTGGTGGAGCGCTTACCTTAC 722
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RESULT 10
US-09-981-876-63
; Sequence 63, Application US/09981876
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/ Patent No. US20020164669A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Rosen et al.  
/ TITLE OF INVENTION: 70 Human Secreted Proteins  
/ FILE REFERENCE: PZ001P1  
/ CURRENT APPLICATION NUMBER: US/09/981,876  
/ CURRENT FILING DATE: 2001-10-19  
/ PRIOR APPLICATION NUMBER: 09/148,545  
/ PRIOR FILING DATE: 1998-09-04  
/ PRIOR APPLICATION NUMBER: 60/040,162  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,333  
/ PRIOR FILING DATE: 1997-03-07  
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/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,626  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,334  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,336  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,163  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/047,615  
/ PRIOR FILING DATE: 1997-05-23  
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/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,597  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,502  
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/ PRIOR APPLICATION NUMBER: 60/057,761  
/ PRIOR FILING DATE: 05-sep-1997  
/ PRIOR APPLICATION NUMBER: 60/047,599

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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,585
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; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1478

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## Alignment Scores:

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Score: 1300.00 Matches: 244
Percent Similarity: 77.19% Conservative: 47
Best Local Similarity: 64.72% Mismatches: 84
Query Match: 53.32% Indels: 5
DB: 10 Gaps: 1

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US-09-719-601-5 (1-444) x US-09-981-876-63 (1-1478)

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Qy 89 LeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSerLys 108
Db 76 CTGTGTTGGAGAGCTGGCTCCGGAACACCCAGCCAGGATGGACCCCTGATG--CGC 133
Qy 109 IleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLysThr 128

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## RESULT 11

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US-09-148-545-63
; Sequence 63, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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Qy 149 PheThrValPheTyrPheGlyAsnGlyTTPilleProThrLeulle-ThrAlaPheValle 168
Db 254 CTCCTTATCTACCTCTCTGGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 313
Qy 168 uAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTy 188
Db 314 GGCCATCTCTCAGCTCAGTCTCTGGTGTCTGCAAGCATGACCTGGGCGATGC-TCCATCTT 372
Qy 188 rArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAl 208
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Db 790 CTTGAAAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
Qy 348 pGlnGluAlaTyrArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsnValGluGI 368
Db 850 CCAGAGAAGCACCGGACCTGGTCACTCTCAGCTGGCAGCCACCTGCAACGTGGAGCC 909
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Db 1030 CAAGCACGCGCTCAGCTACGAATG-AAAGCCCTCTCTCAGCGCGCTGGTGGACATCGTCAG 1088
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|--|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
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| TITLE OF INVENTION: 70 Human Secreted Proteins |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| FILE REFERENCE: P2001P1                        |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| CURRENT APPLICATION NUMBER: US/09/148,545      |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| PRIOR FILING DATE: 1998-09-04                  |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| CURRENT FILING DATE: 1998-09-04                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: PCT/US98/04482     |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1998-03-06                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,162         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,333         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/038,621         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,161         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,626         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,334         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,336         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/040,163         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-03-07                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,615         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,600         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,597         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,502         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,633         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,583         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,617         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,618         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,503         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,592         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,581         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,584         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,500         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,587         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,492         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,598         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,613         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,582         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,596         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,612         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,632         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/047,601         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-05-23                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,580         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,568         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,314         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,569         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,311         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,671         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,674         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,669         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,312         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,313         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,672         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/043,315         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-04-11                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/048,974         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-06-06                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/056,886         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-08-22                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/056,877         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-08-22                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/056,889         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-08-22                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/056,893         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-08-22                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/056,630         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-08-22                |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER APPLICATION NUMBER: 60/056,878         |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
| EARLIER FILING DATE: 1997-08-2                 |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |



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/ SEQ ID NO 119
/ LENGTH: 2016

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; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: P2001P1  
; CURRENT APPLICATION NUMBER: US/09/148,545  
; CURRENT FILING DATE: 1998-09-04  
; EARLIER APPLICATION NUMBER: PCT/US98/04482  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
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; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22

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EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 280  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 119  
LENGTH: 2016

Alignment Scores:  
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Score: 1162.00 Matches: 248  
Percent Similarity: 54.88% Conservative: 50  
Best Local Similarity: 45.67% Mismatches: 97  
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US-09-719-601-5 (1-444) x US-09-148-545-119 (1-2016)

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QY 81 PheValGlyPheLeuLysProLeuLeuIleGlyGluLeuAlaProGluProSer 100  
Db 194 TTTGTGCG-CAATTCCTACAGCCCTGTTGATGAGAGCTGCTCCGGAAGACCCAGC 252  
QY 101 GlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeuArgLysThrAla 120  
Db 253 CAKGATGGACCCCTGAATG-CGCATGGTCGAGGACTTCGAGCCCTGCACCGAGCGCC 310  
QY 121 GluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHisIle 140  
Db 311 GAGGACATGAAGCTGTTGATGCCAGTCCCACTTCCTTTGCTTCTATCTGGCCACATC 370  
QY 141 IleAlaLeuGluSerIleAlaThrPheThrValPheTyrPheGlyAsnGlyTrpIlePro 160  
Db 371 CTGCGCATGGAGGTGCTGGCTGGCTCTTATCTACTCTGCTGCTCTGCTGGTGGCC 430  
QY 161 ThrLeuIle-ThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHi 180  
Db 431 AGTCCCTCGNCCGCTTCATCTCCGCTCAGTCTCAGGCTCAGTCTGCTGCTGAGCA 490  
QY 180 sAspTyrGlyHisLeuSerValTyrArgLysProLysTyrAsnHisLeuValHisLysPh 200  
Db 491 TGACCTGGGCCATGC-TCCATCTTCAAGAGTCTCTGTGAACACACGTCGCCAGAGTT 549  
QY 200 eValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHi 220  
Db 550 CGTGATGGGCGAGCTAAAGGGCTTCTCCGCGCCACTGGTGGAACTTCGCCACATCTCCAGCA 609  
QY 220 sHisAlaLysProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheVa 240  
Db 610 CCAGCCCAAGCCCAACATCTTCCAAAGAGCCAGAGCTGAGCGTGGCGGCCGCTTCTCT 659  
QY 240 lLeuGlyGluTrpGlnProIleGluTyrGly-LysLysLysLysLysLysLysLysLys 260  
Db 670 CCTGGGGGAG---TCATCCGTCGAGTATGNCAGAGAAAGAACACGATACCTACCTTACA 726  
QY 260 snHisGlnHisGluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheG 280  
Db 727 ACCAGCAGCAGCTGTACTTTTCTGATCGCGCCGCGCTGCTCACCTCGTGAACCTTG 786  
QY 280 lntyrGlnIleIleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlav 300  
Db 787 AAGTGGAAATCTGGCGTACATGCTGCTGTCATGTCAGTGGCGGAGTTTCTCTGGGCCG 846  
QY 300 alserTyrTrpIleAcPhePheIleThrTrpIleProPheTyrGlyIleLeuGlyAlaAl 320  
Db 847 CCAGCTTCTATGCGCCGCTTCTTCTTACCTACCTCCCTCTTACGCGGCTCCCTGGGGTGC 906

EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,936  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 05-Sep-1997  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650



QY 415 GlnGluLysProLeuLeuArgAlaLeuLeuAspIleLeuAserLeuLysSerGly 434  
 Db 772 CAGTCCAGCCCTGCTGCGACCTTCGCGACATCATCCACTCACTAAAGGAGTCAGG 831  
 QY 435 LysLeuTrpLeuAspAlaTyrlleuHisLys 444  
 Db 832 CAGCTCTGGCTAGATGCCTATCTTCCACCA 861

## RESULT 15

US-10-191-513A-34  
 ; Sequence 34, Application US/10191513A  
 ; Publication No. US20030104596A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pardip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; APPLICANT: Tapas, Das  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.D3  
 ; CURRENT APPLICATION NUMBER: US/10/191,513A  
 ; CURRENT FILING DATE: 2002-09-25  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 34  
 ; LENGTH: 990  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-191-513A-34

Alignment Scores:  
 Pred. No.: 2,37e-102 Length: 990  
 Score: 960.00 Matches: 176  
 Percent Similarity: 69.54% Conservative: 50  
 Best Local Similarity: 54.15% Mismatches: 73  
 Query Match: 39.38% Indels: 26  
 DB: 15 Gaps: 4

US-09-719-601-5 (1-444) x US-10-191-513A-34 (1-990)

QY 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27  
 Db 19 GCGCGCGAGACCGCGGCTCAGGACCTACCCCGCTACTTCCCTGGGACGAGGTGGCC 78  
 QY 28 LysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTrsAnlleThr 47  
 Db 79 CAGCGCTCAGGGTCCGAGGAGCGGTGGCTAGTCATCGCGTAAAGGTGACACATCAGC 138  
 QY 48 LysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTrValaGlyGluAsp 67  
 Db 139 GAGTTACCGCGGCTACAGGGGCTCCGGGTATCAGCACCTACCGCGGCGAGGAT 198  
 QY 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87  
 Db 199 GCCACGGATCCCTTTGTGGCTTCCATCAACAAAGGCGCTTGTGAAGAAGTATATGAAC 258  
 QY 88 ProLeuLeuIleGlyGluLeuAlaProGluProSerGlnAspHisGlyLysAsnSer 107  
 Db 259 TCTCTCTGATTGGAGAACTGTCTCCAGAGCAGCCGAGCTTGAGCCCAAGATATAA 318  
 QY 108 LysIleThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127  
 Db 319 GAGCTGACAGATGAGTTCGGGAGCTCGGCGCCACAGTGGAGCGGATGGGCTCATGAAG 378  
 QY 128 ThrAsnHisValPhePheLeuLeuAlaHisIleIleAlaLeuGluSerIleAla 147

Db 379 GCCAACCATGTCTTCTCTCTGCTGCTACCTGCTGCACATCTTCTGCTGGATGGTCAGCC 438  
 QY 148 TrpPheThrValPheTyrlleGlyAsnGlyTrpIleProThrLeuIleThrAlaPheVal 167  
 Db 439 TGCTCACCTCTGGGCTCTTTGGGAGCGTCTTTTGGCCCTTCTCTCTCTGTCGGGTGTCG 498  
 QY 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrlleGlyHisLeuSerVal 187  
 Db 499 CTGAGTGCAGTTCAGGCCCGGCTGGCTGGCTGCAGCATGCTTTGGGACCTGTCGGTC 558  
 QY 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGly 207  
 Db 559 TTCAGCACCTCAAAAGTGAACCATCTGCTACATCATTTTGTGATGGCCACCTGAAGGG 618  
 QY 208 AlaserAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePhe 227  
 Db 619 GCGCCCGCGAGTTGGTGGAAACCATGCTCTCCAGCACCATGCCAGCCCACTGCTTC 678  
 QY 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245  
 Db 679 CGCAAGACCCAGACATCAACATG---CATCCCTTCTCTCTGCTTGGGGAAGATCCTC 735  
 QY 246 ProIleGluTyrlleGlyLysLysLeuLysTyrlleProTyrlleAsnHisGlnHisGluTyrl 265  
 Db 736 TCTGTGAGCTTGGGAAACAGAAATAATATATCGGTACCAACCCAGCACCAATATC 795  
 QY 266 PhePheLeuIleGly-----ValPheValLeuGlyGluTrpGln 270  
 Db 796 TTCTTCTTAATTGGGCGCCCGCAGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTAT 855  
 QY 271 -----ProProLeuLeuIleProMetTyrlleGlnTyrlleGlnIleMet 285  
 Db 856 TTTGTTATCCAGCGACCCCGCAGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTAT 915  
 QY 286 ThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrlleArg 305  
 Db 916 TTTGTTATCCAGCGAAAGAGTGGTGGACTTGGCTGGATGATTACCTTCTACGTCGCG 975  
 QY 306 PhePheIleThrTyrl 310  
 Db 976 TTCTTCTCTCACTTAT 990  
 RESULT 16  
 US-10-191-513A-35  
 ; Sequence 35, Application US/10191513A  
 ; Publication No. US20030104596A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pardip  
 ; APPLICANT: Leonard, Amanda E.  
 ; APPLICANT: Huang, Yung-Sheng  
 ; APPLICANT: Tapas, Das  
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 ; FILE REFERENCE: 6295.US.D3  
 ; CURRENT APPLICATION NUMBER: US/10/191,513A  
 ; CURRENT FILING DATE: 2002-09-25  
 ; PRIOR APPLICATION NUMBER: US 09/227,613  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422  
 ; PRIOR FILING DATE: 1998-04-10  
 ; PRIOR APPLICATION NUMBER: US 08/833,610  
 ; PRIOR FILING DATE: 1997-04-11  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 35  
 ; LENGTH: 960  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-191-513A-35  
 Alignment Scores:  
 Pred. No.: 3,33e-99 Length: 960  
 Score: 933.00 Matches: 170

Percent Similarity: 73.38%  
Best Local Similarity: 58.02%  
Query Match: 38.27%  
DB: 15  
Conservative: 45  
Matches: 72  
Indels: 6  
Gaps: 3

US-09-719-601-5 (1-444) x US-10-191-513A-35 (1-960)

```
Qy 11 AlaAlaGluArgGluValSerValProThr-----PheSerTrpGluGluLeuGln 27
Db 49 GCGGCGAGACCGCGGCTCAGGACCTACCCGCGCTACTTACCTGGGAGGAGTGGCC 108
Qy 28 LysHisLeuArgThrAspSerGlyLeuValLeuAspArgLysValTyrAsnLeuThr 47
Db 109 CAGCGCTCAGCGTCCGAGGAGCGGTGCTAGTATGACCGTAAAGTGTACAACTCAGC 168
Qy 48 LysTrpSerLeuGlnHisProGlyGlyGlnArgValLeuGlyHisTyrAlaGlyGluAsp 67
Db 169 GAGTTCACCGCGGCTCAGGCGGCTCCGCGGTCTATCAGCCACTACGCGCGGAGGAT 228
Qy 68 AlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeuLys 87
Db 229 GCCACGATCCCTTTGGCGCTTCCACATCAACAGGCGCTTGTGAAGAGTATATGAAC 288
Qy 88 ProLeuLeuGlyGluLeuAlaProGluGluProSerGlnAspHisGlyLysAsnSer 107
Db 289 TCTCTCTGATTGAGACTGTCTCCAGACAGCGGCTTTCAGCCCAAGATATAA 348
Qy 108 LysLeuThrGluAspPheArgAlaLeuArgLysThrAlaGluAspMetAsnLeuPheLys 127
Db 349 GAGGTGACATGATGTTCCGAGAGTCCGCGGAGTCCGCGGAGTGGGCTCATGAAG 408
Qy 128 ThrAsnHisValPhePheLeuLeuLeuAlaHisLeuLeuAlaLeuGluSerLeuAla 147
Db 409 GCCAACCATGCTCTCTCTGCTGTACTGCTGCACATCTTGTGCTGAGTGTGAGCC 468
Qy 148 TrpPheThrValPheTyrPheGlyAsnGlyTrpLeuProThrLeuLeuThrAlaPheVal 167
Db 469 TGGCTCACCTTGGGCTTGGGAGCTCTTTTGGCCCTTCTCTCTCTGCGGTGCTG 528
Qy 168 LeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerVal 187
Db 529 CTCAGTGAGTTCAGGCGGCGGCTGGCTGGCTGAGCATGACTTTGGGCGCCTGTGCTC 588
Qy 188 TyrArgLysProLysTrpAsnHisLeuValHisLysPheValLeuGlyHisLeuLysGly 207
Db 589 TTCAGCACTCAAGTGAACCATCTGCTACATCATTTTGTGATGGCCACCTGAAGGG 648
Qy 208 AlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnLeuPhe 227
Db 649 CCCCCCGCAGTTGGTGAACCATGCTCCAGCACCATGTCGAAGCCCAACTGCTTC 708
Qy 228 HisLysAspProAspValAsnMetLeuHis-----ValPheValLeuGlyGluTrpGln 245
Db 709 CGCAAGAGCCAGACATCAATG---CATCCCTTCTTCTTGGCTTGGGAGAGTCTC 765
Qy 246 ProLeuGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyr 265
Db 766 TCTGTGGAGCTTGGGAACAGAGAATAATATGCGGTACAAACCCAGCACAATAC 825
Qy 266 PhePheLeuLeuGlyProProLeuLeuProMetTyrPheGlnTyrGlnLeuMet 285
Db 826 TCTCTCTTAATGGGCCCCCGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTAT 885
Qy 286 ThrMetLeuValHisLysAsnTrpValAspLeuAlaTrp 298
Db 886 TTTGTTATCCAGCAAGAGTGGTGGACTTGGCTGG 924
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RESULT 17

US-10-191-513A-5  
; Sequence 5, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories

```
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapes, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (755)...(755)  
; OTHER INFORMATION: x = g or a at position 755  
US-10-191-513A-5  
Alignment Scores:  
Pred. No.: 4.62e-98 Length: 918  
Score: 923.00 Matches: 167  
Percent Similarity: 74.04% Conservative: 44  
Best Local Similarity: 58.60% Mismatches: 68  
Query Match: 37.86% Indels: 6  
DB: 15 Gaps: 3  
US-09-719-601-5 (1-444) x US-10-191-513A-5 (1-918)  
Qy 19 ProThr-----PheSerTrpGluGluLeuGlnLysHisAsnLeuArgThrAspSer 35  
Db 7 CCTACCCGCGGCTACTTCACTGGGAGGAGTGGCCAGCGCTCAGGCTGGGAGGCGG 66  
Qy 36 GlyLeuValLeuAspArgLysValTyrAsnLeuThrLysTrpSerLeuGlnHisProGly 55  
Db 67 TGGCTAGTATCGACCGTAAAGTGTACAACTACAGAGTTCACCCCGCGGCACTCAGG 126  
Qy 56 GlyGlnArgValLeuGlyHisTyrAlaGlyGluAspAlaThrAspAlaPheArgAlaPhe 75  
Db 127 GACTCCCGGCTCATCAGCCACTACGCGGCGGAGGATGCCAGGATCCCTTTGTGCGCTTC 186  
Qy 76 HisProAspLeuGluPheValGlyLysPheLeuLysProLeuLeuLeuGlyLeuAla 95  
Db 187 CACATCAACAAGGCGCTTGTGAAGAAGTATATGAATCTCTCTCTGATGGAGAACTGTCT 246  
Qy 96 ProGluGluProSerGlnAspHisGlyLysAsnSerLysLeuThrGluAspPheArgAla 115  
Db 247 CAGAGAGCGCCAGCTTTGAGCCCAACCAAGATAAAGAGCTGACAGATGAGTTCGGGAG 306  
Qy 116 LeuArgLysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPheLeuLeu 135  
Db 307 CTGCGGCGCACAGTGGAGCGGATGGGCTCATGAAGGCCAACCACTGTCTTTCTTCGTGTG 366  
Qy 136 LeuLeuAlaHisLeuLeuAlaLeuGluSerLeuAlaTrpPheThrValPheTyrPheGly 155  
Db 367 TACCTGTGCACATTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426  
Qy 156 AsnGlyTrpProThrLeuLeuThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175  
Db 427 AGGTCTCTTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486  
Qy 176 GlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHis 195  
Db 487 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 546  
Qy 196 LeuValHisLysPheValLeuGlyHisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHis 215
```

Db 547 CTGCTACATCATTTTGTGATTTGGCCACCTGAGGGGGCCCCCGCAGTTGGTGAACAC 606  
Qy 216 ArgHisPheGlnHisHisAlaLysProAsnTlePheHisLysAspProAspValAsnMet 235  
Db 607 ATGCACCTTCCAGCACCATGCGCAAGCCCACTGCTTCCGCAAGAGCCAGACATCAACATG 666  
Qy 236 LeuHis-----ValPheValLeuGlyGlnProLeuGlnProLeuGlyGlyLeuLysLys 253  
Db 667 ---CACTCCTCTCTTTTGGCTTGGGGAAGATCCTCTCTGTTGGAGCTTGGGAACAGAG 723  
Qy 254 LeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhePheLeuLeuGlyProProLeu 273  
Db 724 AAAAAATATATGCGGTACCAACACCCAGCACACATCTTCTCTTAATTTGGGCCCCCAGCC 783  
Qy 274 LeuLeuProMetTyrPheGlnTyrGlnTlelleMetThrMetIleValHisLysAsnTyr 293  
Db 784 TTGCTGCTCTCTACTTCCAGTGTATATTTCTATTTTGTATCCAGCGAAGAGTGG 843  
Qy 294 ValAspLeuAlaTyr 298  
Db 844 GTGGACTTGGCCTGG 858

## RESULT 18

US-09-604-287A-425  
; Sequence 425, Application US/09604287A  
; Patent No. US20020064872A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-425

Alignment Scores:  
Pred. No.: 4e-88 Length: 446  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 9 Gaps: 0

US-09-719-601-5 (1-444) x US-09-604-287A-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
Db 2 CACTTAAAGGGTGCCTCTGCAACTGGTGAATCATCGCACTTCCAGCACCCAGCAAG 61  
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 62 CCTTAAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCAGCTGTTTCTGGGCGAA 121  
Qy 244 TrpGlnProIleGluTyrGlyLysLysLeuLysLeuLysTyrLeuProTyrAsnHisGlnHis 263  
Db 122 TGGCAGCCCATCGATCGGCAAGAGAGTGAATACCTGCTTACATCACCAGCAC 181  
Qy 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283  
Db 182 GAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCCATGATTTCAGTACCAGATC 241

Qy 284 IleMetThrMetIleValHisLysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyr 303  
Db 242 ATCATGACCATCATGTCCTCAATGAACCTGGGTGGACCTGGCTGGGCGCTCAGCTACTAC 301  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaIleLeuPheLeu 323  
Db 302 ATCCGGTTCCTTCATCACCCTACATCCCTTTCTACGGCATCCTGGGAGCCCTCTTTCCTC 361  
Qy 324 AsnPheIleArgPheLeuGluSerHisTyrPheValTyrValThrGlnMetAsnHisIle 343  
Db 362 AACTTCATCAGGTTCTGGAGAGCCACTGGTTTGTGTGGGTACACACAGATGAATCACATC 421  
Qy 344 ValMetGluIleAspGlnGlu 350  
Db 422 GTCATGGAGATTGACCAAGGAG 442

## RESULT 19

US-09-551-621-425  
; Sequence 425, Application US/09551621  
; Publication No. US20030104366A1  
; GENERAL INFORMATION:  
; APPLICANT: Yuqiu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C5  
; CURRENT APPLICATION NUMBER: US/09/551,621  
; CURRENT FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 479  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-551-621-425

Alignment Scores:  
Pred. No.: 4e-88 Length: 446  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 11 Gaps: 0

US-09-719-601-5 (1-444) x US-09-551-621-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTyrTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
Db 2 CACTTAAAGGGTGCCTCTGCAACTGGTGAATCATCGCACTTCCAGCACCCAGCAAG 61  
Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 62 CCTTAAACATCTTCCACAAGGATCCCGATGTGAACATGCTGCAGCTGTTTGTTCGGCGAA 121  
Qy 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263  
Db 122 TGGCAGCCCATCGAGTACGCAAGAGAGTGAATACCTGCTTACATCACCAGCAC 181  
Qy 264 GluTyrPhePheLeuLeuGlyProProLeuLeuLeuProMetTyrPheGlnTyrGlnIle 283  
Db 182 GAATACCTTCTCTGATTTGGCGCGCGCTGCTCATCCCCATGATTTCAGTACCAGATC 241  
Qy 284 IleMetThrMetIleValHisLysAsnTyrValAspLeuAlaTyrAlaValSerTyrTyr 303  
Db 242 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGGCGCTCAGCTACTAC 301  
Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaIleLeuPheLeu 323  
Db 302 ATCCGGTTCCTTCATCACCCTACATCCCTTTCTAGGGCATCTCTGGAGGCCCTCTTTCCTC 361



Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
Db 362 AACTTCATCAGGTCTCTGGAGGCCACTGGTTGTGTGGGTCCACAGAGATCATCATC 421

Qy 344 ValMetGluIleAspGlnGlu 350  
Db 422 GTCATGGAGATTGACCAAGGAG 442

## RESULT 20

US-10-124-805-425  
; Sequence 425, Application US/10124805  
; Publication No. US2003016602A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C12  
; CURRENT APPLICATION NUMBER: US/10124.805  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-124-805-425

Alignment Scores:  
Pred. No.: 4e-88 Length: 446  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 13 Gaps: 0

US-09-719-601-5 (1-444) x US-10-124-805-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223  
Db 2 CACTTAAGGGTGCTCTGCCAATCTGTGGATCATGCCACTCCAGCCCAAG 61

Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 62 CCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTGTTGTCTGGCGAA 121

Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLys 263  
Db 122 TGGCAGCCCATCGAGTACGGCAGAGAGAGCTGAATACCTGCCCTACATCCAGAC 181

Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
Db 182 GAATACTTCTCTGATGGCGCGCTGCTCATCCCCATGATATTCAGTACCATC 241

Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuIleValPheValSerTyrTyr 303  
Db 242 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGAGCTACTAC 301

Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323  
Db 302 ATCCGGTTCTTCACTACATCCCTTCACGGCATCTGGAGGCCCTCCCTTTCCCTC 361

Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
Db 362 AACTTCATCAGGTCTCTGGAGGCCACTGGTTGTGTGGGTCCACAGAGATCATCATC 421

Qy 344 ValMetGluIleAspGlnGlu 350  
Db 422 GTCATGGAGATTGACCAAGGAG 442

## RESULT 21

US-10-007-805-425

; Sequence 425, Application US/10076622

; Publication No. US20030023036A1

; Sequence 425, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007.805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 425  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-007-805-425

Alignment Scores:  
Pred. No.: 4e-88 Length: 446  
Score: 834.00 Matches: 147  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 34.21% Indels: 0  
DB: 14 Gaps: 0

US-09-719-601-5 (1-444) x US-10-007-805-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisAlaLys 223  
Db 2 CACTTAAGGGTGCTCTGCCAATCTGTGGATCATGCCACTCCAGCCCAAG 61

Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
Db 62 CCTAACATCTTCCACAGGATCCCGATGTGAACATGCTGCACGTGTTGTCTGGCGAA 121

Qy 244 TrpGlnProIleGluTyrGlyLysLysLysLysLysLysLysLysLysLysLys 263  
Db 122 TGGCAGCCCATCGAGTACGGCAGAGAGAGCTGAATACCTGCCCTACATCCAGAC 181

Qy 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
Db 182 GAATACTTCTCTGATGGCGCGCTGCTCATCCCCATGATATTCAGTACCATC 241

Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuIleValPheValSerTyrTyr 303  
Db 242 ATCATGACCATGATCGTCCATAAGAACTGGGTGGACCTGGCGCTGAGCTACTAC 301

Qy 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323  
Db 302 ATCCGGTTCTTCACTACATCCCTTCACGGCATCTGGAGGCCCTCCCTTTCCCTC 361

Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
Db 362 AACTTCATCAGGTCTCTGGAGGCCACTGGTTGTGTGGGTCCACAGAGATCATCATC 421

Qy 344 ValMetGluIleAspGlnGlu 350  
Db 422 GTCATGGAGATTGACCAAGGAG 442

GENERAL INFORMATION:  
 APPLICANT: Houghton, Raymond L.  
 APPLICANT: Sleath, Paul R.  
 APPLICANT: Persing, David H.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
 FILE REFERENCE: 210121.470C11  
 CURRENT APPLICATION NUMBER: US/10/076,622  
 CURRENT FILING DATE: 2002-02-13  
 NUMBER OF SEQ ID NOS: 627  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 425  
 LENGTH: 446  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-076-622-425

Alignment Scores:  
 Pred. No.: 4e-88 Length: 446  
 Score: 834.00 Matches: 147  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 34.21% Indels: 0  
 DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-076-622-425 (1-446)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
 Db 2 CACTTAAAGGGTCCCTCTGCAACTGGTGGATCATCGCCACTTCCAGCACCACCCCAAG 61  
 Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
 Db 62 CCTAACATCTTCCACAGGATCCCGATGGAATGCTGCAGTGTGTTCTTGGGCGAA 121  
 Qy 244 TrpGlnProIleGluTyGlyLysLysLysLeuLysTyLeuProTyrAsnHisGlnHis 263  
 Db 122 TGGCAGCCCATCAGTACGCGCAAGAGAGCTGAAATACCTGCCCTTACATCACCAGCAC 181  
 Qy 264 GluTyPhePheLeuIleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIle 283  
 Db 182 GAATACCTCTCTGATTTGGCGCGCTCTCATCCCATGATTTTCCAGTACCATGATC 241  
 Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTy 303  
 Db 242 ATCATGACCATGATCGTCCATAAGAACTGGTGGACCTGGCTGGCGCTGAGTACTAC 301  
 Qy 304 IleArgPhePheIleThrTyIleProPheTyGlyIleLeuGlyAlaLeuLeuPheLeu 323  
 Db 302 ATCCGGTTCATCATCACCTACATCCCTTTCTACGGCATCTGGAGCCCTCTTTTCCATC 361  
 Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
 Db 362 AACTTCATCAGTTCCTGGAGAGCCACTGTTTGTGTGGTCCACACAGATGATCATCATC 421  
 Qy 344 ValMetGluIleAspGlnGlu 350  
 Db 422 GTCATGGAGATTGACCCAGGAG 442

RESULT 23  
 US-09-604-287A-313  
 Sequence 313, Application US/09604287A  
 Patent No. US20020064872A1  
 GENERAL INFORMATION:  
 APPLICANT: Jiang, Yugu  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Hepler, William T.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
 FILE REFERENCE: 210121.470C7

CURRENT APPLICATION NUMBER: US/09/604,287A  
 CURRENT FILING DATE: 2000-06-22  
 NUMBER OF SEQ ID NOS: 489  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 313  
 LENGTH: 456  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-604-287A-313

Alignment Scores:  
 Pred. No.: 4.15e-88 Length: 456  
 Score: 834.00 Matches: 147  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 34.21% Indels: 0  
 DB: 9 Gaps: 0

US-09-719-601-5 (1-444) x US-09-604-287A-313 (1-456)

Qy 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223  
 Db 3 CACTTAAAGGGTCCCTCTGCAACTGGTGGATCATCGCCACTTCCAGCACCACCCCAAG 62  
 Qy 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
 Db 63 CCTAACATCTTCCACAGGATCCCGATGGAATGCTGCAGTGTGTTCTTGGGCGAA 122  
 Qy 244 TrpGlnProIleGluTyGlyLysLysLysLeuLysTyLeuProTyrAsnHisGlnHis 263  
 Db 123 TGGCAGCCCATCAGTACGCGCAAGAGAGCTGAAATACCTGCCCTTACATCACCAGCAC 182  
 Qy 264 GluTyPhePheLeuIleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIle 283  
 Db 183 GAATACCTCTCTGATTTGGCGCGCTCTCATCCCATGATTTTCCAGTACCATGATC 242  
 Qy 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTy 303  
 Db 243 ATCATGACCATGATCGTCCATAAGAACTGGTGGACCTGGCTGGCGCTGAGTACTAC 302  
 Qy 304 IleArgPhePheIleThrTyIleProPheTyGlyIleLeuGlyAlaLeuLeuPheLeu 323  
 Db 303 ATCCGGTTCATCATCACCTACATCCCTTTCTACGGCATCTGGAGCCCTCTTTTCCATC 362  
 Qy 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343  
 Db 363 AACTTCATCAGTTCCTGGAGAGCCACTGTTTGTGTGGTCCACACAGATGATCATCATC 422  
 Qy 344 ValMetGluIleAspGlnGlu 350  
 Db 423 GTCATGGAGATTGACCCAGGAG 443

RESULT 24  
 US-09-339-338-313  
 Sequence 313, Application US/09339338A  
 Patent No. US20020102602A1  
 GENERAL INFORMATION:  
 APPLICANT: Yugu, Jiang  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Xu, Jiangchun  
 TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
 TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
 FILE REFERENCE: 210121.470C2  
 CURRENT APPLICATION NUMBER: US/09/339,338A  
 CURRENT FILING DATE: 1999-06-23  
 NUMBER OF SEQ ID NOS: 315  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 313  
 LENGTH: 456  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-339-338-313

```
Alignment Scores:
Pred. No.: 4.15e-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 10 Gaps: 0

US-09-719-601-5 (1-444) x US-09-339-338-313 (1-456)
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAGGGTGCTCTGCCAATCGGTGGATCATCGCACTTCCAGCACCGCCAAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGCAGTGTGTCTGGGGGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 123 TGGAGCCCATCGATCGGCAAGAGCTGAATACCTGCCCTTACCAATCACCAGCAC 182
QY 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACCTTCTCTGATTTGGCGCGCGCTGCTATCCCATGATATTTCCAGTACCAGATC 242
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303
Db 243 ATCATGACCATGATCGTCCATAAGAACTGGGGGACCTGGGCGCTGAGCTACTAC 302
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACCTTCATCAGTCTCTGGAGAGCCACTGGTTGTGGGTCCACAGATGAATCACATC 422
QY 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGGAGATTGACCAGGAG 443

RESULT 26
US-10-124-805-313
; Sequence 313, Application US/10124805
; Publication No. US2003016022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; NUMBER OF SEQ ID NOS: 627
; CURRENT FILING DATE: 2002-04-15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-313

Alignment Scores:
Pred. No.: 4.15e-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 13 Gaps: 0

US-09-719-601-5 (1-444) x US-10-124-805-313 (1-456)
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAGGGTGCTCTGCCAATCGGTGGATCATCGCACTTCCAGCACCGCCAAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGCAGTGTGTCTGGGGGAA 122

Alignment Scores:
Pred. No.: 4.15e-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 11 Gaps: 0

US-09-551-621-313
QY 204 HisLeuLysGlyAlaSerAlaAsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLys 223
Db 3 CACTTAAGGGTGCTCTGCCAATCGGTGGATCATCGCACTTCCAGCACCGCCAAAG 62
QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243
Db 63 CCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGCAGTGTGTCTGGGGGAA 122
QY 244 TrpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263
Db 123 TGGAGCCCATCGATCGGCAAGAGCTGAATACCTGCCCTTACCAATCACCAGCAC 182
QY 264 GluTyrPhePheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283
Db 183 GAATACCTTCTCTGATTTGGCGCGCGCTGCTATCCCATGATATTTCCAGTACCAGATC 242
QY 284 IleMetThrMetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyr 303
Db 243 ATCATGACCATGATCGTCCATAAGAACTGGGGGACCTGGGCGCTGAGCTACTAC 302
QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeu 323
Db 303 ATCCGGTTCTTCATCACCTACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrpPheValTrpValThrGlnMetAsnHisIle 343
Db 363 AACCTTCATCAGTCTCTGGAGAGCCACTGGTTGTGGGTCCACAGATGAATCACATC 422
QY 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGGAGATTGACCAGGAG 443

RESULT 25
US-09-551-621-313
; Sequence 313, Application US/09551621
; Publication No. US20030104366A1
; GENERAL INFORMATION:
; APPLICANT: Yuqi, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621
; NUMBER OF SEQ ID NOS: 479
; CURRENT FILING DATE: 2000-04-17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-621-313

Alignment Scores:
Pred. No.: 4.15e-88 Length: 456
Score: 834.00 Matches: 147
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.21% Indels: 0
DB: 11 Gaps: 0
```

QY 244 TtpGlnProIleGluTyrGlyLysLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263  
 DB 123 TGGCAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAATCACCAGCAC 182  
 QY 264 GluTyrPhePheLeuLeuGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
 DB 183 GAATACCTTCTTCCTGATTGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242  
 QY 284 IleMetThrMetIleValHisLysAsnTtpValAspLeuAlaTtpAlaValSerTyrTyr 303  
 DB 243 ATCATGACCATGATCGTCCATAGAACTGGGTGGAGCTGGCGCTGAGCTACTAC 302  
 QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeuLeuPheLeu 323  
 DB 303 ATCCGGTTCTTCATCACCTACATCCCTTTCTAGCGCATCTGGAGCCCTCCTTTTCCTC 362  
 QY 324 AsnPheIleArgPheLeuGluSerHisTtpPheValTtpValThrGlnMetAsnHisIle 343  
 DB 363 AACTTCATCAGGTTCTCGAGAGCCACTGGTTTGTGGGTCCACAGATGATCATCATC 422  
 QY 344 ValMetGluIleAspGlnGlu 350  
 DB 423 GTCATGGAGATTGACCAGGAG 443

## RESULT 27

US-10-007-805-313

; Sequence 313, Application US/10007805  
 ; Publication No. US20020150581A1

## GENERAL INFORMATION:

; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Durham, Margarita  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.470C10  
 ; CURRENT APPLICATION NUMBER: US/10/007,805  
 ; CURRENT FILING DATE: 2001-12-07  
 ; NUMBER OF SEQ ID NOS: 593  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 313  
 ; LENGTH: 456  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-10-007-805-313

## Alignment Scores:

Pred. No.: 4,15e-88 Length: 456  
 Score: 834.00 Matches: 147  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 34.21% Indels: 0  
 DB: 14 Gaps: 0

US-09-719-601-5 (1-444) x US-10-007-805-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTtpTtpAsnHisArgHisPheGlnHisAlaLys 223  
 DB 3 CACTTAAAGGGTGCCTCTGCAACTGGTGAATCATCGGCACATCCAGCACCAGCAAG 62  
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
 DB 63 CCTAACATCTTCACAGAGATCCGATGTGAACATCTGCACGTGTGTCTTGGGCGAA 122  
 QY 244 TtpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263

DB 123 TGGCAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAATCACCAGCAC 182  
 QY 264 GluTyrPhePheLeuLeuGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
 DB 183 GAATACCTTCTTCCTGATTGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242  
 QY 284 IleMetThrMetIleValHisLysAsnTtpValAspLeuAlaTtpAlaValSerTyrTyr 303  
 DB 243 ATCATGACCATGATCGTCCATAGAACTGGGTGGAGCTGGCGCTGAGCTACTAC 302  
 QY 304 IleArgPhePheIleThrTyrIleProPheTyrGlyLeuGlyAlaLeuLeuPheLeu 323  
 DB 303 ATCCGGTTCTTCATCACCTACATCCCTTTCTAGCGCATCTGGAGCCCTCCTTTTCCTC 362  
 QY 324 AsnPheIleArgPheLeuGluSerHisTtpPheValTtpValThrGlnMetAsnHisIle 343  
 DB 363 AACTTCATCAGGTTCTCGAGAGCCACTGGTTTGTGGGTCCACAGATGATCATCATC 422  
 QY 344 ValMetGluIleAspGlnGlu 350  
 DB 423 GTCATGGAGATTGACCAGGAG 443

## RESULT 28

US-10-076-622-313

; Sequence 313, Application US/10076622

; Publication No. US20030023036A1

## GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.  
 ; APPLICANT: Sleath, Paul R.  
 ; APPLICANT: Persing, David H.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.470C11  
 ; CURRENT APPLICATION NUMBER: US/10/076,622  
 ; CURRENT FILING DATE: 2002-02-13  
 ; NUMBER OF SEQ ID NOS: 627  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 313  
 ; LENGTH: 456  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-10-076-622-313

## Alignment Scores:

Pred. No.: 4,15e-88 Length: 456  
 Score: 834.00 Matches: 147  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 34.21% Indels: 0  
 DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-076-622-313 (1-456)

QY 204 HisLeuLysGlyAlaSerAlaAsnTtpTtpAsnHisArgHisPheGlnHisAlaLys 223  
 DB 3 CACTTAAAGGGTGCCTCTGCAACTGGTGAATCATCGGCACATCCAGCACCAGCAAG 62  
 QY 224 ProAsnIlePheHisLysAspProAspValAsnMetLeuHisValPheValLeuGlyGlu 243  
 DB 63 CCTAACATCTTCACAGAGATCCGATGTGAACATCTGCACGTGTGTCTTGGGCGAA 122  
 QY 244 TtpGlnProIleGluTyrGlyLysLysLeuLysTyrLeuProTyrAsnHisGlnHis 263  
 DB 123 TGGCAGCCCATCGAGTACGGCAAGAGCTGAATACCTGCCCTCAATCACCAGCAC 182  
 QY 264 GluTyrPhePheLeuLeuGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIle 283  
 DB 183 GAATACCTTCTTCCTGATTGGCGCGCTGCTCATCCCATGTATTTCCAGTACCAGATC 242  
 QY 284 IleMetThrMetIleValHisLysAsnTtpValAspLeuAlaTtpAlaValSerTyrTyr 303  
 DB 243 ATCATGACCATGATCTTCATAGAACTGGGTGGAGCTGGCGCTGAGCTACTAC 302

```
QY 304 ileArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeu 323
Db 303 ATCCGTTCTTTCATCACCTACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTTTCCTC 362
QY 324 AsnPheIleArgPheLeuGluSerHisTrrPheValTrrPheValThrGlnMetAsnHisIle 343
Db 363 AACCTTCATCAGGTTCCTCGAGAGCCACTGGTTTGTGTGGTGCACACAGATGAATCATC 422
QY 344 ValMetGluIleAspGlnGlu 350
Db 423 GTCATGGAGATTGACCAGAG 443

RESULT 29
US-09-918-995-29095
; Sequence 29095, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29095
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(453)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29095

Alignment Scores:
Pred. No.: 5,698-73 Length: 453
Score: 705.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.92% Indels: 0
DB: 11 Gaps: 0

US-09-719-601-5 (1-444) x US-09-918-995-29095 (1-453)
QY 98 GluProSerGlnAspHisGlyIleSerHisTrrPheValThrGluAspPheArgAlaLeuArg 117
Db 73 GAGCCAGCCAGGACACGCGAAGAACTCAAGATCACTGAGGACTTCGCGGCCCTGAGG 132
QY 118 LysThrAlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeu 137
Db 133 AAGCGCTGAGGACATGAACCTGTTCAAGACCAACACGCTGTTCTTCTCTCTCTG 192
QY 138 AlaHisIleIleAlaLeuGluSerIleAlaTrrPheThrValPheTyrPheGlyAsnGly 157
Db 193 GCCACATCATCGCCCTGGAGAGCATTGCATGTTTCACTGCTTTTACATTGGCAATGC 252
QY 158 TrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrr 177
Db 253 TGGATTCTACCTCATACGCGCTTGTCTTGTGTACTCTCTGAGCCCAAGCTGGATGG 312
QY 178 LeuGlnHisAspTyrGlyHisLeuSerValTrrArgLysProLysTrrPheAsnHisLeuVal 197
Db 313 CTGCACATGATTATGGCCACTGTCTGTCTACAGAAAACCAAGTGGAAACCACTTGTG 372
QY 198 HisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrrPheAsnHisArgHis 217
Db 373 CACAAATTCGTATTGGCCACTTAAAGGTGCTCTGCAACTGCTGGATCAATCGCCAC 432
QY 218 PheGlnHisHisAlaLysPro 224
```

```
Db 433 TTCCAGCACCACGCCAAGCCT 453

RESULT 30
US-10-191-513A-36
; Sequence 36, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-36

Alignment Scores:
Pred. No.: 5,798-63 Length: 473
Score: 620.00 Matches: 108
Percent Similarity: 81.17% Conservative: 17
Best Local Similarity: 70.13% Mismatches: 29
Query Match: 25.43% Indels: 0
DB: 15 Gaps: 0

US-09-719-601-5 (1-444) x US-10-191-513A-36 (1-473)
QY 291 LysAsnTrrValAspLeuAlaTrrPheValSerTrrTyrIleArgPhePheIleThrTrr 310
Db 9 AAGAGTGGGTGACCTTGGCCTGGATGATTACCTTCTAGTCGGCTTCTCTCACTTAT 68
QY 311 IleProPheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeuGlu 330
Db 69 GTCCCACTATTGGGCTGAAAGCCTTCCTGGGCCCTTTCTTCATAGTCAGGTTCTGGAA 128
QY 331 SerHisTrrPheValTrrPheValThrGlnMetAsnHisIleValMetGluIleAspGlnGlu 350
Db 129 AGCAACTGTTGTGTGGGTGACACAGATGAACCATATTCCCATGTCACATTGATGAC 188
QY 351 AlaTyrArgAspTrrPheSerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhe 370
Db 189 CGGAACATGAGTCTGGGTTTCCACCCAGCTCTCTGGCCACATGCAATGTCACCAAGTCTGC 248
QY 371 PheAsnAspTrrPheSerGlyHisLeuAsnPheGlnIleGluHisLeuPheProThr 390
Db 249 TTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTGAGCACCATCTTTTCCCAG 308
QY 391 MetProArgHisAsnLeuHisLysIleAlaProLeuValLysSerLeuCysAlaLysHis 410
Db 309 ATGCTTCGACACATATTACCAAGAGGCTCCCTGGTGGAGTCTCTTGTGTCCCAAGCT 368
QY 411 GlyIleGlyTrrGlnGlyLysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeu 430
Db 369 GGCATAGAGTACCAAGTCCCAAGCCCTCTGCTGTGTCAGCTTCGCGGACATCATCCACTCA 428
QY 431 LysLysSerGlyLysLeuTrrPheAspAlaTrrLeuHisLys 444
Db 429 AAGGATGACGGGCTCTGCTGTAGTGCCTATCTTACCAA 470
```

```

RESULT 31
US-10-191-513A-4
; Sequence 4, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-4
Alignment Scores:
Pred. No.: 3,63e-59 Length: 304
Score: 585.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.00% Indels: 0
DB: 15 Gaps: 0
US-09-719-601-5 (1-444) x US-10-191-513A-4 (1-304)
QY 151 ValPheTyrPheGlyAsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThr 170
Db 1 GTCTTTTACTTTGGCAATGGCTGGATTCTTACCTCATCAGCGCTTTGTCTTGCTACC 60
QY 171 SerGlnAlaGlnAlaGlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLys 190
Db 61 TCTCAGGCCCAAGCTGGATGGCTGCMACATGATTATGGCCACCTCTGTCTCAGAGAAA 120
QY 191 ProGlyTrpAsnHisLeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAla 210
Db 121 CCCAAGTGAACACACCTTGTCCACAAATTCGTCAITGGCCACTTAAAGGGTGCCTCTGCC 180
QY 211 AsnTrpTrpAsnHisArgHisPheGlnHisHisAlaLysProAsnIlePheHisLysAsp 230
Db 181 AACTGTGTGNATCATCGCCACTTCCAGCACCAAGCCCAACATCTTCCACAGGAT 240
QY 231 ProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGluTyrGly 250
Db 241 CCCGATGTGAACATGTCACGTGTTTGTCTGGGCGAATGCAGCCCATCGAGTAGCGGC 300
QY 251 Lys 251
Db 301 AAG 303
RESULT 32
US-10-191-513A-37
; Sequence 37, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-37
Alignment Scores:
Pred. No.: 1.16e-56 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 15 Gaps: 0
US-09-719-601-5 (1-444) x US-10-191-513A-37 (1-449)
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTACGTCCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGG 68
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisIleTrpPheValTyrValThrGlnMet 340
Db 69 GCCTTTTCTTCATA-GTCAGGTTCCTGGAAAGCAACTGGTTTGTGTGGGTGACACAGATG 127
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 128 AACCATATATCCCATGTGCACATTCATGATGACCGGAACATGAGCTGGTTCACCCAGCTC 187
QY 361 ThrAlaThrCysAsnValGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 188 CAGGCCACATGCAATGTCCACAGTCTGCCTTCATGACTGGTTTCATGTCGACACCTCAAC 247
QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db 248 TTCCAGATGTAGACCACTCTTTTCCCATGATGCTCGACACAAATTACCAAGTGGCT 307
QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCCTGGTGCAGTCTCTGTGTGCCAAGCATGCGATAGATACCAAGTCCAGCCCTGCTG 367
QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
Db 368 TCAGCCTTTCGGCGACATCATCTCACTAAAGGAGTCAGGGCAGCTCTGGCTAGATGCC 427
QY 441 TyrLeuHisLys 444
Db 428 TATCTTACCAA 439
RESULT 33
US-10-191-513A-3
; Sequence 3, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: k = g or t/u at position 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37
Alignment Scores:
Pred. No.: 1.16e-56 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 15 Gaps: 0
US-09-719-601-5 (1-444) x US-10-191-513A-37 (1-449)
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTACGTCCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGG 68
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisIleTrpPheValTyrValThrGlnMet 340
Db 69 GCCTTTTCTTCATA-GTCAGGTTCCTGGAAAGCAACTGGTTTGTGTGGGTGACACAGATG 127
QY 341 AsnHisIleValMetGluIleAspGlnGluAlaTyrArgAspTrpPheSerSerGlnLeu 360
Db 128 AACCATATATCCCATGTGCACATTCATGATGACCGGAACATGAGCTGGTTCACCCAGCTC 187
QY 361 ThrAlaThrCysAsnValGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsn 380
Db 188 CAGGCCACATGCAATGTCCACAGTCTGCCTTCATGACTGGTTTCATGTCGACACCTCAAC 247
QY 381 PheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeuHisLysIleAla 400
Db 248 TTCCAGATGTAGACCACTCTTTTCCCATGATGCTCGACACAAATTACCAAGTGGCT 307
QY 401 ProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeu 420
Db 308 CCCCTGGTGCAGTCTCTGTGTGCCAAGCATGCGATAGATACCAAGTCCAGCCCTGCTG 367
QY 421 ArgAlaLeuLeuAspIleIleArgSerLeuLysSerGlyLysLeuTrpLeuAspAla 440
Db 368 TCAGCCTTTCGGCGACATCATCTCACTAAAGGAGTCAGGGCAGCTCTGGCTAGATGCC 427
QY 441 TyrLeuHisLys 444
Db 428 TATCTTACCAA 439
RESULT 33
US-10-191-513A-3
; Sequence 3, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: k = g or t/u at position 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37
Alignment Scores:
Pred. No.: 1.16e-56 Length: 449
Score: 566.00 Matches: 102
Percent Similarity: 83.33% Conservative: 18
Best Local Similarity: 70.83% Mismatches: 24
Query Match: 23.22% Indels: 1
DB: 15 Gaps: 0
US-09-719-601-5 (1-444) x US-10-191-513A-37 (1-449)
QY 301 SerTyrTyrIleArgPhePheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeu 320
Db 9 ACCTTCTACGTCCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGG 68
QY 321 LeuPheLeuAsnPheIleArgPheLeuGluSerHisIleTrpPheValTyrValThrGlnMet 340
Db 69 GCCTTTTCTTCATA-GTCAGGTTCCTGGAAAGCAACTGGTTTGTGTGGGTGACACAGATG 1
```





; CURRENT APPLICATION NUMBER: US/09/967,477B  
 ; CURRENT FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: 60/236,303  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: 60/297,562  
 ; PRIOR FILING DATE: 2001-06-12  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1380  
 ; TYPE: DNA  
 ; ORGANISM: Thraustochytrium sp.  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1380)  
 US-09-967-477B-7

| Alignment Scores:      |        | Pred. No.:    | 9e-48 | Length: | 1380 |
|------------------------|--------|---------------|-------|---------|------|
| Score:                 | 497.00 | Matches:      | 132   |         |      |
| Percent Similarity:    | 44.23% | Conservative: | 79    |         |      |
| Best Local Similarity: | 27.67% | Mismatches:   | 176   |         |      |
| Query Match:           | 20.39% | Indels:       | 90    |         |      |
| DB:                    | 10     | Gaps:         | 16    |         |      |

US-09-719-601-5 (1-444) x US-09-967-477B-7 (1-1380)

```

QY   22 SerTrpGlucluleglnlyHisAsnLeuArgThrAspSerSerglyLeuValileAspArg 41
Db   37 AGCTGAAGAGATCCGGACCGCAGCGGCCCGCGCGGTGGTATTCGTTCAATCCACCAC 96
QY   42 LysValTyzAsnlelThrystrpserilleGlnHisProGlyGlyGlnArgVaillegly 61
Db   97 AAGGTCTACGACATCTCCAAGTGGAC---TCGCACCGGGTGCGTCC---GTATGCTC 150
QY   62 HistyAlaclyGluaspalathraspalapheArgAlaphexisProasPleuGluPhe 81
Db   151 ACAGAGCGCGCGAGACGCCAGCGACGCTTCGCGGTTCCTCACCCGCTCTCGCGCGCTC 210
QY   82 ValglyLysPheLeuLysProLeuLeuIleGlyGluLeu----- 94
Db   211 -----AAGCTGCTCGAGCATGTACTCGTCGGCGAGTGGAGAAACCTCCAGGCGGAG 264
QY   95 AlaProgluGluproSerglnasp-----HisGlyLysAsnSerlylleThrGlu--- 111
Db   265 ATCAGGGGAGCGCGCGAGCAGGAGCGCGCGCGCGCGCGCGCATCAACGAGGTC 324
QY   112 -----AspPheArgAlaleuarglystrAlagiuAspMetAsnLephelysThrAsn 129
Db   325 ATCGCGTCCTACGTCGTCTGCGGCTCAAGGTCAAGGCGATGGGCTCTACGACGCCAGC 384
QY   130 HisValphePheLeuLeuLeuAlaHisIlelleAlaLeuGluSerilleAlatrPhe 149
Db   385 GCCTCTACTACGCGTGGAGCTGTGAGACAGTTCGCGATCGCGGTGCTCTCGATGGCG 444
QY   150 ThrValpheTyrrPheglyAsnGlyTrilleProthrLeullelThralapheValleAla 169
Db   445 ATCTGCTTCTCTTC--AACAGTTTCGCATGTATGTTCCGCGCGGTGATTATGGG 501
QY   170 ThrSerClualaclnlaglyTrpleughInHisAsptyrGlyHisLeuSerValtyrArg 189
Db   502 CTCTTCTACAGAGTCCCGATGGTGGCGCAGACTCTTCGCAACACCGAGTGTGGAG 561
QY   190 LysProLystrpAsnHisLeuValHisLysPheValileglyHisLeuLysGlyAlaser 209
Db   562 AACCGCAGCTCGCAACCTTATCGGCTCGCTCGTGGCAACCGCTCGCGGCTTTCAGC 621
QY   210 AlaasnTrpTrpAsnhisPhelGlnHisHisAlalyProasNille----- 226
Db   622 GTGACGTGGTGAAGAACAAGACAACTTCGACACCGCGGTGCCGAACTTCACAGCGCC 681
QY   227 -----PheHisLysAspProAspValAsnMetLeuHisValpheValleugly 242
  
```

Alignment Scores:  
 Pred. No.: 1,15e-46 Length: 1362  
 Score: 487.50 Matches: 133  
 Percent Similarity: 47.27% Conservatives: 92  
 Best Local Similarity: 27.94% Mismatches: 164  
 Query Match: 20.00% Indels: 87  
 DB: 13 Gaps: 19

US-09-719-601-5 (1-444) x US-09-769-863-13 (1-1362)

QY 7 GlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluLe 26  
 DB 7 CAGGGCAAAAGGCGGAGAG-----ATCTCGTGGCGGACCATC 45

QY 27 GlnLysHisAsnLeuLeuThrAspSerGlyLeuValIleAspArgLysValTyAsnIle 46  
 DB 46 CGTGAGCAACACCGCAAGACACCGGTGGATCGTATCCACCAAGAGGTGTACGACATC 105

QY 47 ThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGlu 66  
 DB 106 TCGGCGTTTGAG--GACCACCGCGGGCGGCTC---GTCATGTTTCACGCGCGCGGCGAA 159

QY 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86  
 DB 160 GACGCGACCGATGGTTCGCTCTTCACCGAGCTCGGCGTC-----AGCTCCTC 213

QY 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101  
 DB 214 GACGAGTACTACGTGGCGGACGTGACCGAGTCGACGGCGCGTGCACACGTCGATCTCG 273

QY 102 AsHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuArgLysThr 119  
 DB 274 GACGAGGTCAAGAGAGCGATCGGACTTCATCGCTGCTACCGCAAGCTCGCGCTTGAA 333

QY 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139  
 DB 334 GTCAAGCCCTCGGCTTTAGACTCGAGCAAGCTACTACTCTCAAGTGGCGCTCG 393

QY 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrpIle 159  
 DB 394 ACCTGAGCATGGCTGTGTGGCGGCCATTGGCTCCACTTT---GACTCGACGGCC 450

QY 160 ProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179  
 DB 451 ATGTACATGTGGCGGCTGTATCTTGGCTCTTTTACCAGCAGTCGCGCTGGCTGCC 510

QY 180 HisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHisLys 199  
 DB 511 CATGACTTTCGACCAACCAAGTGTAG-----AACCACTTGTGTGGCGAC 558

QY 200 PheVal-----IleGlyHisLeu---LysGlyAlaSerAlaAsnTrpTrpAsnHis 215  
 DB 559 CTCGTGCGGTCATGTCGGCAACCTCTGGCAGGCTTCTCGGTGCACTGTGGAAGAAC 618

QY 216 ArgHisPheGlnHisHisAlaLysProAsnIle-----PheHis 228  
 DB 619 AAGCACACACACGACCATCGCATCCCACTCCACCGCAGCGCGGATCGCTTCCAC 678

QY 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlu 248  
 DB 679 GGCGACCGGACATGACACATGCCGATTCGCG-----TGG-----717

QY 249 TyrglyLysLysLysLeuLysTyLeuProTyAsnHisGlnHisGluTyPhePheLeu 268  
 DB 718 -----TCGCTCAAGATGGCG-----CAGCAGCGGTCGACTCGGCC 753

QY 269 IleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIleMetThrMetIle 288  
 DB 754 GTCGGG-----CTCTTCTTCATCGCTTACCACCGTACTTACTTCTCCATCTTG 804

QY 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyTrpIleArgPhePheIle 308  
 DB 805 CTC-----TTTGGCGGTATCTCGTGGGTGATCCAGTCGGCCATGTACGCGCTTCTAC 855

QY 309 ThrTyIlePro----- 312  
 DB 856 AACGTTGGCGCGGCGCACCTTTGACAAGTCCAGTACCCTGCTCGAGCGCGCGC 915

QY 313 -----PheTyGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeu 329  
 DB 916 CTCCTCTCTACTACGCTGGAACTCGGCTTGTGTAGCGACCAACATGTCGCTGCTC 975

QY 330 GluSerHisTrpPheValTrpValThrGln----- 339  
 DB 976 CAAGCGCTGCTCTCTCTTTGTGAGCCAGCGCTGTCGCGCTCTTCTCTCGCATGTC 1035

QY 340 -----MetAsnHisIleValMetGluIle---AspGlnGluAlaTyArgAspTrpPhe 356  
 DB 1036 TTTAGCGTCGGCACCAACGGCATGGAGTCTTTGACAGGACAGCAAGCCGATTTTGG 1095

QY 357 SerSerGlnLeuLeuAlaThrCysAsnValGluGlnSerPhePheAsnAspTrpPheSer 376  
 DB 1096 AAGCTGCAAGTCTCTCGACGCGCAACGTGACGTGCTGCTGCTGCTGCTGCTGCT 1155

QY 377 GlyHisLeuAsnPheGlnIleGluHisIleLeuPheProThrMetProArgHisAsnLeu 396  
 DB 1156 GCGGCGCTCACTACAGATCGACCACTTGTTCCTGATGTCGTCGCGGCAACCTC 1215

QY 397 HisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyGlnGlu 416  
 DB 1216 CCGGCGCTCAACGTCTGCTCAAGTCTGCTGCAAGCAGTACGACATCCCATACCAG 1275

QY 417 LysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLys 432  
 DB 1276 ACGGGCTTCATCGCGGATGCGCGAGGTGCTGTCGCTGACCTCGAGCGC 1323

RESULT 37  
 US-10-054-534B-13  
 ; Sequence 13, Application US/10054534B  
 ; Publication No. US20030167525A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Mukerji, Pradip  
 ; APPLICANT: Huang, Yung-Sheng  
 ; APPLICANT: Das, Tapas  
 ; APPLICANT: Thurmond, Jennifer M.  
 ; APPLICANT: Pereira, Suzette L.  
 ; TITLE OF INVENTION: DSATURASE GENES AND USES THEREOF  
 ; FILE REFERENCE: 6763.US.P1  
 ; CURRENT APPLICATION NUMBER: US/10/054,534B  
 ; PRIOR FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: US 09/769,863  
 ; PRIOR FILING DATE: 2001-01-25  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 1362  
 ; TYPE: DNA  
 ; ORGANISM: Saprolegnia diclina  
 ; US-10-054-534B-13

Alignment Scores:  
 Pred. No.: 1,15e-46 Length: 1362  
 Score: 487.50 Matches: 133  
 Percent Similarity: 47.27% Conservatives: 92  
 Best Local Similarity: 27.94% Mismatches: 164  
 Query Match: 20.00% Indels: 87  
 DB: 13 Gaps: 19

US-09-719-601-5 (1-444) x US-10-054-534B-13 (1-1362)

QY 7 GlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluLe 26  
 DB 7 CAGGGCAAAAGGCGGAGAG-----ATCTCGTGGCGGACCATC 45

QY 27 GlnLysHisAsnLeuLeuThrAspSerGlyLeuValIleAspArgLysValTyAsnIle 46  
 DB 46 CGTGAGCAACACCGCAAGACACCGGTGGATCGTATCCACCAAGAGGTGTACGACATC 105

QY 47 ThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGlu 66  
 DB 106 TCGGCGTTTGAG--GACCACCGCGGGCGGCTC---GTCATGTTTCACGCGCGCGGCGAA 159

QY 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86  
 DB 160 GACGCGACCGATGGTTCGCTCTTCACCGAGCTCGGCGTC-----AGCTCCTC 213

QY 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101  
 DB 214 GACGAGTACTACGTGGCGGACGTGACCGAGTCGACGGCGCGTGCACACGTCGATCTCG 273

QY 102 AsHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuArgLysThr 119  
 DB 274 GACGAGGTCAAGAGAGCGATCGGACTTCATCGCTGCTACCGCAAGCTCGCGCTTGAA 333

QY 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139  
 DB 334 GTCAAGCCCTCGGCTTTAGACTCGAGCAAGCTACTACTCTCAAGTGGCGCTCG 393

QY 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrpIle 159  
 DB 394 ACCTGAGCATGGCTGTGTGGCGGCCATTGGCTCCACTTT---GACTCGACGGCC 450

QY 160 ProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179  
 DB 451 ATGTACATGTGGCGGCTGTATCTTGGCTCTTTTACCAGCAGTCGCGCTGGCTGCC 510

QY 180 HisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHisLys 199  
 DB 511 CATGACTTTCGACCAACCAAGTGTAG-----AACCACTTGTGTGGCGAC 558

QY 200 PheVal-----IleGlyHisLeu---LysGlyAlaSerAlaAsnTrpTrpAsnHis 215  
 DB 559 CTCGTGCGGTCATGTCGGCAACCTCTGGCAGGCTTCTCGGTGCACTGTGGAAGAAC 618

QY 216 ArgHisPheGlnHisHisAlaLysProAsnIle-----PheHis 228  
 DB 619 AAGCACACACACGACCATCGCATCCCACTCCACCGCAGCGCGGATCGCTTCCAC 678

QY 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlu 248  
 DB 679 GGCGACCGGACATGACACATGCCGATTCGCG-----TGG-----717

QY 249 TyrglyLysLysLysLeuLysTyLeuProTyAsnHisGlnHisGluTyPhePheLeu 268  
 DB 718 -----TCGCTCAAGATGGCG-----CAGCAGCGGTCGACTCGGCC 753

QY 269 IleGlyProProLeuLeuIleProMetTyPheGlnTyGlnIleMetThrMetIle 288  
 DB 754 GTCGGG-----CTCTTCTTCATCGCTTACCACCGTACTTACTTCTCCATCTTG 804

QY 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyTrpIleArgPhePheIle 308  
 DB 805 CTC-----TTTGGCGGTATCTCGTGGGTGATCCAGTCGGCCATGTACGCGCTTCTAC 855

Db 46 CTGAGCAACCGCCAGACACACCGGTGATCGTATCCACCACCAAGGTGTACGACATC 105  
Qy 47 ThrLysTrpSerIleGlnHisProGlyGlnArgValIleGlyHisTyAlaGlyGlu 66  
Db 106 TCGGCTTTTGAG--GACACACCGCGCGCGTC--GTCATGTTCCACGACGCGCGGAA 159  
Qy 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86  
Db 160 GACGCGACCGATCGTTCGCTCTCCACCGGAGCTGGCGTC-----AGCTCTCTC 213  
Qy 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101  
Db 214 GACGAGTACTAGTCGGCGACCTGACACGAGTCGCGCGCGCTCGACACGTCGATCTCG 273  
Qy 102 AspHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuArgLysThr 119  
Db 274 GACGAGTCAAGAGAGCCAGTCGGACITTCATTGCGTCGACCGCAAGCTGGCGCTTGA 333  
Qy 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139  
Db 334 GTCACGCGCTCGGCTTGTACGACTCGAGCAAGCTCTACTACTCTACAAGTGGCGCTCG 393  
Qy 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheTyPheGlyAsnGlyTrpIle 159  
Db 394 ACCTGAGCATTCGCTTGTGCGCGGCATTCCTCCACTTT--GACTCGACGCCC 450  
Qy 160 ProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179  
Db 451 ATGTACATGTCGCGCTCTCATCTCTGCTTGTACGACGAGTGGCTGGCTGGCTGCC 510  
Qy 180 HisAspTyGlyHisLeuSerValTyArgLysProLysTrpAsnHisLeuValHisLys 199  
Db 511 CATGACTTCTGACCAACCAAGTGTGTAG-----AACCACTGTGTGGCGAC 558  
Qy 200 PheVal-----IleGlyHisLeu--LysGlyAlaSerAlaAsnTrpTrpAsnHis 215  
Db 559 CTCGTCGGGCTCATGTCGCAACCTCTGCGAGGCTTCTCGTGCAGTGTGGAAGAAC 618  
Qy 216 ArgHisPheGlnHisAlaLysProAsnIle-----PheHis 228  
Db 619 AAGCAACACGACCATGATGCCAACCTCCACCGGACGCGCGAGATCGCCTTCAC 678  
Qy 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyGluTrpGlnProIleGlu 248  
Db 679 GCGGACCGGACATTCACACGATGCGGATTCGCG-----TGG----- 717  
Qy 249 TyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 268  
Db 718 -----TCGCTCAAGATGGCG-----CAGCACCGGTCGACTCGCCCC 753  
Qy 269 IleGlyProProLeuLeuIleProMetTyPheGlnTyPheGlnIleMetThrMetIle 288  
Db 754 GTCGGG-----CTCTCTTCATGCGCTACCAAGCTACCTGACCTTCCCATCTTG 804  
Qy 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyTyTyIleArgPhePheIle 308  
Db 805 CTC-----TTTGGCGATATCTCGTGGTGATCCAGTCGGCCATGTACGCTCTTAC 855  
Qy 309 ThrTyIlePro----- 312  
Db 856 AACGTTGGGCGCGCGCACCTTTGACAGGTCCAGTACCCTGCTCGAGCGCGCGCG 915  
Qy 313 -----PheTyGlyIleLeuGlyAlaLeuLeuPheLeuAsnPheIleArgPheLeu 329  
Db 916 CTCCTCTCTACTACGCTCGAACCTCGGCTTGTGTACGACCAACATGTGCTGCTC 975  
Qy 330 GluSerHisTrpPheValTrpValThrGln----- 339  
Db 976 CAAGCGGCTCGTTCCTCTTTGTGAGCGAGCGCTCGTGGCGCTCTCTCTCGCGATGTC 1035  
Qy 340 -----MetAsnHisIleValMetGluIle--AspGlnGluAlaTyArgAspTrpPhe 356  
Db 356 ----- 356

Db 1036 TTTAGCGTCCGCCACCAACCGCATGGAGGTCTTTTACAGGACAGCAAGCCGATTTTGG 1095  
Qy 357 SerSerGlnLeuThrAlaThrCysAsnValGluGlnSerPhePheAsnSpTrpPheSer 376  
Db 1096 AAGCTCAAGTGTCTTCGACGCGCACGACGAGTGCCTCTGGATCGACTGGTTCATG 1155  
Qy 377 GlyHisLeuAsnPheGlnIleGluHisHisLeuPheProThrMetProArgHisAsnLeu 396  
Db 1156 GCGGCGCTCAACTACCAGATCGACCACTTGTTCCTGATGGTGGCGGACCACTTC 1215  
Qy 397 HisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyGlnGlu 416  
Db 1216 CCGGCGCTCAAGTGTCTGCAAGTGCCTCTGCAAGCATGACATCCATCCACCGAG 1275  
Qy 417 LysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLys 432  
Db 1276 ACGGCTTTCATCGCGGCATGGCGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323

## RESULT 38

US-10-431-952-13  
; Sequence 13, Application US/10431952  
; Publication No. US2003019073A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Das, Tapas  
; APPLICANT: Thurmond, Jennifer  
; APPLICANT: Pereira, Suzette L.  
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
; FILE REFERENCE: 6763.US.01  
; CURRENT APPLICATION NUMBER: US/10/431,952  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US/09/769,863  
; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1362  
; TYPE: DNA  
; ORGANISM: Saprolegnia dielina  
US-10-431-952-13

## Alignment Scores:

|                        |          |               |      |
|------------------------|----------|---------------|------|
| Pred. No.:             | 1,15e-46 | Length:       | 1362 |
| Score:                 | 487.50   | Matches:      | 133  |
| Percent Similarity:    | 47.27%   | Conservative: | 92   |
| Best Local Similarity: | 27.94%   | Mismatches:   | 164  |
| Query Match:           | 20.00%   | Indels:       | 87   |
| DB:                    | 13       | Gaps:         | 19   |

US-09-719-601-5 (1-444) x US-10-431-952-13 (1-1362)

Qy 7 GlnGlyGluGlyAlaAlaGluArgGluValSerValProThrPheSerTrpGluGluIle 26  
Db 7 CAGGGGCAAAAGCGCGAGAG-----ATCTGTTGGCGGACCATC 45  
Qy 27 GlnLysHisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyAsnIle 46  
Db 46 CGTGACGACCAACCGCCAAAGCAACGCGTGTGATCCACCACCAAGGTGTACGACATC 105  
Qy 47 ThrLysTrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyAlaGlyGlu 66  
Db 106 TCGGCTTTGAG---GACCACCGCGCGCGCTC---GTATGTTACGACGCGCGCGAA 159  
Qy 67 AspAlaThrAspAlaPheArgAlaPheHisProAspLeuGluPheValGlyLysPheLeu 86  
Db 160 GACGCGACCGATGCTTCTGCTGCTTCTCCACCGGAGCTCGGCGCTC-----AAGCTCTCTC 213  
Qy 87 LysProLeuLeuIleGlyGluLeu-----AlaProGluGluProSerGln 101  
Db 214 GACGAGTACTACGTCGGCGACGTCGACCACTGACGCGGCGCGCTGACGCTGATCTCG 273

Qy 102 AspHisGlyLysAsnSerLys-----IleThrGluAspPheArgAlaLeuAlaGlyThr 119  
Db 274 GACGAGGTCAAGAGAGCCAGTCCGACTTCATTGCGTCGTACCGCAAGCTGCGCTTGAA 333  
Qy 120 AlaGluAspMetAsnLeuPheLysThrAsnHisValPhePheLeuLeuLeuAlaHis 139  
Db 334 GTCAGGCGCTCGGCTTGTACGACTGAGCAAGCTCTACTACCTTACAGTCGCGCTCG 393  
Qy 140 IleIleAlaLeuGluSerIleAlaTrpPheThrValPheThrPheGlyAsnGlyTrpIle 159  
Db 394 ACCTGAGCATTCGCTGTTGTCGGCGCCATTTCCTCCACTT---GACTCGAGCGCC 450  
Qy 160 ProThrIleuThrAlaPheValLeuAlaThrSerGlnAlaGlnAlaGlyTrpLeuGln 179  
Db 451 ATGTACATGTCGGCTGTCATCTTCCTGGCTCTTTTACAGCAGTCCGCTCGCTCGC 510  
Qy 180 HisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHisLeuValHisLys 199  
Db 511 CATGACTTTCGCACCAACCAAGTGTGTAG-----AACACTTGTGTGGCGAC 558  
Qy 200 PheVal-----IleGlyHisLeu---LysGlyAlaSerAlaAsnTrpTrpAsnHis 215  
Db 559 CTCGTGCGCTCATGTCGCGCAACCTCTGCGAGGCTTCTCGGTGCAAGTGTGGAAGAAC 618  
Qy 216 ArgHisPheGlnHisHisAlaLysProAsnIle-----PheHis 228  
Db 619 AAGCACAACAGCAGCATGTCGATCCCACTCCAGCGAGCGCCGAGATCGCTTCAC 678  
Qy 229 LysAspProAspValAsnMetLeuHisValPheValLeuGlyLutTrpGlnProIleGlu 248  
Db 679 GCGCAGCGGACATTCACAGATCGCGATTCCTCGC-----TGG----- 717  
Qy 249 TyrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 268  
Db 718 -----TCGCTCAAGATGGG-----CAGCAGCGGTGACTCGGCC 753  
Qy 269 IleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThrMetIle 288  
Db 754 GTCGGG-----CTCTCTCTCATCGCTACCAAGCTGACTGACTTCCATCTTG 804  
Qy 289 ValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhePheIle 308  
Db 805 CTC-----TTTGGCGTATCTCGTGGTGTATCCAGTCGCGCCATGACGCTTCTAC 855  
Qy 309 ThrTyrIlePro-----312  
Db 856 AACGTTGGCGCGCGCGACCTTTGACAAGTCCAGTACCGCTGCTCGAGCGCGCGCGC 915  
Qy 313 -----PheTyrGlyIleLeuGlyAlaLeuLeuPheLeuAsnPhelleArgPheLeu 329  
Db 916 CTCTCTCTTACTACGCTGGAACCTCGCGCTTGTGTACGACCCCAACATGCTGCTCTC 975  
Qy 330 GluSerHisTrpPheValTrpValThrGln-----339  
Db 976 CAACGCGCTCGTCTCTCTTTGTGAGCAGGCGTCTGCGGCTCTTCTCGCATGCTC 1035  
Qy 340 -----MetAsnHisIleValMetGluIle---AspGlnGluAlaTyrArgAspTrpPhe 356  
Db 1036 TTWAGCTCGGCGCACCAACGCGATGAGGTCTTTGACAAGCAGCAGCAAGCCGATTTGG 1095  
Qy 357 SerSerGlnLeuThrAlaThrCysAsnValGlnSerPhePheAsnAspTrpPheSer 376  
Db 1096 AACCTGCAAGTGTCTCGAGCGCACGTCGCTGCTCTGATCATGCTGCTGCTCATG 1155  
Qy 377 GlyHisLeuAsnPhedGlnIleGluHisLysLeuPheProThrMetProArgHisAsnLeu 396  
Db 1156 GCGGCGCTCAACTACCAAGATCGACCACTTGTTCCTGATGTCGCGCGCACCACTC 1215  
Qy 397 HisLysIleAlaProLeuValLysSerLeuCysAlaLysHisGlyIleGluTyrGlnGlu 416  
Db 1216 CCGCGCTCAAGTGTCTGATAGTCTCTGCAAGCATGACATCCATCCATACCACGAG 1275  
Qy 417 LysProLeuLeuArgAlaLeuLeuAspIleIleArgSerLeuLysLys 432

Db 1276 ACGGCTTCATCGCGCGCATGCCGAGTCTGCTGTCACCTCGAGCGC 1323

## RESULT 39

US-10-278-391-3  
; Sequence 3, Application US/10278391  
; Publication No. US20030159164A1  
; GENERAL INFORMATION:  
; APPLICANT: KOPCHIK, JOHN J.  
; KELDER, BRUCE  
; HUANG, YUNG-SHENG  
; KIRCHNER, STEPHEN J.  
; MUKERJI, PRADIP  
; TITLE OF INVENTION: SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM PRODUCTS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/278,391  
; FILING DATE: 23-Oct-2002  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,578  
; FILING DATE: 29-MAY-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-03349  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1374 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-278-391-3

Alignment Scores:  
Pred. No.: 2,58e-43 Length: 1374  
Score: 459.00 Matches: 118  
Percent Similarity: 43.55% Conservative: 88  
Best Local Similarity: 24.95% Mismatches: 183  
Query Match: 18.83% Indels: 84  
Gaps: 14

US-09-719-601-5 (1-444) x US-10-278-391-3 (1-1374)

Qy 17 SerValProThrPheSerTrpGluGluIle-----GlnLys 28  
Db 16 AGTGTGAGGACGTTTACTCGGCGCGAGTTTGAATCCGAGGCTCTGATGAGGCAAG 75  
Qy 29 HisAsnLeuArgThrAspSerGlyLeuValIleAspArgLysValTyrAsnIleThrLys 48  
Db 76 AAGGATCCGAGGACCCCTTCTTGTATGATCATCGACAAAGGTGTACGATGTCGCGAG 135  
Qy 49 TrpSerIleGlnHisProGlyGlyGlnArgValIleGlyHisTyrAlaGlyGluAspAla 68



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Qy 44 TyrAsnIleThrLysTrpSerIleGlnHisProGlyGlyClnArgValIleGlyHisTyr 63
Db 137 TAGATGTTTCGGATTTCGGTGAAGACCATCCAGGTGGCAGCTTCCCTTGAAGAGCTTT 196
Qy 64 AlAGlyGluAspAlaThrAspAlaPheArgAlaPheHisPro----- 77
Db 197 GCTGGTCAAGAGGTAACTGATGATTTGTTGCAATTCATCCCTGCTTACATGGAGAAT 256
Qy 78 --AspLeuGluPheValGlyLysPheLeuLysProLeuLeuLeuLeuLeuAlaPro 96
Db 257 CTTGATAAGTTTTTCACCTGGGTATTATCTTAAAGATTACTCTGTT----- 301
Qy 97 GluGluProSerGlnAspHisGlyLysAsnSerLysIleThrGluAspPheArgAlaLeu 116
Db 302 -----TCGAGGTTCTAAAGATTATAGGAAGCTT 331
Qy 117 ArgLysThrAlaGluAspMetAsnLeuPhe---LysThrAsnHisValPhePheLeuLeu 135
Db 332 GTGTTTGAGTTTCTAAATGGGTTTGTATGACAAAAAGGTCATATTATGTTT---GCA 388
Qy 136 LeuLeuAlaHisIleLeuLeuGluSerIleAlaTrpPheThrValPheTyrPheGly 155
Db 389 ACTTGTGCTTTATAGCAATGCTGTTTCTGATGAGTGTATGGGTTTGTG---TTTTGT 445
Qy 156 AsnGlyTrpIleProThrLeuIleThrAlaPheValLeuAlaThrSerGlnAlaGlnAla 175
Db 446 GAGGGTGTGTTTGTACATTTGTTTCTGGGTGTTGATGGGTTTCTTTGGATTGAGT 505
Qy 176 GlyTrpLeuGlnHisAspTyrGlyHisLeuSerValTyrArgLysProLysTrpAsnHis 195
Db 506 GGTGGATTGGACATGATGCTGGGCATTTATGCTAGTGTCTGATTCAAGGCTTAAATAG 565
Qy 196 LeuValHisLysPheValIleGlyHisLeuLysGlyAlaSerAlaAsnTrpAsnHis 215
Db 566 TTATGGGTATTTTGTGCAAAATGCTCTTCAGGAATAAGTATTGTTGGTGGAAATGG 625
Qy 216 ArgHisPheGlnHisIleAlaLysProAsnIlePheHisLysAspProAspValAsnMet 235
Db 626 AACCATATGCACATCACATGCTGCTGTAATAGGCTTGAATATGACCTGATTTACAATAT 685
Qy 236 LeuHisValPheValLeu-----GlyGluTrpGlnProIleGluTyrGly 250
Db 686 ATACCATCTGTTGTTGCTTCCAAAGTTTTTTGGTTCACTCACCTCTCATTTCTATGAG 745
Qy 251 LysLys-----LysLeuLysTyrLeuProTyrAsnHisGlnHisGluTyrPhe 266
Db 746 AAAAGGTTGACTTTTGACTCTTTTATCAAGATTCTTTGTAAGTTATCAACATTGGACATT 805
Qy 267 PheLeuIleGlyProProLeuLeuIleProMetTyrPheGlnTyrGlnIleIleMetThr 286
Db 806 TACCTTATTATGTGCTGCTGAGCTCAATATGATGTACAA---TCTCTCATATG--- 859
Qy 287 MetIleValHisLysAsnTrpValAspLeuAlaTrpAlaValSerTyrTyrIleArgPhe 306
Db 860 TTGTTGACCAAGAGAAAT-----GTGCTCATCGAGCTCAG--- 895
Qy 307 PheIleThrTyrIleProPheTyrGlyIleLeuGlyAlaLeuPheLeuAsnPheIle 326
Db 896 -----GRACCTTGGGATGCTAGTGTCTCGATTGGTAC 931
Qy 327 ArgPheLeuGluSer-----HisTrp-----PheVal----- 335
Db 932 CGGTCCTGTTGTTCTGTTTTCCTAATATGGGGTGAAGAAATTATGTTTGTATTGCAAGT 991
Qy 336 ---TrpValThrGlnMetAsnHisIleValMetGluIleAsp-----GlnGluAla 351
Db 992 TTATCAGTGACTGGAATGACACAGTTCAGTCTCTCTGACACACTTCTCTCAAGTGT 1051
Qy 352 Tyr-----ArgAspTrpPheSerSerGlnLeuThrAlaThrCysAsn 365
Db 1052 TATGTTGGAAGCCTAAAGGGAATAATGTTTGAGAAAAACACGATGGGACACTTGAC 1111
```

```
Qy 366 ValGluGlnSerPhePheAsnAspTrpPheSerGlyHisLeuAsnPheGlnIleGluHis 385
Db 1112 ATTTCTTTGTCCTCCTTGGATGGATTGGTTTCATGGTGGATTGCAATTCCAATTGAGCAT 1171
Qy 386 HisLeuPheProThrMetProArgHisAsnLeuHisLysIleAlaProLeuValLysSer 405
Db 1172 CATTTGTTTCCCAAGATGCCCTAGATGCAACCTTAGGAAATCTCGCCCTAGTGTGATCGAG 1231
Qy 406 LeuCysAlaLysHisGlyIleGluTyrGlnGluLysProLeuLeuArgAlaLeuLeuAsp 425
Db 1232 TTATGCAAGAAACATAAATTTGCCCTTACAATATATCATCTTTCTCCAAGGCCAATGAAATG 1291
Qy 426 IleIleArgSerLeuLysLysSer 433
Db 1292 ACATCAGACATTGAGAACACA 1315
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Search completed: December 10, 2003, 21:04:18  
Job time : 367 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2003, 12:23:27 ; Search time 7608 Seconds  
(without alignments)  
17120.958 Million cell updates/sec

Title: US-09-719-601-11

Perfect score: 3184

Sequence: 1 ccccgagcgaggcgagag.....aggaaattttaaaaaaaaaa 3184

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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38: em\_sy.\*  
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40: em\_hgo\_mus.\*  
41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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| 24         | 1830.4 | 57.5        | 1843   | 6     | BD082654 Methods a |
| 25         | 1830.4 | 57.5        | 1843   | 6     | BD082933 Methods a |
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# ALIGNMENTS

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DEFINITION Homo sapiens fatty acid desaturase 2 (FADS2) mRNA, complete cds.  
ACCESSION AF084559  
VERSION AF084559.1  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 3149)  
AUTHORS Marquardt A., Stohr H., White K. and Weber B.H.  
TITLE cDNA cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family



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JOURNAL      Genomics 66 (2), 175-183 (2000).
MEDLINE      20318619
PUBMED       10860662
REFERENCE    2 (bases 1 to 3149)
AUTHORS      Marquardt A., Stoeckl H., Passmore, L.A., Kraemer, P., Rivera, A. and
              Weber, B.H.F.
TITLE        Direct Submission
JOURNAL      Submitted (05-AUG-1998) Institute of Human Genetics, University of
              Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany
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1410 GGCATTGAATACCGAGAGAGCGGCTACTGAGGGCCCTGCTGGACATCATCAGGTTCCCTG 1469
1381 GGCATTGAATACCGAGAGAGCGGCTACTGAGGGCCCTGCTGGACATCATCAGGTTCCCTG 1440
1470 AAGAAAGTCTGGAGAGCTGTGGCTGAGCGCTTACATTCACAAATGAAGCAGAGCCCGG 1529
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| Qy | 1710 | CTGCCCTCCCTCAGCCGTCAGCCATCAGCCATGGCCCTCCACAGTGCTCTTAGCCCTTTC  | 1769 |
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| Qy | 1830 | CTAAAGATGGGAGAGACCAACGGGTGCATAGGHTTGGCCCTGTGAGTCTCCCTTTGCAGCC | 1889 |
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| Db | 1861 | TGGTCACTAGGCATCACCCCGCTTTTGGTCTTTCAGATGCTCTGTGGGGTTCATAGGGCA  | 1920 |
| Qy | 1950 | GGTCTTAGTGGGACAGGCGCCCTGACCCCTCCGGCCCTGGGTTCACCTCCCTGACGGCTG  | 2009 |
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| Qy | 2010 | CCATTGGTCCACCCCTTTCATAGAGAGCCTGCTTTGTTTACAAAGCTCGGGTCTCCCTTCT | 2069 |
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| LOCUS      |  |   | PAT 18-SEP-2002   |
| DEFINITION |  |   | Primer for synthesizing full-length cDNA and use thereof. |
| ACCESSION  | BD127375   |   |   |
| VERSION    | BD127375.1   | GI:32222320   |   |
| KEYWORDS   | JP 2002017375-A/2806   |   |   |
| SOURCE     | Homo sapiens (human)   |   |   |
| ORGANISM   | Homo sapiens   |   |   |
| REFERENCE  |  |   |   |
| AUTHORS    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 3083) |   |   |
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| JOURNAL    | Primer for synthesizing full-length cDNA and use thereof   |   |   |
| COMMENT    |  |   |   |
|            | Patent: JP 2002017375-A 2806 22-JAN-2002;  |   |   |
|            | HELEX RESEARCH INSTITUTE   |   |   |
|            | OS Homo sapiens (human)  |   |   |
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|            | PD 22-JAN-2002   |   |   |
|            | PF 07-JUL-2000 JP 2000253172   |   |   |
|            | PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO   |   |   |
|            | PI ISHII,  |   |   |
|            | PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI  |   |   |
|            | SHINICHI KOJIMA,   |   |   |
|            | PI TETSUO OTSUKI, HISASHI KOGA   |   |   |
|            | PC   |   |   |
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|            | PC CL2P21/02, C12Q1/68/CL2P21/08, G06F17/30, C12N15/00, C12N5/00 CC  |   |   |
|            | Primer for synthesizing full-length cDNA and use thereof   |   |   |
|            | PH Key   |   |   |
|            | Location/Qualifiers  |   |   |
|            | (91) . (1422).   |   |   |
| FT         | CDS  |   |   |

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| Matches 3078; Conservative | 0;     | Mismatches 5; Indels 1; Gaps 1;                                   |
| Qy                         | 90     | GCACACACCGCGCTGGGAGGACGCGTCTGTGCAGCAGCAGCCGGCGCGGGGAGCGCGCA 149   |
| Db                         | 1      | GCACACACCGCGCTGGGAGGACGCGTCTGTGCAGCAGCAGCCGGCGCGGGGAGCGCGCA 60    |
| Qy                         | 150    | GTGCACGGGCGGTACACAGTCGGCAGCAGCATGGGGAAGGAGGAGGACCCAGGGCGAGGG 209  |
| Db                         | 61     | GTGCACGGGCGGTACACAGTCGGCAGGAGCATGGGGAAGGAGGAGGACCCAGGGCGAGGG 120  |
| Qy                         | 210    | GCGCCGAGCGCGAGGAGTGTGGTGTGCCACCTTCAGCTGGGAGGAGATTCAGAAGCATAAC 269 |
| Db                         | 121    | GCGCCGAGCGCGAGGAGTGTGGTGTGCCACCTTCAGCTGGGAGGAGATTCAGAAGCATAAC 180 |
| Qy                         | 270    | CTGGCACCCACAGTCGGGCGTGTATTCAGCCGCGAAGCTTTACACATCACCAATGTGTC 329   |
| Db                         | 181    | CTGGCACCCACAGTCGGGCGTGTATTCAGCCGCGAAGCTTTACACATCACCAATGTGTC 240   |
| Qy                         | 330    | ATCCAGCACCCGGGGGCCAGCGGGTCATCGGCACCTACGCTGGAGAAGATGCAACCGGAT 389  |
| Db                         | 241    | ATCCAGCACCCGGGGGCCAGCGGGTCATCGGCACCTACGCTGGAGAAGATGCAACCGGAT 300  |
| Qy                         | 390    | GCCTTCGCGCCCTTCCACCCCTGCACTCGAATTCGTGGGCAAGTCTTTGAACCCCTGCTG 449  |
| Db                         | 301    | GCCTTCGCGCCCTTCCACCCCTGCACTCGAATTCGTGGGCAAGTCTTTGAACCCCTGCTG 360  |
| Qy                         | 450    | ATTGGTGAATGGCCCCGGAGGACCCAGCGCAGGACCAACGCAAGAACTCAAGATCACT 509    |
| Db                         | 361    | ATTGGTGAATGGCCCCGGAGGACCCAGCGCAGGACCAACGCAAGAACTCAAGATCACT 420    |
| Qy                         | 510    | GAGGACTTCGGGGCCCTGAGGAAGACCGCTGAGGACATGAACCTGTTTCAAGACCAACAC 569  |
| Db                         | 421    | GAGGACTTCGGGGCCCTGAGGAAGACCGCTGAGGACATGAACCTGTTTCAAGACCAACAC 480  |
| Qy                         | 570    | GTGTTCTTCCTCTCTCTGGCCCCACATCATATCGCCCTGGAGAGCATGATGTTCACT 629     |
| Db                         | 481    | GTGTTCTTCCTCTCTCTGGCCCCACATCATATCGCCCTGGAGAGCATGATGTTCACT 540     |
| Qy                         | 630    | GTCTTCTACTTTGGCAATGGCTGGATTCCTTACCCCTCATCGGCGCTTTGCTTGTCTACC 689  |
| Db                         | 541    | GTCTTCTACTTTGGCAATGGCTGGATTCCTTACCCCTCATCGGCGCTTTGCTTGTCTACC 600  |
| Qy                         | 690    | TCTCAGGCCCAAGCTGGATGCTGCAACATGATTTATGGCCACCTGTCTGTCTACAGAAA 749   |
| Db                         | 601    | TCTCAGGCCCAAGCTGGATGCTGCAACATGATTTATGGCCACCTGTCTGTCTACAGAAA 660   |
| Qy                         | 750    | CCCAAGTGGAAACCACTTGTCCACAAATTCGTCAATGGCCACTTTAAAGGGTGCTCTGCC 809  |
| Db                         | 661    | CCCAAGTGGAAACCACTTGTCCACAAATTCGTCAATGGCCACTTTAAAGGGTGCTCTGCC 720  |
| Qy                         | 810    | AACCTGTGGAAATCATCGGCATTCGAGCACACCGCAAGCCCTAACATCTTCCACAAGAT 869   |
| Db                         | 721    | AACCTGTGGAAATCATCGGCATTCGAGCACACCGCAAGCCCTAACATCTTCCACAAGAT 780   |
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| Db                         | 781    | CCCGATGTGAACATGCTGCAGTGTGTTGTTCTGGGCGAATGGCAGCCCATCGAGTACGGC 840  |
| Qy                         | 930    | AAGAAGAGCTGAATACCTGCCCTACATTCACACGACGCAATCTTCTTCTGATTTGGG 989     |
| Db                         | 841    | AAGAAGAGCTGAATACCTGCCCTACATTCACACGACGCAATCTTCTTCTGATTTGGG 900     |
| Qy                         | 990    | CCGCGGCTGCTCATCCCCCATGTATTTCCAGTACCAGATCATCATGACATGATCGTGCAT 1049 |

|      |  |      |
|------|--|------|
| 1981 | GCAGCTCGGTAAGTACCCGAGGCGCTCTCTTTAAGATGTCAGGGCCCAAGCGCCCGCGGGC  | 2041 |
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| Qy   | ACCTTGGGCTTTACAGGGCCCAATTCACACGCGCTCCCAACTTCAGCCTGTGACCTTGGG   | 2249 |
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| Qy   | TCCAAGATTCTGGAGCAATTCGACCCCTTCTCCAAAGGCTCTGTATTACAGCTGGGCACTGC | 2429 |
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| Qy   | CAGCCAAATCCCTGGCCATTGGCCCCCAGAGGGAAGTGGGCCCTCGAGGCTCAGAGGGC    | 2489 |
| Db   | CAGCCAAATCCCTGGCCATTGGCCCCCAGAGGGAAGTGGGCCCTCGAGGCTCAGAGGGC    | 2399 |
| Qy   | ACTGGAGCTGGAGGCTCTGCTCCAGACCCCTCCCATCTCGGGGCTGCTGTGTGACGGCG    | 2549 |
| Db   | ACTGGAGCTGGAGGCTCTGCTCCAGACCCCTCCCATCTCGGGGCTGCTGTGTGACGGCG    | 2459 |
| Qy   | CTGCCTCAGGCACCTCTCTGTCTGAACTTGCCCTTACTGTGTTTAACTGTGTCTCCAGG    | 2609 |
| Db   | CTGCCTCAGGCACCTCTCTGTCTGAACTTGCCCTTACTGTGTTTAACTGTGTCTCCAGG    | 2519 |
| Qy   | ATGCATTCTGATAGAGGGGCGCAGGGCTGGGCCCTTGTGACAACTCTGCTTTCAACC      | 2669 |
| Db   | ATGCATTCTGATAGAGGGGCGCAGGGCTGGGCCCTTGTGACAACTCTGCTTTCAACC      | 2579 |
| Qy   | ATGCGCTTGCCCTCGGTGCCCTGACTGTCTAGGGAGGGCCAGGAGGAGAGCGGGAGGA     | 2729 |
| Db   | ATGCGCTTGCCCTCGGTGCCCTGACTGTCTAGGGAGGGCCAGGAGGAGAGCGGGAGGA     | 2639 |
| Qy   | GTCTCAGGAGAGGCTGCCCTGAGGGGCTGGGAGGGGGTACCTCATGATGAGGACGAGGGTG  | 2789 |
| Db   | GTCTCAGGAGAGGCTGCCCTGAGGGGCTGGGAGGGGGTACCTCATGATGAGGACGAGGGTG  | 2699 |
| Qy   | CAGCTGAGAACAGGAGAGGTGGGGCTGGAGGTGCTGTAGCTGAGGGGACCGGGCAAGT     | 2849 |
| Db   | GAGCTGAGAACAGGAGAGGTGGGGCTGGAGGTGCTGTAGCTGAGGGGACCGGGCAAGT     | 2759 |
| Qy   | GAGAGGGAGGGAGGGAAGTCTCTGGGAGGATCTGTGAGCTGCTGTGTGAGTCTTAACCCACT | 2909 |
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| Db   | GGTTGCCATGGCAATGCGATGCCCGCAGCTACTGTATGCCCGGACCCCGCAGAGGCA      | 2999 |
| Qy   | GAATGAACCCATAGGAGCTGATCGTAATGTTTATCATGTACTTCCCCACCCCTACATT     | 3149 |
| Db   | GAATGAACCCATAGGAGCTGATCGTAATGTTTATCATGTACTTCCCCACCCCTACATT     | 3059 |
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| Db   | TTTTGAAATAAATAAGGAATTTT  | 3083 |

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 Homo sapiens (human)  
 Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,  
 Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,  
 Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,  
 Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,  
 Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and  
 Nanamiya,K.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 3083)  
 Isogai,T. and Otsuki,T.  
 Direct Submission  
 Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology; cDNA library construction:  
 Institute of Medical Science, University of Tokyo, Laboratory of  
 Genome Structure, Human Genome Center; cDNA 5' - 3'-end one pass  
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 615 a 937 c 884 g 647 t

BASE COUNT 615 a 937 c 884 g 647 t  
 ORIGIN

Query Match 96.2%; Score 3064; DB 9; Length 3083;  
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Qv 150 GTGCACGGGGCGCTCACAGTCTGGCAGCAGCATCGGGAGAGGGAGGAAACACGAGCGCAGGGG 209

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RESULT 8

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Db 2073 GTGCCAGCCAAATCCCTGGCCATTTGGCCCCA-GGGGACGTGGGCCCGCAGGCTGCAAG 2131  
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Db 2132 GGGCACTGGAGCTGGAGGCTCTGCTCCAGCCCTCCCACTCTCGGGCTCTGTGTGGAC 2191  
QY 2546 GGCCTGCTCAGCACTCTCTCTGTGTGAACCTGCCCTTACTGTGTTTAACTTGTGCTC 2605  
Db 2192 GGCCTGCTCAGCACTCTCTCTGTGTGAACCTGCCCTTACTGTGTTTAACTTGTGCTC 2251  
QY 2606 CAGATGCATTTCTGATAGGAGGGGGGGAGGCTGGGCCCTTGTGACAACTTCCCTTTCA 2665  
Db 2252 CAGATGCATTTCTGATAGGAGGGGGGGAGGCTGGGCCCTTGTGACAACTTCCCTTTCA 2311  
QY 2666 CCACATGCTTCTGCTCGTGGCCCTGACTGTCTGAGGAGGGGCCAGGAGGAGCGGGA 2725  
Db 2312 CCACATGCTTCTGCTCGTGGCCCTGACTGTCTGAGGAGGGGCCAGGAGGAGCGGGA 2371  
QY 2726 GGGAGTCTCAGGAGGCTGCTCTGAGGGCTGGGGAGGGGTACTCTATGAGGACCAG 2785  
Db 2372 GGGAGTCTCAGGAGGAGGCTGCTCTGAGGGCTGGGGAGGGGTACTCTATGAGGACCAG 2431  
QY 2786 GGTGGAGCTGAGAGAGGAGGAGTGGGGCTGGAGGTGCTGTAGCTGAGGGAGCGGGC 2845  
Db 2432 GGTGGAGCTGAGAGAGGAGGAGTGGGGCTGGAGGTGCTGTAGCTGAGGGAGCGGGC 2491  
QY 2846 AAGTGAGGGGAGGAGGAGTCTCTGGAGGATCTCTGAGCTGTGTTGCACTTAACC 2905  
Db 2492 AAGTGAGGGGAGGAGGAGTCTCTGGAGGATCTCTGAGGAGTCTCTGAGCTTAACC 2551  
QY 2906 CACTTAATCAGTTCTTAGATTGAGGGAAGGGCAGGCAACCAACTCAGAACTGGGGCTT 2965  
Db 2552 CACTTAATCAGTTCTTAGATTGAGGGAAGGGCAGGCAACCAACTCAGAACTGGGGCTT 2611  
QY 2966 TCGGGAGGGGCTAGTTCCTCCCTCAGCTCTAAGCAGCAGGAGGAGCTGCTTAAGCA 3025  
Db 2612 TCGGGAGGGGCTAGTTCCTCCCTCAGCTCTAAGCAGCAGGAGGAGCTGCTTAAGCA 2671  
QY 3026 TCTGGGTGGCAATGGCAATGGCATGCCCCAGCTACTGTATGCCCGCCGACCCCGCAG 3085  
Db 2672 TCTGGGTGGCATGGCATGGCATGCCCCAGCTACTGTATGCCCGCCGACCCCGCAG 2731  
QY 3086 GGCAGATGAACCCATGAGGAGCTGATCGTAATGTTTATCTGTTATCTTCCCGACCCCTA 3145  
Db 2732 GGCAGATGAACCCATGAGGAGCTGATCGTAATGTTTATCTGTTATCTTCCCGACCCCTA 2791  
QY 3146 CATTTTTCGAATAAATAAGGAAATTTTA 3174  
Db 2792 CATTTTTCGAATAAATAAGGAAATTTTA 2820













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| 901  | AGCCACAGACCCCGGGACACTGTGGGAAAGGGGTGCAGGTGGGTGATGCCACAGGAAT     | 960  |
| 1575 | GATGGGCTTTGTGCTGAGGGGTGTCGAGAGGCTGTGTATGCACTGCTCACGGACCCC      | 1634 |
| 961  | GATGGGCTTTGTGCTGAGGGGTGTCCGAGAGGCTGTGTATGCACTGCTCACGGACCCC     | 1020 |
| 1635 | ATGTTGATCTTTCTCCCTTCTCCTCTCTCTTTTCTCTTTCACATCTCCGCCATAGCACC    | 1594 |
| 1021 | ATGTTGATCTTTCTCCCTTCTCCTCTCTTTTCTCTTTCACATCTCCGCCATAGCACC      | 1080 |
| 1595 | CTGCCCTATGGGACCTTGCCCTCTCCCTCAGCCGTGAGCCATCAGCCATGGGCCCTCCAGTG | 1754 |
| 1081 | CTGCCCTCATGGGACCTGCCCTCTCCCTCAGCCGTGAGCCATCAGCCATGGGCCCTCCAGTG | 1140 |
| 1755 | CCTCCTAGCCCCCTTCTTCCAAAGGACGAGAGGTGGCCACCGGGGTGGCTCTGTCTCTAC   | 1814 |
| 1141 | CCTCCTAGCCCCCTTCTTCCAAAGGACGAGAGGTGGCCACCGGGGTGGCTCTGTCTCTAC   | 1200 |
| 1815 | CTCCACACTCTGCGCCCTTAAAGATGGGAGAGACAGCGGTCCATGGGTCTGGCCTGTGAG   | 1874 |
| 1201 | CTCCACACTCTGCGCCCTTAAAGATGGGAGAGACAGCGGTCCATGGGTCTGGCCTGTGAG   | 1260 |
| 1875 | TCTCCCTTGAGCCTGGTCACTAGGCATCACCCCGCTTTGGTTCTTCAGATGCTCTTG      | 1934 |
| 1261 | TCTCCCTTGAGCCTGGTCACTAGGCATCACCCCGCTTTGGTTCTTCAGATGCTCTTG      | 1320 |
| 1935 | GGGTTCATAGGGGAGGCTCTTAGTTCGGGACGGGCCCTGACCTCCCGGCTGGCTTCAC     | 1994 |
| 1321 | GGGTTCATAGGGGAGGCTCTTAGTTCGGGAGGGGCCCTGACCTCCCGGCTGGCTTCAC     | 1380 |
| 1995 | TCTCCCTGAGGCTGCCATTGGTCCACCCCTTTCATAGAGAGGCGCTGTTTGTTCACAAAGC  | 2054 |
| 1381 | TCTCCCTGAGGCTGCCATTGGTCCACCCCTTTCATAGAGAGGCGCTGTTTGTTCACAAAGC  | 1440 |
| 2055 | TCGGGTCTCCCTCTGTGAGCTCGGTTAAGTACCCGAGGCGCTCTCTTAAGATGTCAGGCG   | 2114 |
| 1441 | TCGGGTCTCCCTCTGTGAGCTCGGTTAAGTACCCGAGGCGCTCTCTTAAGATGTCAGGCG   | 1500 |
| 2115 | CCCAGGCCCGGGCACAGCAGCCCCAAAACCTTGGGCCCTTGGAGAGTCTCTCCACCCCAT   | 2174 |
| 1501 | CCCAGGCCCGGGCACAGCAGCCCCAAAACCTTGGGCCCTTGGAGAGTCTCTCCACCCCAT   | 1560 |
| 2175 | CACCTAGAGTCTCTGACCTTGGCTTTTCAGGGGCCCATTCACCGGCTCCCAACTTGA      | 2234 |
| 1561 | CACCTAGAGTCTCTGACCTTGGCTTTTCAAGGGCCCCATTCACCGGCTCCCAACTTGA     | 1620 |
| 2235 | GCCTGTGACCTTGGGACAAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCAGAGGCAGT     | 2294 |
| 1621 | GCCTGTGACCTTGGGACAAAGGGGAGTCCCTGCTCTCTTGTGACTCAGCAGAGGCAGT     | 1680 |
| 2295 | GGCCACGTTTCAGGAGAGGGCGGCTGGCTGGAGGCTCAGCCACCTCCAGGCTTTTCTCT    | 2354 |
| 1681 | GGCCACGTTTCAGGAGAGGGCGGCTGGCTGGAGGCTCAGCCACCTCCAGGCTTTTCTCT    | 1740 |
| 2355 | CAGGGTCTCTGAGGTCCAGATTCTGGAGCAATCTGACCTCTCTCAAGGCTCTGTTA       | 2414 |
| 1741 | CAGGGTCTCTGAGGTCCAGATTCTGGAGCAATCTGACCTCTCTCAAGGCTCTGTTA       | 1800 |
| 2415 | TCAGCTGGGAGTGCCACAGCCAAATCCCTGGCCATTGGCCCCCAGGGGACGTGGGCCCTGC  | 2474 |
| 1801 | TCAGCTGGGAGTGCCACAGCCAAATCCCTGGCCATTGGCCCCA-GGGGACGTGGGCCCTGC  | 1859 |
| 2475 | AGGCTGAGAGGGGACATGAGCTGGAGGTCTCGTCCGAGCCCTCCCACTCTGGGGCT       | 2534 |
| 1860 | AGGCTGAGAGGGGACCGGAGCTGGAGGTCTCGTCCGAGCCCTCCCACTCTGGGGCT       | 1919 |
| 2535 | GCTGTGTGGACGGGCGCTCTCAGGCACTCTCTGTCTGAACTGCGCTTACTGTGTTA       | 2594 |
| 1920 | GCTGTGTGGACGGGCGCTCTCAGGCACTCTCTGTCTGAACTGCGCTTACTGTGTTA       | 1979 |
| 2595 | ACCTGTGCTCCAGGATGCATTTCTGATAGAGGGGGCGGAGGGCTCGGCGCTGTGACAA     | 2654 |
| 1980 | ACCTGTGCTCCAGGATGCATTTCTGATAGAGGGGGCGGAGGGCTCGGCGCTGTGACAA     | 2039 |

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|----|------|--|------|
| Qy | 2655 | TCGCGCTTTACACATGGCCCTTGCCTCGGTGCCCTGACTGTCAAGGAGGGCCACGGGAG    | 2714 |
| Db | 2040 | TCGCGCTTTACACATGGCCCTTGCCTCGGTGCCCTGACTGTCAAGGAGGGCCACGGGAG    | 2099 |
| Qy | 2715 | GCAGAGCGGAGGGAGTGCTCAGAGGAGGCTGCCCTGAGGGGCTGGGAGGGGGGTACCTC    | 2774 |
| Db | 2100 | GCAGAGCGGAGGGAGTGCTCAGAGGAAGCTGCCCTGAGGGGCTGGGAGGGGGTACCTC     | 2159 |
| Qy | 2775 | ATAGGACCAGGCTGGAGCTTGAGAAGAGGAGGAGGTGGGGCTGGAGGTGCTGGTAGCTG    | 2834 |
| Db | 2160 | ATGAGGACCAAGGTGGAGCTTGAGAAGAGGAGGAGGTGGGGCTGGAGGTGCTGGTAGCTG   | 2219 |
| Qy | 2835 | AGGGGACGGGCAAGTGAAGAGGGAGGAGGAAAGTCCCTGGGAGGATCCTCAGAGCTGCTGTT | 2894 |
| Db | 2220 | AGGGGACGGGCAAGTGAAGAGGGAGGAGGAAAGTCCCTGGGAGGATCCTCAGAGCTGCTGTT | 2279 |
| Qy | 2895 | GCAGTCTAACCCACTAATCATGTTCTTAGATTACGGGAAGGGCACCAACAACCTCAG      | 2954 |
| Db | 2280 | GCAGTCTAACCCACTAATCATGTTCTTAGATTACGGGAAGGGCACCAACAACCTCAG      | 2339 |
| Qy | 2955 | AATGGGGGCTTTTCGGGGAGGGCGCTAGTCCCCCAGCTCTAAGACGCCAGGAGGGACCT    | 3014 |
| Db | 2340 | AATGGGGGCTTTTCGGGGAGGGCGCTAGTCCCCCAGCTCTAAGACGCCAGGAGGGACCT    | 2399 |
| Qy | 3015 | GCATCTAAGCATCTGGGTTGCCATGGCAATGGCAATGCCCCCAGCTACTGTATGCCCGCG   | 3074 |
| Db | 2400 | GCATCTAAGCATCTGGGTTGCCATGGCAATGGCAATGCCCCCAGCTACTGTATGCCCGCG   | 2459 |
| Qy | 3075 | ACCCCCCAGAGGCAGAAATGAAACCCATAGGGAGCTGATCGTAATGTTTTATCATGTTACTT | 3134 |
| Db | 2460 | ACCCCCCAGAGGCAGAAATGAAACCCATAGGGAGCTGATCGTAATGTTTTATCATGTTACTT | 2519 |
| Qy | 3135 | CCCCACCCCTACATTTTTTGAATAAATAAAGGAATTTT                         | 3173 |
| Db | 2520 | CCCCACCCCTACATTTTTTGAATAAATAAAGGAATTTT                         | 2558 |

RESULT 11

|            |   |             |      |        |                 |
|------------|---|-------------|------|--------|-----------------|
| AK074925   | AK074925  | 2558 bp     | mrna | linear | PRI 03-SEP-2002 |
| LOCUS      |   |             |      |        |                 |
| DEFINITION | Homo sapiens cDNA FLJ90444 fis, clone NT2RP3001159.               |             |      |        |                 |
| ACCESSION  | AK074925  |             |      |        |                 |
| VERSION    | AK074925.1  | GI:22750689 |      |        |                 |
| KEYWORDS   | oligo capping; fis (full insert sequence).                        |             |      |        |                 |
| SOURCE     | Homo sapiens (human)  |             |      |        |                 |
| ORGANISM   | Homo sapiens  |             |      |        |                 |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |             |      |        |                 |
|            | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.          |             |      |        |                 |

REFERENCE  
AUTHORS

Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sawaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.

**TITLE** NEPO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2558)

**AUTHORS** Isogai, T. and Otsuki, T.

| TITLE           | Direct Submission |
|-----------------|-------------------|
| 1. <u>THE</u>   |                   |
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| 98. <u>THE</u>  |                   |
| 99. <u>THE</u>  |                   |
| 100. <u>THE</u> |                   |

JOURNAL

COMMENT

## FEATURES

Location

1. .2558



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Db 1920 GCTGTGTGAGCGGCTGCCTCAGCACTCTCCTGTCTGAACCTGCCCTTACTGTGTGA 1979
Qy 2595 ACCTGTTCTCCAGATGTCATTCATAGAGGGGGGGGCGGAGGCTGGCTGTGTGACAA 2654
Db 1980 ACCTGTTCTCCAGATGTCATTCATAGAGGGGGGGGCGGAGGCTGGCTGTGTGACAA 2039
Qy 2655 TCTGCTTTACCACTGCTTCCCTCGGTGGCCCTGACTGTGCTGAGGAGGGGCGAGGAG 2714
Db 2040 TCTGCTTTACCACTGCTTCCCTCGGTGGCCCTGACTGTGCTGAGGAGGGGCGAGGAG 2099
Qy 2715 GCAGAGCGGGAGGAGTCTCAGGAGGAGGCTGCTCCTGAGGGGCTGGGAGGGGATCCTC 2774
Db 2100 GCAGAGCGGGAGGAGTCTCAGGAGGAGGCTGCTCCTGAGGGGCTGGGAGGGGATCCTC 2159
Qy 2775 ATGAGGACCCAGGGTGGAGCTCAGAGAGGAGGAGGCTGGGGCTGGAGGTCTGCTGAGCTG 2834
Db 2160 ATGAGGACCCAGGGTGGAGCTCAGAGAGGAGGAGGCTGGGGCTGGAGGTCTGCTGAGCTG 2219
Qy 2835 AGGGAGCGGGCAAGTGAAGAGGGGAGGAGGAGTCTCTGGAGGATCCTGAGCTGCTGTT 2894
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Qy 2955 AATGGGGCTTTCCGGGAGGGGCTGAGTCCCTCCAGCTCTAAGCAGCCAGGAGGAGGAGGAGGAG 3014
Db 2340 AATGGGGCTTTCCGGGAGGGGCTGAGTCCCTCCAGCTCTAAGCAGCCAGGAGGAGGAGGAGGAG 2399
Qy 3015 GCATCTAAGCATCTGGGTTCATGCGCAATGGCATGGCATGGCATGGCATGGCATGGCATGGCAT 3074
Db 2400 GCATCTAAGCATCTGGGTTCATGCGCAATGGCATGGCATGGCATGGCATGGCATGGCATGGCAT 2459
Qy 3075 ACCCCCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3134
Db 2460 ACCCCCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2519
Qy 3135 CCCACCCCTACATTTTGTGAATTAATAAGGAATTTT 3173
Db 2520 CCCACCCCTACATTTTGTGAATTAATAAGGAATTTT 2558

RESULT 12
LOCUS BD158110 2190 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD158110
VERSION BD158110.1 GI:27863868
KEYWORDS JP 2002191363-A/12953.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2190)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 12953 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/12953
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/00 CC
10,
PC C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
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Primer for synthesizing full-length cDNA and use thereof FH Key
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN
Query Match 68.3%; Score 2174.2; DB 6; Length 2190;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
983 GATTGGGGCGCGCTCATCCCATGTATTTCCAGTACCAGATCATCATGACCATCAT 1042
Db 1 GATTGGGGCGCGCTCATCCCATGTATTTCCAGTACCAGATCATCATGACCATCAT 60
1043 CTTCCATTAAGAACTGGGTGGACCTGGCTGGCCGTAGCTACTACATCCGGTCTTCAT 1102
61 CTTCCATTAAGAACTGGGTGGACCTGGCTGGCCGTAGCTACTACATCCGGTCTTCAT 120
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1163 CTTGAGAGCCACTGGTTTGTGGTCAACAGATGAATCAGATCGTCATGGAGATTGA 1222
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241 CCAGGAGCCCTACCGTGAAGTTCAGTAGCAGCTGACAGCCACCTCAACAGTGGAGCA 300
1283 GTCTTTCTTAACGACTGGTTTCAAGTGGACACCTTAACCTTCAGATTTGAGCACCCTCTT 1342
301 GTCTTTCTTAACGACTGGTTTCAAGTGGACACCTTAACCTTCAGATTTGAGCACCCTCTT 360
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1823 TCTGCCCTTAAAGATGGGAGGAGCAGCGGTCCATGGGTCTGGCTCTGTGATGTCCCTT 1882
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|    |      |     |    |    |     |    |    |      |     |     |     |    |    |    |    |    |    |    |     |    |    |     |    |     |     |      |      |    |      |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|----|------|-----|----|----|-----|----|----|------|-----|-----|-----|----|----|----|----|----|----|----|-----|----|----|-----|----|-----|-----|------|------|----|------|------|------|------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Db | 841  | TC  | TG | CC | CT  | AA | GA | TG   | GA  | GA  | GA  | CA | CG | GT | CC | AT | GG | GT | CT  | GG | CC | TG  | TG | AG  | TC  | TG   | CC   | CT | 900  |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 1883 | TG  | CA | GC | CT  | TG | CA | CT   | AT  | AG  | CA  | TG | CA | CC | CC | CG | CT | TG | TT  | GT | CT | TT  | CA | GA  | TG  | CT   | TT   | GG | GT   | CA   | 1942 |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 901  | TG  | CA | GC | CT  | TG | CA | CT   | AT  | AG  | CA  | TG | CA | CC | CC | CG | CT | TG | TT  | GT | CT | TT  | CA | GA  | TG  | CT   | TT   | GG | GT   | CA   | 960  |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 1943 | AG  | GG | CA | GT  | CT | TA | GT   | CG  | GA  | GG  | CC | CT | GA | CC | CT | CG | CC | TG  | GG | CC | TG  | GT | CA  | CT  | TC   | CC   | CT | G    | 2002 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 961  | AG  | GG | CA | GT  | CT | TA | GT   | CG  | GA  | GG  | CC | CT | GA | CC | CT | CG | CC | TG  | GG | CC | TG  | GT | CA  | CT  | TC   | CC   | CT | G    | 1020 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2003 | AC  | GG | CT | GC  | CA | TG | GT   | CC  | AC  | CC  | CT | TT | CA | TG | AG | AG | GC | CT  | GT | TT | GT  | TT | CA  | AA  | AG   | CT   | CG | GT   | 2062 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1021 | AC  | GG | CT | GC  | CA | TG | GT   | CC  | AC  | CC  | CT | TT | CA | TG | AG | AG | GC | CT  | GT | TT | GT  | TT | CA  | AA  | AG   | CT   | CG | GT   | 1080 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2063 | CC  | CT | CT | CA  | GT | CG | TT   | AA  | GT  | CA  | CC | GA | GG | CC | CT | TT | AA | GA  | TG | CA | GG  | CC | CC  | CA  | GG   | CC   | CC | CA   | GG   | CC   | 2122 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1081 | CC  | CT | CT | CA  | GT | CG | TT   | AA  | GT  | CA  | CC | GA | GG | CC | CT | TT | AA | GA  | TG | CA | GG  | CC | CC  | CA  | GG   | CC   | CC | CA   | GG   | CC   | 1140 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2123 | CG  | GG | CA | CAG | CA | GC | CC   | CA  | AA  | CC  | TT | GG | CC | CT | GA | AG | AG | TG  | CC | CT | CA  | CC | CC  | CA  | CT   | CA   | CT | AG   | 2182 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1141 | CG  | GG | CA | CAG | CA | GC | CC   | CA  | AA  | CC  | TT | GG | CC | CT | GA | AG | AG | TG  | CC | CT | CA  | CC | CC  | CA  | CT   | CA   | CT | AG   | 1200 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2183 | TG  | CT | CT | GA  | CC | CT | TG   | GG  | CT  | TT  | CA | GG | CC | CC | AT | TC | CA | CG  | CC | TT | CC  | CA | CT  | TT  | CG   | CA   | CT | TT   | CG   | CA   | 2242 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1201 | TG  | CT | CT | GA  | CC | CT | TG   | GG  | CT  | TT  | CA | GG | CC | CC | AT | TC | CA | CG  | CC | TT | CC  | CA | CT  | TT  | CG   | CA   | CT | TT   | CG   | CA   | 1260 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2243 | CT  | TT | GG | GA  | CC | AA | AA   | GG  | GA  | GC  | CC | CT | CG | TC | CT | GT | GA | CT  | CA | GA | GG  | CA | GT  | GG  | CC   | AC   | GT | 2302 |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1261 | CT  | TT | GG | GA  | CC | AA | AA   | GG  | GA  | GC  | CC | CT | CG | TC | CT | GT | GA | CT  | CA | GA | GG  | CA | GT  | GG  | CC   | AC   | GT | 1320 |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2303 | TC  | AG | GG | AG  | GG | CC | GG   | CT  | TG  | AG  | GT | CA | GG | CC | CC | CT | CA | GG  | CT | TT | CC  | CT | CAG | GG  | GT   | 2362 |    |      |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1321 | TC  | AG | GG | AG  | GG | CC | GG   | CT  | TG  | AG  | GT | CA | GG | CC | CC | CT | CA | GG  | CT | TT | CC  | CT | CAG | GG  | GT   | 1380 |    |      |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2363 | CT  | CA | GG | TC  | CA | AG | AT   | TC  | GA  | AG  | CA | AT | CT | GA | CC | TT | TC | CA  | AA | GG | CT  | CT | GT  | TA  | TC   | AG   | CT | GG   | 2422 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1381 | CT  | CA | GG | TC  | CA | AG | AT   | TC  | GA  | AG  | CA | AT | CT | GA | CC | TT | TC | CA  | AA | GG | CT  | CT | GT  | TA  | TC   | AG   | CT | GG   | 1440 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2423 | GC  | AG | TG | CC  | AG | CA | CA   | T   | CC  | CT  | GG | CC | AT | TT | GG | CC | CC | AG  | GG | CA | CG  | TG | GG  | CC  | CT   | CA   | GG | CT   | GC   | CA   | 2482 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1441 | CC  | AG | TG | CC  | AG | CA | CA   | T   | CC  | CT  | GG | CC | AT | TT | GG | CC | CC | AG  | GG | CA |     |    |     |     |      |      |    |      | 1499 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2483 | GG  | GG | CA | CT  | GA | AG | CT   | GG  | AG  | GT  | CT | CG | TC | CA | GG | CC | CT | CC  | CA | CT | CT  | CG | GG  | GC  | TG   | CT   | GT | GT   | 2542 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1500 | GG  | GG | CA | CT  | GA | AG | CT   | GG  | AG  | GT  | CT | CG | TC | CA | GG | CC | CT | CC  | CA | CT | CT  | CG | GG  | GC  | TG   | CT   | GT | GT   | 1559 |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2543 | GAC | GG | CG | TG  | CC | TC | CAGG | CAC | TCT | CCT | GT | CT | GA | CC | TG | CC | CT | TAC | TG | TT | TAA | CC | TG  | TTG | 2602 |      |    |      |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Db | 1560 | GAC | GG | CG | TG  | CC | TC | CAGG | CAC | TCT | CCT | GT | CT | GA | CC | TG | CC | CT | TAC | TG | TT | TAA | CC | TG  | TTG | 1619 |      |    |      |      |      |      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Qy | 2603 | CT  | C  | A  | G   | A  | N  | T    | G   | A   | T   | T  | C  | T  | G  | A  | T  | A  | G   | A  | G  | G   | G  | G   | G   | G    | G    | G  | G    | G    | G    | G    | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G | G |

|    |      |   |      |
|----|------|---|------|
| QY | 2963 | CTTTTCGGGGAGGGCGCGCTAGTCCCCCGAGCTTAAGCAGCAGCAGGAGGAGCCTGCATCTAA | 3023 |
| DB | 1980 | CTTTTCGGGGAGGGCGCGCTAGTCCCCCGAGCTTAAGCAGCAGCAGGAGGAGCCTGCATCTAA | 2039 |
| QY | 3023 | GCATCTCGGTTGCCATGGCAATGCATGCCCCCGAGCTACTGTATGCCCGCCGACCCCCCGC   | 3082 |
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| QY | 3083 | AGAGGCGAGATGAACCCATAGGGAGCTGATCGTAAATGTTTATCATGTTATCTCCCAACC    | 3142 |
| DB | 2100 | AGAGGCGAGAATGAACCCATAGGGAGCTGATCGTAAATGTTTATCATGTTATCTCCCAACC   | 2159 |
| QY | 3143 | CTACATTTTGTGAATAAAATAAGGAATTTT                                  | 3173 |
| DB | 2160 | CTACATTTTGTGAATAAAATAAGGAATTTT                                  | 2190 |

RESULT 13

AK027577

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AK027577

Homo sapiens cDNA FLJ14671 fis, clone NT2RP2003466, highly similar to Homo sapiens delta-6 fatty acid desaturase mRNA.

AK027577.1

GI:14042349

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 2190)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@ri.co.jp, Tel:81-438-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center, Helix and Department of Virology, Institute of Medical Science, University of Tokyo).

Location/Qualifiers

1..2190

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="NT2RP2003466"

/cell\_line="NT2"

/cell\_type="teratocarcinoma"

/clone\_1lb="NT2RP2"

/notes="Cloning vector: pWE18FL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."

BASE COUNT 412 a 657 c 634 g 477 t

ORIGIN

Query Match 68.3%; Score 2174.2; DB 9; Length 2190;

Best local similarity 99.8%; Pred. No. 0;

Matches 2187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 983 GATTGGCGCGCGCTCTCATCCCATGTATTTCAGTACCAGATCATCATGACCATGAT 1042

DB 1 GATTGGCGCGCGCTCTCATCCCATGTATTTCAGTACCAGATCATCATGACCATGAT 60



QY 1043 CGTCCATGAAGAACTGGGTGGACCTGGCCCTGGCCCGTCACTACTACATCGGTTCTTTCAT 1102  
Db 61 CGTCCATGAAGAACTGGGTGGACCTGGCCCTGGCCCGTCACTACTACATCGGTTCTTTCAT 120  
QY 1103 CACCTACATCCCTTCTACAGCAGTCTGGGAGCCCTGCTTTCTCAACTTCATCAGGTT 1162  
Db 121 CACCTACATCCCTTCTACAGCAGTCTGGGAGCCCTGCTTTCTCAACTTCATCAGGTT 180  
QY 1163 CCGAGAGCCACTGGTTTGTGTGGGTACACAGATGAATCACATCGTCAATGAGATTGA 1222  
Db 181 CCGAGAGCCACTGGTTTGTGTGGGTACACAGATGAATCACATCGTCAATGAGATTGA 240  
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Db 241 CCAGAGCCCTACCGTGAATGCTGGTACAGTGGTACAGCCACTGGCAACGTGGAGCA 300  
QY 1283 GTCCCTTCTTCAACGACTGGTTCACTGGACACCTTAACTTCCAGATTCAGCACCACTCTT 1342  
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Db 1800 GGTGGGGCTGGAGGTGCTGTAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1859

Qy 2868 GTCTGGGAGGATCTGAGCTGCTGTTGAGCTTAACTTAACTTAACTTAACTTAACTTAACTT 2927

Db 1860 GTCTGGGAGGATCTGAGCTGCTGTTGAGCTTAACTTAACTTAACTTAACTTAACTTAACTT 1919

Qy 2928 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2987

Db 1920 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1979

Qy 2988 CCAGCTCTAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3047

Db 1980 CCAGCTCTAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2039

Qy 3048 ATGCCCCCAGCTACTGTATGCCCCGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3107

Db 2040 ATGCCCCCAGCTACTGTATGCCCCGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2099

Qy 3108 CTGATGCTGAATGTTTATCATGCTTACTTCCCGACCCCTACATTTTGGAAATATAAATAGG 3167

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Qy 3168 AATTTT 3173

Db 2160 AATTTT 2165

RESULT 15

AK027513

LOCUS AK027513 2165 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14607 f1s, clone NT2RP1000609.

ACCESSION AK027513

VERSION AK027513.1 GI:14042243

KEYWORDS oligo capping; f1s (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shitatori, A., Sudo, H., Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2165)

AUTHORS Isogai, T. and Otsuki, T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yano, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

Location/Qualifiers

1..2165

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="NT2RP1000609"

/cell\_line="NT2"

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/note="cloning vector; pUC19FL3-mRNA from NT2 neuronal precursor cells after 48-hours retinoic acid (RA) induction."

1..507

/note="unnamed protein product"

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BASE COUNT 410 a 655 c 629 g 471 t

ORIGIN

Query Match 67.3%; Score 2144.4; DB 9; Length 2165;  
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Db 1 ATGTATTTCCAGTACAGATCATCATGACCATGATGCTCCATAGAACTGGGTGACCTG 60

Qy 1068 GCGTGGCGCTCAGCTACTACATCCGTTCTTCATCACCCTACATCCCTTTCTACCGCATC 1127

Db 61 GCGTGGCGCTCAGCTACTACATCCGTTCTTCATCACCCTACATCCCTTTCTACCGCATC 120

Qy 1128 CTGGGAGCCCTCTCTTTCTCAACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGG 1187

Db 121 CTGGGAGCCCTCTCTTTCTCAACTTCATCAGTTCTCTGGAGAGCCACTGGTTTGTGG 180

Qy 1188 GTACACAGATGAATCAGATCGTCATGGAGTTGACAGGAGGCGCTACGTCAGCTGTTTC 1247

Db 181 GTACACAGATGAATCAGATCGTCATGGAGTTGACAGGAGGCGCTACGTCAGCTGTTTC 240

Qy 1248 AGTAGCCAGCTGACAGCCACTCTGCAACCTGGAGAGCAGTCTCTTCTCAACGACTGTTCA 1307

Db 241 AGTAGCCAGCTGACAGCCACTCTGCAACCTGGAGAGCAGTCTCTTCTCAACGACTGTTCA 300

Qy 1308 GGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCAACCATGCCCGGCGACACTTA 1367

Db 301 GGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCAACCATGCCCGGCGACACTTA 360

Qy 1368 CACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTAATACAGAGG 1427

Db 361 CACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTAATACAGAGG 420

Qy 1428 AGCGCGCTACTAGGAGGCGCTCTGTCAGATCATCATGAGTCTCTGAGAGAGTCTGGGAAGCTG 1487

Db 421 AAGCGCGCTACTAGGAGGCGCTCTGTCAGATCATCATGAGTCTCTGAGAGAGTCTGGGAAGCTG 480

Qy 1488 TGGCTGGAGCGCTTACCTTCAAAATGAAGCCACAGCCCGGCGACACCGTGGGGAAGGG 1547

Db 481 TGGCTGGAGCGCTTACCTTCAAAATGAAGCCACAGCCCGGCGACACTGTGGGAAGGG 540

Qy 1548 TGCAGGTGGGTGATGGCCAGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCGAGAGG 1607



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| Best Local Similarity    | 99.8%;       | Pred. No.  | 0;         |       |        |       |      |    |  |
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| Db                       | 1            | TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGGCCGTGAGTACT        | 60         |       |        |       |      |    |  |
| QY                       | 1087         | ACATCCGGTCTTTCATACACTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTTCC   | 1146       |       |        |       |      |    |  |
| Db                       | 61           | ACATCCGGTCTTTCATACACTACATCCCTTTCTACGGCATCTGGGAGCCCTCTTTTCC   | 120        |       |        |       |      |    |  |
| QY                       | 1147         | TCNACTTCATCAGGTCTCTGGAGAGCCACTGGTTTGTGGGTACACAGATGAATCACA    | 1206       |       |        |       |      |    |  |
| Db                       | 121          | TCAACTTCATCAGGTCTCTGGAGAGCCACTGGTTTGTGGGTACACAGATGAATCACA    | 180        |       |        |       |      |    |  |
| QY                       | 1207         | TCGTATGAGGATTCACAGGAGGACCTACCGTGTACTGGTTGAGTACAGCTGACGCCA    | 1266       |       |        |       |      |    |  |
| Db                       | 181          | TCGTATGAGGATTCACAGGAGGACCTACCGTGTACTGGTTGAGTACAGCTGACGCCA    | 240        |       |        |       |      |    |  |
| QY                       | 1267         | CCTGCAACGTGGAGCAGTCCCTTTCAACGACTGGTTCACTGGACACTTAACTTCAGA    | 1326       |       |        |       |      |    |  |
| Db                       | 241          | CCTGCAACGTGGAGCAGTCCCTTTCAACGACTGGTTCACTGGACACTTAACTTCAGA    | 300        |       |        |       |      |    |  |
| QY                       | 1327         | TTGAGCACCACTCTTCCCAACCATGCCCCGGGCAAACTTACAAAGATGCCGCCGTGG    | 1386       |       |        |       |      |    |  |
| Db                       | 301          | TTGAGCACCACTCTTCCCAACCATGCCCCGGGCAAACTTACAAAGATGCCGCCGTGG    | 360        |       |        |       |      |    |  |
| QY                       | 1387         | TGAAGTCTCTATGTGCAAGCATGCAATGATACAGAGAGAACCGCTACTGAGGSCC      | 1446       |       |        |       |      |    |  |
| Db                       | 361          | TGAAGTCTCTATGTGCAAGCATGCAATGATACAGAGAGAACCGCTACTGAGGSCC      | 420        |       |        |       |      |    |  |
| QY                       | 1447         | TGCTGGACATCATCAGTCCCTGAAGAGTCTGGGAAGCTGTGGCTGGAGCCCTACCTTC   | 1506       |       |        |       |      |    |  |
| Db                       | 421          | TGCTGGACATCATCAGTCCCTGAAGAGTCTGGGAAGCTGTGGCTGGAGCCCTACCTTC   | 480        |       |        |       |      |    |  |
| QY                       | 1507         | ACAAATGAGCCACAGCCCCGGGACACCGTGGGAGGGGTGAGGTGGGTGATGGCC       | 1566       |       |        |       |      |    |  |
| Db                       | 481          | ACAAATGAGCCACAGCCCCGGGACACCGTGGGAGGGGTGAGGTGGGTGATGGCC       | 540        |       |        |       |      |    |  |
| QY                       | 1567         | AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGCTCA  | 1626       |       |        |       |      |    |  |
| Db                       | 541          | AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGGTGTATGCACTGCTCA  | 600        |       |        |       |      |    |  |
| QY                       | 1627         | CGGACCCCATGTTGGATCTTTCTCCCTTCTCCTCTCCTTTTCTCTTCATCTCCCC      | 1686       |       |        |       |      |    |  |
| Db                       | 601          | CGGACCCCATGTTGGATCTTTCTCCCTTCTCCTCTCCTTTTCTCTTCATCTCCCC      | 660        |       |        |       |      |    |  |
| QY                       | 1687         | ATAGCACCCCTGCCCTCATGGACCTGCCCTCCCTCAGCCGTGAGCCATGAGCCATGGCCC | 1746       |       |        |       |      |    |  |
| Db                       | 661          | ATAGCACCCCTGCCCTCATGGACCTGCCCTCCCTCAGCCGTGAGCCATGAGCCATGGCCC | 720        |       |        |       |      |    |  |
| QY                       | 1747         | TCCAGTGCCTCTAGCCCTTCTCCAGGAGCAGAGAGTGGCCACCGGGGTGGCTC        | 1806       |       |        |       |      |    |  |
| Db                       | 721          | TCCAGTGCCTCTAGCCCTTCTCCAGGAGCAGAGAGTGGCCACCGGGGTGGCTC        | 780        |       |        |       |      |    |  |
| QY                       | 1807         | TGTCCTACTCCACTCTCTGCCCTTAAAGATGGGAGGAGACAGCGGTCCATGGTCTGG    | 1866       |       |        |       |      |    |  |
| Db                       | 781          | TGTCCTACTCCACTCTCTGCCCTTAAAGATGGGAGGAGACAGCGGTCCATGGTCTGG    | 840        |       |        |       |      |    |  |
| QY                       | 1867         | CCTGTAGTCTCCCTTTCAGGCTGGTCACTAGGCAATCACCCCGCTTTGGTCTTTCAGA   | 1926       |       |        |       |      |    |  |
| Db                       | 841          | CCTGTAGTCTCCCTTTCAGGCTGGTCACTAGGCAATCACCCCGCTTTGGTCTTTCAGA   | 900        |       |        |       |      |    |  |
| QY                       | 1927         | TGCTCTTGGGGTTCATAGGGGACAGGTCTTAGTCCGGGACAGGGCCCTGACCTCCCGGCT | 1986       |       |        |       |      |    |  |
| Db                       | 901          | TGCTCTTGGGGTTCATAGGGGACAGGTCTTAGTCCGGGACAGGGCCCTGACCTCCCGGCT | 960        |       |        |       |      |    |  |

|    |      |   |      |
|----|------|---|------|
| QY | 1987 | GGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCTTTTCATAGAGAGGCTCTCTTTGT    | 2046 |
| Db | 961  | GGCTTCACTCTCCCTGACGGCTGCCATTGGTCCACCTTTTCATAGAGAGGCTCTCTTTGT    | 1020 |
| QY | 2047 | TACAAAGCTCGGTCTCCCTCTGACGTGGTTAAGTTACCGAGGCTCTCTTAAAGATG        | 2106 |
| Db | 1021 | TACAAAGCTCGGTCTCCCTCTGACGTGGTTAAGTTACCGAGGCTCTCTTAAAGATG        | 1080 |
| QY | 2107 | TCCAGGGCCCCAGGCCCGGGGCAAGCCACCAAACTTTGGGCCCTTGGAGAGTCTCTC       | 2166 |
| Db | 1081 | TCCAGGGCCCCAGGCCCGGGGCAAGCCACCAAACTTTGGGCCCTTGGAGAGTCTCTC       | 1140 |
| QY | 2167 | CACCCCATCTAGAGTCTCTGACCTGGGCTTTCAGGGCCCATTCACCCGCTCCC           | 2226 |
| Db | 1141 | CACCCCATCTAGAGTCTCTGACCTGGGCTTTCAGGGCCCATTCACCCGCTCCC           | 1200 |
| QY | 2227 | CAACTTTGAGCCTGTGACCTTTGGGACCAAAAGGGGGAGTCCCTCGTCTCTTTGTACTCAGCA | 2286 |
| Db | 1201 | CAACTTTGAGCCTGTGACCTTTGGGACCAAAAGGGGGAGTCCCTCGTCTCTTTGTACTCAGCA | 1260 |
| QY | 2287 | GAGGAGTGGCCAGCTTCAGGGAGGGCCGGCTGGCTGGAGGCTCAGCCACCCCTCCAG       | 2346 |
| Db | 1261 | GAGGAGTGGCCAGCTTCAGGGAGGGCCGGCTGGCTGGAGGCTCAGCCACCCCTCCAG       | 1320 |
| QY | 2347 | CTTTTCTCAGGGTGTCTGAGGTCCAAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG    | 2406 |
| Db | 1321 | CTTTTCTCAGGGTGTCTGAGGTCCAAAGATTCTGGAGCAATCTGACCCCTTCTCCAAAGG    | 1380 |
| QY | 2407 | CTCTGTTATCAGCTGGGAGTGCAGCCAAATCCCTGGCCATTTGGCCCCAGGGGACCTG      | 2466 |
| Db | 1381 | CTCTGTTATCAGCTGGGAGTGCAGCCAAATCCCTGGCCATTTGGCCCCAGGGGACCTG      | 1439 |
| QY | 2467 | GGCCCTGACGGTGCAGGAGGSCACTGGAGCTGGAGGTCTCGTCCAGGCTCTCCCATC       | 2526 |
| Db | 1440 | GGCCCTGACGGTGCAGGAGGSCACTGGAGCTGGAGGTCTCGTCCAGGCTCTCCCATC       | 1499 |
| QY | 2527 | TGGGGCTGTCTGTGGACGGCGTGCCTCAGGCACTCTCTGTGTAACTGCCCTTAC          | 2586 |
| Db | 1500 | TGGGGCTGTCTGTGGACGGCGTGCCTCAGGCACTCTCTGTGTAACTGCCCTTAC          | 1559 |
| QY | 2587 | TGTGTTTAACTTGTCTCCAGGATGCATTTCTGATAGAGGGGGGGGAGGCTGGGCT         | 2646 |
| Db | 1560 | TGTGTTTAACTTGTCTCCAGGATGCATTTCTGATAGAGGGGGGGGAGGCTGGGCT         | 1619 |
| QY | 2647 | TGTGCAATCTCCCTTTTCCACATGGCTTGCCTCGGTGGCCCTGACTGTGAGGAGGG        | 2706 |
| Db | 1620 | TGTGCAATCTCCCTTTTCCACATGGCTTGCCTCGGTGGCCCTGACTGTGAGGAGGG        | 1679 |
| QY | 2707 | CCAGGAGGACAGCGGGAGGAGTCTCAGGAGGAGGCTGCCCTGAGGGCTGGGGAGGG        | 2766 |
| Db | 1680 | CCAGGAGGACAGCGGGAGGAGTCTCAGGAGGAGGCTGCCCTGAGGGCTGGGGAGGG        | 1739 |
| QY | 2767 | GGTACCTCATAGGACCGAGGTGGAGTCTGAGAGGAGGAGGTGGGGCTGGAGGTCT         | 2826 |
| Db | 1740 | GGTACCTCATAGGACCGAGGTGGAGTCTGAGAGGAGGAGGTGGGGCTGGAGGTCT         | 1799 |
| QY | 2827 | GGTAGCTAGGGAGCGGGCAAGTGTAGAGGGGAGGAGGAGTCTCTGGAGGATCTCTGAG      | 2886 |
| Db | 1800 | GGTAGCTAGGGAGCGGGCAAGTGTAGAGGGGAGGAGGAGTCTCTGGAGGATCTCTGAG      | 1859 |
| QY | 2887 | CTGCTTTTCAGTCTAAACCCACTTAATCAGTTCTTAGATTTCAGGGGAAGGGCAGGCCAA    | 2946 |
| Db | 1860 | CTGCTTTTCAGTCTAAACCCACTTAATCAGTTCTTAGATTTCAGGGGAAGGGCAGGCCAA    | 1919 |
| QY | 2947 | CAACTCAGAAATGGGGCTTTCCGGGAGGGCGCTAGTCCCCCAGCTCTAAGCAGCCAGG      | 3006 |
| Db | 1920 | CAACTCAGAAATGGGGCTTTCCGGGAGGGCGCTAGTCCCCCAGCTCTAAGCAGCCAGG      | 1979 |
| QY | 3007 | AGGACCTTCATCTAAGCATCTGGGTTCACATGGCAATGGCATGCCCCCAGCTACTGTA      | 3066 |
| Db | 1980 | AGGACCTTCATCTAAGCATCTGGGTTCACATGGCAATGGCATGCCCCCAGCTACTGTA      | 2039 |







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|----|------|-------|-----------------------------------|---------------------------------|------|
| QY | 1190 | CA    | CACAGATGAATCATCTGTCATGGAGATTGA    | CACCAGAGGCCCTACCGTGACTGTGTTCCAG | 1249 |
| DB | 975  | CACA  | CAGATGAATCACATCTGTCATGGAGATTGA    | CACAGAGGCCCTACCGTGACTGTGTTCCAG  | 1034 |
| QY | 1250 | TAGC  | CAGCTGCAGCCACTGCAACGTCGGACAGTCT   | CTTCTTAACACACTGGTTCAGTGG        | 1309 |
| DB | 1035 | TAGC  | CAGCTGCAGCCACTGCAACGTCGGACAGTCT   | CTTCTTAACACACTGGTTCAGTGG        | 1094 |
| QY | 1310 | ACAC  | CTTAACCTTCAGATTGAGCACCACTCTCTTCCC | ACCATGCCCCGGGCACAACTTACA        | 1369 |
| DB | 1095 | ACAC  | CTTAACCTTCAGATTGAGCACCACTCTCTTCCC | ACCATGCCCCGGGCACAACTTACA        | 1154 |
| QY | 1370 | CAAGA | TCGCCCCGCTGGTGAGTCTCTATGTGCCAAG   | CATGGCATTAATAACAGAGAA           | 1429 |
| DB | 1155 | CAAGA | TCGCCCCGCTGGTGAGTCTCTATGTGCCAAG   | CATGGCATTAATAACAGAGAA           | 1214 |
| QY | 1430 | GCCG  | CTACTGAGGGCCCTGCTGGACATCATCAGGT   | CCCTGCAAGAAGTCTGGGAAGCTGTG      | 1489 |
| DB | 1215 | GCCG  | CTACTGAGGGCCCTGCTGGACATCATCAGGT   | CCCTGCAAGAAGTCTGGGAAGCTGTG      | 1274 |
| QY | 1490 | GCTG  | GACGCTTACCTTCACAATGAGGCCACAGCCCC  | GGGACHACCTGTGGGGAAGGGGTG        | 1549 |
| DB | 1275 | GCTG  | GACGCTTACCTTCACAATGAGGCCACAGCCCC  | GGGACHACCTGTGGGGAAGGGGTG        | 1334 |
| QY | 1550 | CAGGT | GGGGTGATGCCACAGAGAAATGATGGSCITTT  | TGTCTGAGGGGTGTCCAGAGGCT         | 1609 |
| DB | 1335 | CAGGT | GGGGTGATGCCACAGAGAAATGATGGSCITTT  | TGTCTGAGGGGTGTCCAGAGGCT         | 1394 |
| QY | 1610 | GGTGT | ATGCATGCTACAGAACCCATGTTGGATCTTTT  | CTCCCTTCTCCTCTCCTTTTT           | 1669 |
| DB | 1395 | GGTGT | ATGCATGCTACAGAACCCATGTTGGATCTTTT  | CTCCCTTCTCCTCTCCTTTTT           | 1454 |
| QY | 1670 | CTCTT | CAATCTCCCCCATAGCACCCCTCATGGAGCT   | GTGCCCTCCCTCAGCCGTCA            | 1729 |
| DB | 1455 | CTCTT | CAATCTCCCCCATAGCACCCCTCATGGAGCT   | GTGCCCTCCCTCAGCCGTCA            | 1514 |
| QY | 1730 | GCCAT | CAGCATGGCCCTCCAGTGCTCTTAGGCCCTT   | CTTCAAAGGACGACAGAGGTG           | 1789 |
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| QY | 1790 | GCCAC | CGGGGTGGCTCTGTCTTACTACCTCCA       | CTCTGCCCCCTAAGATGGGAGACCA       | 1849 |
| DB | 1575 | GCCAC | CGGGGTGGCTCTGTCTTACTACCTCCA       | CTCTGCCCCCTAAGATGGGAGACCA       | 1634 |
| QY | 1850 | GCGGT | CCATGGGCTGCGCTGTAGTCTCCCTTGCAG    | CGCTGGTCACTAGGCATCACCC          | 1909 |
| DB | 1635 | GCGGT | CCATGGGCTGCGCTGTAGTCTCCCTTGCAG    | CGCTGGTCACTAGGCATCACCC          | 1694 |
| QY | 1910 | CGCTT | TGGTCTTCAGATGCTCTTGGGTTCA         | TAGGGGAGGTCCTAGTCGGGACGGGC      | 1969 |
| DB | 1695 | CGCTT | TGGTCTTCAGATGCTCTTGGGTTCA         | TAGGGGAGGTCCTAGTCGGGACGGGC      | 1754 |
| QY | 1970 | CTTG  | AACCTCCCGSCCTGGCTTCACTCTCCCT      | GACCGCTGCCATGGTCCACCCCTTTCAT    | 2029 |
| DB | 1755 | CTTG  | AACCTCCCGSCCTGGCTTCACTCTCCCT      | GACCGCTGCCATGGTCCACCCCTTTCAT    | 1814 |
| QY | 2030 | AGAG  | AGCCCTCTTTGTTTACAAGCTCGGCTCTCC    | CTCTGAGCTCGGTTAAGTACCG          | 2089 |
| DB | 1815 | AGAG  | AGCCCTCTTTGTTTACAAGCTCGGCTCTCC    | CTCTGAGCTCGGTTAAGTACCG          | 1874 |
| QY | 2090 | AGG   | CCTCTTAAGATGTCCAGGGCCCCAGCGCC     | GGGGCACAGCCAGCCCAAACTTCG        | 2149 |
| DB | 1875 | AGG   | CCTCTTAAGATGTCCAGGGCCCCAGCGCC     | GGGGCACAGCCAGCCCAAACTTCG        | 1934 |
| QY | 2150 | GGCC  | TGGAAGTCTTCCACCCCATCATAGAGTG      | CTCTGAACCTGGGCTTTCACGGGCC       | 2209 |
| DB | 1935 | GGCC  | TGGAAGTCTTCCACCCCATCATAGAGTG      | CTCTGAACCTGGGCTTTCACGGGCC       | 1994 |
| QY | 2210 | CCAT  | TCACCGCCTCCCCACITTTAGCCTGTGAC     | TTTGGACCAAGGGGAGTCCCTCG         | 2269 |
| DB | 1995 | CCAT  | TCACCGCCTCCCCACITTTAGCCTGTGAC     | TTTGGACCAAGGGGAGTCCCTCG         | 2054 |
| QY | 2270 | TCCT  | TGTGACTCAGCAGAGGACGTGGCCAC        | GTTTCAGGAGGGGGCGGCTGGCCCTGGAGG  | 2329 |

| Db         | 2055  | TCCTCTGTGACTCAGCAGAGCGAGTGCACAGTTTCAGGGAGGGCGCGCTGGCTCGAGG     | 2114                       |  |  |
|------------|---|--|----------------------------|--|--|
| Qy         | 2330  | CTCAGGCCACCCCTCCAGCTTTTCCTCAGGGTGTCCCTGAGTCCAAAGATTCTCGAGCAATC | 2389                       |  |  |
| Db         | 2115  | CTCAGGCCACCCCTCCAGCTTTTCCTCAGGGTGTCCCTGAGTCCAAAGATTCTCGAGCAATC | 2174                       |  |  |
| Qy         | 2390  | TGACCTCTTCCTCCAAAGCTCTGTATCAGCTGGGAGTGCACAGCAATCCTCGGCATTT     | 2449                       |  |  |
| Db         | 2175  | TGACCTCTTCCTCCAAAGCTCTGTATCAGCTGGGAGTGCACAGCAATCCTCGGCATTT     | 2234                       |  |  |
| Qy         | 2450  | GGCCCCAGGGGACGTGGGCCCTG  | 2473                       |  |  |
| Db         | 2235  | GGCCCCA-GGGGACGTGGGCCCTG                                       | 2257                       |  |  |
| RESULT 19  |   |  |                            |  |  |
| LOCUS      | BD082640  | 2257 bp  | DNA linear PAT 27-AUG-2002 |  |  |
| DEFINITION | Methods and compositions for synthesis of long chain poly-unsaturated fatty acids.  |  |                            |  |  |
| ACCESSION  | BD082640  |  |                            |  |  |
| VERSION    | BD082640.1  | GI:22628250  |                            |  |  |
| KEYWORDS   | JP 2001523091-A/20.   |  |                            |  |  |
| SOURCE     | unidentified  |  |                            |  |  |
| ORGANISM   | unclassified.   |  |                            |  |  |
| REFERENCE  | 1 (bases 1 to 2257)   |  |                            |  |  |
| AUTHORS    | Knutzen,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Loenard,A.E.Y.  |  |                            |  |  |
| TITLE      | Methods and compositions for synthesis of long chain poly-unsaturated fatty acids   |  |                            |  |  |
| JOURNAL    | Patent: JP 2001523091-A/20 20-NOV-2001;   |  |                            |  |  |
| COMMENT    | CALGENE LLC,ABBOTT LABORATORIES<br>PN JP 2001523091-A/20<br>PD 20-NOV-2001<br>PF 10-APR-1998 JP 1998544053<br>PR 11-APR-1997 US 08/834655<br>PI DEBORAH KNUTZEN,PRADIP MUKERJI,YUNG SHENG HUANG,JENNIFER PI THURMOND,<br>PI SUNITA CHAUDHARY,ANANDA EUN YEONG LOENARD<br>PC C12N15/53,C12N15/81,C12N9/02,C12N5/10,C12M1/19,C12P7/64 PC<br>C1B1/00,A61K31/20,<br>PC A23L1/30<br>CC Strandedness: Single;<br>CC Topology: Linear;<br>FH Key Location/Qualifiers.<br>FEATURES<br>source<br>1..2257<br>/organism="unidentified"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:32644"<br>BASE COUNT 438 a 719 c 596 g 504 t<br>ORIGIN<br>Query Match 60.9%; Score 1937.6; DB 6; Length 2257;<br>Best Local Similarity 92.1%; Pred No. 0;<br>Matches 2066; Conservative 0; Mismatches 174; Indels 4; Gaps 2;<br>QY 233 GCCACCTTCAGCTGGAGGAGATTCAAGACATAACCTGCACACCGACAGTGGCTGGT 292<br>Db 15 GCGCTACTTCACCTGGGACGAGGTGGCCCGCTCAGGGTCCGAGGAGCGGTGGCTAGT 74<br>QY 293 CATTCAGCCGCAAGGTTTCAACATCACCAAAATGGTCCATCCAGCACCCGGGGGCCACGG 352<br>Db 75 GATCGACCGTAAAGTGTACNACATCAGCGAGTTACCCCGCGGATCCAGGGGGTCCCG 134<br>QY 353 GGTCTATCGGGCACTACGCTGGAGAAGATGCACCGATGCCCTTCGCGCCTTCCACCCGTGA 412<br>Db 135 GGTCTATCAGCCACTACGCGGGGAGATGCCACCGATCCCTTTGTGGGCTTCCACATCAA 194<br>QY 413 CCTGGAATTCTGGGGCAAGTTCTTGAAACCCCTGCTGATTGCTGAACCTGCGCCCGGAGGA 472 |  |                            |  |  |





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KEYWORDS JP 2001523092-A/15.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2257)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids
JOURNAL Patent: JP 2001523092-A 15 20-NOV-2001; CALGENE LLC,ABBOTT LABORATORIES
COMMENT PN JP 2001523092-A/15 PD 20-NOV-2001 PF 10-APR-1998 JP 1998544176 PR 11-APR-1997 US 08/833610 PI DEBORAH KNUZZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND, PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD PC
C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
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  Leonard, A.E.Y.
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  Methods and compositions for synthesis of long chain
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REFERENCE 1 (bases 1 to 1843)  
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.  
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JOURNAL Patent: US 6428990-A 7 06-AUG-2002;  
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RESULT 23  
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LOCUS  
DEFINITION 1843 bp DNA linear PAT 27-AUG-2002  
Methods and compositions for synthesis of long chain  
poly-unsaturated fatty acids.  
ACCESSION  
BD082639  
VERSION  
BD082639.1 GI:22628249  
KEYWORDS  
JP 2001523091-A/19.  
SOURCE  
unidentified  
ORGANISM  
unidentified  
unclassified.  
REFERENCE  
1 (bases 1 to 1843)  
AUTHORS  
Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and  
Loenard,A.E.Y.  
TITLE  
Methods and compositions for synthesis of long chain  
poly-unsaturated fatty acids  
JOURNAL  
Patent: JP 2001523091-A 19 20-NOV-2001;  
COMMENT  
CALGENE LUC,ABBOTT LABORATORIES  
FN JP 2001523091-A/19  
PD 20-NOV-2001  
PF 10-APR-1998 JP 1998544053  
PR 11-APR-1997 US 08/834655  
PI DESORAH KNUZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI  
THURMOND,  
PI SUNITA CHAUDHARY, AMANDA EUN YOUNG LOENARD  
PC C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC  
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## RESULT 24

BD082654

LOCUS

DEFINITION

BD082654

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD082654 1843 bp DNA linear PAT 27-AUG-2002  
Methods and compositions for synthesis of long chain  
polyunsaturated fatty acids.

BD082654  
BD082654.1 GI:22628264

JP 2001523092-A/14.

unidentified

unclassified.

1 (bases 1 to 1843)

Knutson, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and

Leonard, A.E.Y.

Methods and compositions for synthesis of long chain

polyunsaturated fatty acids

Patent: JP 2001523092-A 14 20-NOV-2001;

CALGENE LLC, ABBOTT LABORATORIES

PN JP 2001523092-A/14

PD 20-NOV-2001

PF 10-APR-1998 JP 1998544176

PR 11-APR-1997 US 08/833610

PI DESORAH KNUTSON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI

THURMOND,

PC SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD

C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC







ACCESSION BD092933  
 VERSION BD092933.1 GI:22638544  
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 AUTHORS Knutzen, D., Mukerji, P., Huang, Y. S., Thurmond, J., Chaudhary, S. and Leonard, A. E. Y.  
 TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants  
 JOURNAL Patent: JP 2001527395-A 20 25-DEC-2001; CALGENE LLC ABBOTT LABORATORIES  
 COMMENT PN JP 2001527395-A/20  
 PD 25-DEC-2001  
 PF 10-APR-1998 JP 1998544175  
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 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD  
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RESULT 26

AC084857/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

133683 bp

DNA

linear

HTG 22-NOV-2000

13 unbrordered pieces.

GI:11276215

HTG; HTGS\_PHASE1; HTGS\_DRAFT.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 133683)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Barna,N., Bastien,V., Bada,P., Boguslavskiy,L., Bouckgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heatford,A., Horton,L., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Horton,L., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Minova,I., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisan,C., Pollara,V., Raymond,C., Rieback,M., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zairoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (22-NOV-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smith, A.P.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L11038

Center clone name: 3231\_N5

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

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Db 59880 GGCTGGCTTCACTCTCCCTGAGGCTGCCATTTGGTCCACCTTTTCATAGAGGCGCTGC 59821
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Db 59820 TTTGTTACAAAGCTCGGCTCTCCCTCTGAGCTCGGTTAAGTACCCGAGGCTCTCTTA 59761
QY 2102 AGATGTCCAGGGCCCGAGGCGCGGCGACAGCCAGCCAAACCTTGGGCGCTGGAGAG 2161
Db 59760 AGATGTCCAGGGCCCGAGGCGCGGCGACAGCCAGCCAAACCTTGGGCGCTGGAGAG 59701
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QY 2462 ACGTGGCCCTGCAGGCTGCAGGAGGCACTGGAGCTGGAGGTCTCGTCCCGACCCCTCC 2521
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QY 2522 CCATCTCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2581
Db 59341 CCATCTCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 59282
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Db 59281 CTTTACTGTGTTAAACCTGTTGCTCCAGGATGCATTTCTATAGGAGGGGCGGCGAGGCTG 59222
QY 2642 GSCCTTGTGACAACTGCTGCTTTTACCAATGCGCTTGTGCTCGTGGGCTCTGACTGTACG 2701
Db 59221 GSCCTTGTGACAACTGCTGCTTTTACCAATGCGCTTGTGCTCGTGGGCTCTGACTGTACG 59162
QY 2702 GAGGCGCAGGAGGAGGAGGAGGAGGAGTCTCAGGAGGAGGCTGCCCTGAGGGGCTGG 2761
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QY 2762 GAGGCGTACCTCATGAGGACCAAGGTGTAGCTGTGAGAGAGGAGGAGTGGGGGCTGGAG 2821
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QY 2882 CTGAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2941
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QY 3062 CTGTATGCCCCCGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3121
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QY 3122 TATCATGTTTACTTCCCGACCCCTACATTTTGTGAATAAAATAAGGAATTTTA 3174
Db 58741 TATCATGTTTACTTCCCGACCCCTACATTTTGTGAATAAAATAAGGAATTTTA 58689

RESULT 27
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LOCUS
DEFINITION Homo sapiens clone pDU759j12 chromosome 11 map 11q13, complete
sequence.
ACCESSION AF139813
VERSION AF139813.1 GI:4633837
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 142092)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142092)
Petrushin, K., Koisci, M. J., Bakali, B., Li, W., Xie, G., Marknell, T.,
Sandgren, O., Forsman, K., Holmgren, G., Andreasson, S., Vujic, M.,
Bergan, A. A., McGarty-Dugan, V., Figueroa, D., Austin, C. P.,
Metzger, M. L., Caskey, C. T. and Wadelius, C.
Identification of the gene responsible for Best macular dystrophy
Nat. Genet. 19 (3), 241-247 (1998)
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QY 3002 CCAGGAGGACCTGATCAATGACATCTGGGTTGCCATGCGCAATGCGATGCCCGCCCGACCTA 3061
Db 120496 CCAGGAGGACCTGATCAATGACATCTGGGTTGCCATGCGCAATGCGATGCCCGCCCGACCTA 120437
QY 3062 CTGTATGCCCGGACCGCCGAGGCGAGATGACCCATAGGAGCTGATCGTAATGTT 3121
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QY 3122 TATCATGTTACTTCCCAACCCCTACATCTTTTGAATAAAATAAGGAATTTTA 3174
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RESULT 28
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ACCESSION AC004770.1 GI:3212836
VERSION AC004770
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 185035)
AUTHORS Lamerdin,J.E., McCreedy,P.M., Coleman,M., Skowronski,E., Adamson,A.W., Burkhardt-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stilwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Gaines,J., Danganan,L., Poundstone,P., Christensen,M., Georgescu,A., Avila,J., Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A.S., Montgomery,M., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.
TITLE Sequence analysis of a human BAC containing the FEN1 DNA repair gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 185035)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
REFERENCE 3 (bases 1 to 185035)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
COMMENT On Jun 12, 1998 this sequence version replaced gi:3169154.
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1652..1753
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53074 5'; (339..438); 89% identity.-(1865..1987) AA621878
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IMAGE:1144737; (394..273); 100% identity.-(1910..1987)
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cDNA clone 468915 5'; (79..139); 93%
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cDNA clone 468915 5'; (140..216); 94% identity.-W56243
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3536..3598
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IMAGE:1144737; (134..72); 100% identity.-AA035970
ml70h02.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus
cDNA clone 468915 5'; (217..314); 81%
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QY 2582 CTTACTGTCTTTAACTGTCTGTCCAGATGATCTCTGATAGAGAGGGCGCGCAGGGCTG 2641
Db 13599 CTTACTGTCTTTAACTGTCTGTCCAGATGATCTCTGATAGAGAGGGCGCGCAGGGCTG 13540
QY 2642 GGCCTTGTGACAACTGTGCTTTTCCACCACTGCTTGCCTCGGTGGCCCTGACTGTGAGG 2701
Db 13539 GGCCTTGTGACAACTGTGCTTTTCCACCACTGCTTGCCTCGGTGGCCCTGACTGTGAGG 13480
QY 2702 GAGGGCCAGGGAGGAGAGGGAGGAGTCTCAGAGAGAGCTGCTCCTGAGGGCTGGG 2761
Db 13479 GAGGGCCAGGGAGGAGAGGGAGGAGTCTCAGAGAGAGCTGCTCCTGAGGGCTGGG 13420
QY 2762 GAGGGGTACCTCATGAGGACAGGGGTGGAGTCTGAGAGAGAGAGGAGGGTGGGGCTGGAG 2821
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QY 2822 GTGCTGTGTAGTGGGAGCGGGCAAGTGAAGGGAGGAGGAGGAGTCTCTGGGAGGATC 2881
Db 13359 GTGCTGTGTAGTGGGAGCGGGCAAGTGAAGGGAGGAGGAGGAGTCTCTGGGAGGATC 13300
QY 2882 CTGAGCTGTGTGTGAGTCTAACCACCTAATCAGTCTTGTAGATTCAGGGAGGGCAGGC 2941
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QY 2942 ACCAACAATCAGATGAGGGGCTTTGGGGAGGGCGCTTAGTCCCGCCAGCTCTAAGCAG 3001
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LOCUS Homo sapiens genomic DNA, chromosome 11 clone:RP11-467L20, complete
DEFINITION sequence.
ACCESSION APO02380
VERSION APO02380.3 GI:28189480
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2000)
REFERENCE 2 (bases 1 to 188788)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Jan 31, 2003 this sequence version replaced gi:23821513.
FEATURES Location/Qualifiers

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## ORIGIN

## Query Match

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1721; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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QY 1442 GGGCCCTGCTGGACATCATCAGGTCCCTGAAGAAGTCTGGGAAGCTCTGGCTGAGACCCCTA 1501
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QY 1502 CTTTCAAAATGAAGCCACAGCCCCCGGGACACCGTGGGGAAGGGGTGAGGTGGGGTGA 1561
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| Qy | 1922  | TCAGATGCTCTTTGGGGTTCTATAGGGGACAGGTCCTAGTCTGGGACAGGGCCCTGACCCCTCC | 1981  |
| Db | 95223 | TCAGATGCTCTTTGGGGTTCTATAGGGGACAGGTCCTAGTCTGGGACAGGGCCCTGACCCCTCC | 95282 |
| Qy | 1982  | GGCCTGGCTTCACTCTCCCTCAGCGCTGCCATTGGTCCACCCCTTTCATAGAGAGGGCTGC    | 2041  |
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| Db | 95343 | TTTGTTTAAAGAGCTCGGGTCTCCCTCTCTGACAGTCTGGTTAAGTACCGAGGGCTCTCTTTA  | 95402 |
| Qy | 2102  | AGATGTCCAGGGCCCCAGGCCCGGGGSCACAGCCAGCCCAACCTTGGGCCCTTGGAGAG      | 2161  |
| Db | 95403 | AGATGTCCAGGGCCCCAGGCCCGGGGSCACAGCCAGCCCAACCTTGGGCCCTTGGAGAG      | 95462 |
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| Qy | 2222  | CTCCCCAACTTAGCCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTTGTGACT       | 2281  |
| Db | 95523 | CTCCCCAACTTAGCCTGTGACCTTGGGACCAAGGGGAGTCCCTGCTCTCTTTGTGACT       | 95582 |
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| Db | 95703 | AAAGGCTCTGTTATCAGCTGGGACGTGCCAGCCATCCCTGGCCATTTCGCCCCCAGGGGG     | 95761 |
| Qy | 2462  | ACGTGGGCCCTTGACGGCTGCAGAGGGCACTGAGTCTGGAGGTCTGCTCCAGCCCTCC       | 2521  |
| Db | 95762 | ACGTGGGCCCTTGACGGCTGCAGAGGGCACTGAGTCTGGAGGTCTGCTCCAGCCCTCC       | 95821 |
| Qy | 2522  | CCATCTCGGGGCTGCTGTGTGACGGCGCTGCTCAGGCACATCTCTGTGCTCAACCTGCC      | 2581  |
| Db | 95822 | CCATCTCGGGGCTGCTGTGTGACGGCGCTGCTCAGGCACATCTCTGTGCTCAACCTGCC      | 95881 |
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| Qy | 2642  | GGCCTTGTGACAACTGTGCCCTTTCACACATGGCTTCGCTCGTGGCCCTGACTGTGAGG      | 2701  |
| Db | 95942 | GGCCTTGTGACAACTGTGCCCTTTCACACATGGCTTCGCTCGTGGCCCTGACTGTGAGG      | 96001 |
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| Db | 96062 | GAGGGGTACCTTCATGAGGACACAGGTTGAGCTGAGAGAGAGAGGTGGGGCTGGAG         | 96121 |
| Qy | 2822  | GTGCTGCTAGCTCAGGGGACGGGCAAGTCAGAGGGGAGGGAGGTAAGTCTCTGGGAGGATC    | 2881  |
| Db | 96122 | GTGCTGCTAGCTCAGGGGACGGGCAAGTCAGAGGGGAGGGAGGTAAGTCTCTGGGAGGATC    | 96181 |
| Qy | 2882  | CTGAGCTGCTGTGAGCTTACCCACTAATCAGTCTTAGATTACGGGGAGGGCAGGC          | 2941  |
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VERSION AF000591.3 HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE Homo sapiens 138,627 genomic DNA of 11q13  
JOURNAL Published Only in DataBase (1999)  
REFERENCE 2 (bases 1 to 138627)  
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
Japan (E-mail:hattori@gsc.riken.go.jp,  
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,  
Fax:81-42-778-9924)  
COMMENT On May 31, 2000 this sequence version replaced gi:6997481.

## CENTER

Center: RIKEN Genomic Sciences Center (GSC)  
Center code: RIKEN  
Web site: http://hgp.gsc.riken.go.jp/  
Contact: hattori@gsc.riken.go.jp  
Center project name: HumDraff11  
Center clone name: CMB9-22K5  
----- Summary Statistics  
Sequencing vector: PCR products; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 12298 bases at least Q40  
Consensus quality: 13048 bases at least Q30  
Consensus quality: 134094 bases at least Q20  
Insert size: 135927; sum-of-contigs

Quality coverage: 4.0ix in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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34767 46065 contig of 11299 bp in length
46166 53516 contig of 7351 bp in length
53617 61065 contig of 7449 bp in length
61166 67999 contig of 6833 bp in length
68099 74526 contig of 6428 bp in length
74627 81299 contig of 6673 bp in length
81400 87316 contig of 5917 bp in length
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Sequence updated (26-May-2000).

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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#### FEATURES

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Mukerji,P., Leonard,A.E.Y., Huang,Y.-S. and Parker-Barnes,J.M.

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Db 1141 TGTCTTGGGTTCATAGGGCAGTCTGCTGCGGAGGAGGAGCAGCGGTCCATGGGTGG 1200  
QY 1987 GGTTCACCTCTCCCTGAGCGTGCCTATGGTTCACCTTTTCATAGAGAGGCTGCTTGT 2046  
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QY 2047 TACAAAGTCTCGGTCTCCTCTGAGCTCGGTAACTGAGTACCGAGGCTCTCTTAAGATG 2106  
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QY 2107 TCCAGGGCCCCAGGCCCCGGGCGACAGCCAGCCCAACCTTTGGGCTTGGAGAGTCTCTC 2166  
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QY 2167 CACCCCATCATAGAGTCTGCTGAGCTGGGCTTTCAGCGGCCCATTCACCGGCTCCC 2226  
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QY 2227 CAACTTGAAGCTGTGACCTTGGGACCAAGGGGAGTCCCTCTCTCTTGTGACTCAGCA 2286  
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QY 2287 GAGGAGTGGCCAGCTTTCAGGAGGGGCGCTGGCTTGGAGGCTCAGCCACCTCCAG 2346  
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QY 2347 CTTTTCCTCAGGCTGCTGAGTCTCAGATTCCTGAGCAATCTGACCTTCTCAGAGG 2406  
Db 1561 CTTTTCCTCAGGCTGCTGAGTCTCAGATTCCTGAGCAATCTGACCTTCTCAGAGG 1620  
QY 2407 CTTGTTATCAGCTGGGAGTGGCAGTCCAGCCCAATCCCTGGCCATTTGGCCCCAGGGAGG 2466  
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QY 2467 GGCCTG 2473  
Db 1680 GGCCTG 1686

RESULT 34  
BD082638  
LOCUS  
DEFINITION 1686 bp DNA linear PAT 27-AUG-2002  
Methods and compositions for synthesis of long chain  
poly-unsaturated fatty acids.  
ACCESSION BD082638  
VERSION BD082638.1 GI:22628248  
KEYWORDS JP 2001523091-A/18.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1686)  
AUTHORS Knutson, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and  
Loenard, A.E.Y.  
TITLE Methods and compositions for synthesis of long chain  
poly-unsaturated fatty acids  
JOURNAL Patent: JP 2001523091-A 18 20-NOV-2001;

|   |                          |   |                 |       |  |            |  |  |  |  |
|---|--------------------------|---|-----------------|-------|--|------------|--|--|--|--|
| CALGENE LLC, ABBOTT LABORATORIES                              |                          |   |                 |       |  |            |  |  |  |  |
| COMMENT   | PN                       | JP  | 2001523091-A/18 |       |  |            |  |  |  |  |
|   | PD                       | 20-NOV-2001   |                 |       |  |            |  |  |  |  |
|   | PF                       | 10-APR-1998   | JP              |       |  | 1998544053 |  |  |  |  |
|   | PR                       | 11-APR-1997   | US              |       |  | 08/834655  |  |  |  |  |
|   | PI                       | DEBORAH KNUZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND, |                 |       |  |            |  |  |  |  |
|   | PI                       | SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD                              |                 |       |  |            |  |  |  |  |
|   | PC                       | C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64            | PC              |       |  |            |  |  |  |  |
|   | PC                       | C11B1/00, A61K31/20,  |                 |       |  |            |  |  |  |  |
|   | PC                       | A23L1/30  |                 |       |  |            |  |  |  |  |
|   | CC                       | Strandedness: Single;   |                 |       |  |            |  |  |  |  |
|   | CC                       | Topology: Linear;   |                 |       |  |            |  |  |  |  |
| FEATURES  | Key                      | Location/Qualifiers.  |                 |       |  |            |  |  |  |  |
| source  | 1.                       | .1686   |                 |       |  |            |  |  |  |  |
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|   | /mol_type="genomic DNA"  |   |                 |       |  |            |  |  |  |  |
|   | /db_xref="taxon:32644"   |   |                 |       |  |            |  |  |  |  |
| BASE COUNT  | 322 a                    | 551 c   | 435 g           | 378 t |  |            |  |  |  |  |
| ORIGIN  |                          |   |                 |       |  |            |  |  |  |  |
| Query Match 52.6%; Score 1675; DB 6; Length 1686;             |                          |   |                 |       |  |            |  |  |  |  |
| Best Local Similarity 99.9%; Pred. No. 0;                     |                          |   |                 |       |  |            |  |  |  |  |
| Matches 1686; Conservative 0; Mismatches 0; Indels 1; Gaps 1; |                          |   |                 |       |  |            |  |  |  |  |
| QY  | 787                      | GCACCTTAAGGGTGCCTCGCAACTGTCGAATCATCGCACTTCAGCACACAGCCA                  | 846             |       |  |            |  |  |  |  |
| Db  | 1                        | GCACCTTAAGGGTGCCTCGCAACTGTCGAATCATCGCACTTCAGCACACAGCCA                  | 60              |       |  |            |  |  |  |  |
| QY  | 847                      | AGCCTAACATCTTCCACAGGATCCGATGTGAACATGTCACATGTTTGTCTGGGCG                 | 906             |       |  |            |  |  |  |  |
| Db  | 61                       | AGCCTAACATCTTCCACAGGATCCGATGTGAACATGTCACATGTTTGTCTGGGCG                 | 120             |       |  |            |  |  |  |  |
| QY  | 907                      | AATGGCAGCCATCAGATACGGCAGAGAGAGCTGAATACCTGCGCTTACAAATCACACAGC            | 966             |       |  |            |  |  |  |  |
| Db  | 121                      | AATGGCAGCCATCAGATACGGCAGAGAGAGCTGAATACCTGCGCTTACAAATCACACAGC            | 180             |       |  |            |  |  |  |  |
| QY  | 967                      | ACGAATACCTTCTCTGATGGGCGCGCGCTCTCATCCCATGTATTTTCAGTACCAGA                | 1026            |       |  |            |  |  |  |  |
| Db  | 181                      | ACGAATACCTTCTCTGATGGGCGCGCGCTCTCATCCCATGTATTTTCAGTACCAGA                | 240             |       |  |            |  |  |  |  |
| QY  | 1027                     | TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCGCGCGCTGAGCTACT               | 1086            |       |  |            |  |  |  |  |
| Db  | 241                      | TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTGGCGCGCGCTGAGCTACT               | 300             |       |  |            |  |  |  |  |
| QY  | 1087                     | ACATCGGTTCTTTCATCACTACATCCCTTCTACGGCATCTGGAGCCCTCTCTTTTC                | 1146            |       |  |            |  |  |  |  |
| Db  | 301                      | ACATCGGTTCTTTCATCACTACATCCCTTCTACGGCATCTGGAGCCCTCTCTTTTC                | 360             |       |  |            |  |  |  |  |
| QY  | 1147                     | TCAACTTCATCAGGTTCTCGAGAGCCACTGGTTTGTGGGTACACAGATGAATCACA                | 1206            |       |  |            |  |  |  |  |
| Db  | 361                      | TCAACTTCATCAGGTTCTCGAGAGCCACTGGTTTGTGGGTACACAGATGAATCACA                | 420             |       |  |            |  |  |  |  |
| QY  | 1207                     | TGCTCATGAGATTGACAGAGGCGCTACCGTACGTGGTTCACTAGCAGCTGACGCCA                | 1266            |       |  |            |  |  |  |  |
| Db  | 421                      | TGCTCATGAGATTGACAGAGGCGCTACCGTACGTGGTTCACTAGCAGCTGACGCCA                | 480             |       |  |            |  |  |  |  |
| QY  | 1267                     | CTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTTCAGTGGACACCTTAACTTCCAGA             | 1326            |       |  |            |  |  |  |  |
| Db  | 481                      | CTGCAACGTGGAGCAGTCTTCTTCAACGACTGGTTTCAGTGGACACCTTAACTTCCAGA             | 540             |       |  |            |  |  |  |  |
| QY  | 1327                     | TTGAGCACCATCTTTCGCCACATGCCCCGAGCAACTTACACAGATCCCGCGCTGG                 | 1386            |       |  |            |  |  |  |  |
| Db  | 541                      | TTGAGCACCATCTTTCGCCACATGCCCCGAGCAACTTACACAGATCCCGCGCTGG                 | 600             |       |  |            |  |  |  |  |
| QY  | 1387                     | TGAAGTCTCTATGTGCCAAGCATGGCAATGAAATACAGGAGGCGCTACTGAGGGCCC               | 1446            |       |  |            |  |  |  |  |
| Db  | 601                      | TGAAGTCTCTATGTGCCAAGCATGGCAATGAAATACAGGAGGCGCTACTGAGGGCCC               | 660             |       |  |            |  |  |  |  |
| QY  | 1447                     | TGCTGGACATCATAGGTCCTTGAAGAAGTCTGGGAAGCTGTGGTGGACGCTTACCTTC              | 1506            |       |  |            |  |  |  |  |
| Db  | 661                      | TGCTGGACATCATAGGTCCTTGAAGAAGTCTGGGAAGCTGTGGTGGACGCTTACCTTC              | 720             |       |  |            |  |  |  |  |

|      |  |      |
|------|--|------|
| 1507 | ACAAATGAAGCCACACAGCCCCCGGACACACCGTGGGAAAGGGGTGCAGGTGGGGTGAATGGCC   | 1566 |
| 721  | ACAAATGAAGCCACACAGCCCCCGGACACACCGTGGGAAAGGGGTGCAGGTGGGGTGAATGGCC   | 780  |
| 1567 | AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGCTGGTGTATGCACTGCTCA   | 1626 |
| 781  | AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGCTGGTGTATGCACTGCTCA   | 840  |
| 1627 | CGGACCCCATGTTGATCTTTCTCCCTTTTCCTCTCTCTTTCT |      |

RESULT 35  
BD082653  
LOCUS

BD082653 1686 bp DNA linear PAT 27-AUG-2002

|                       |  |
|-----------------------|--|
| DEFINITION            | Methods and compositions for synthesis of long chain   |
| ACCESSION             | polyunsaturated fatty acids.   |
| VERSION               | BD082653   |
| KEYWORDS              | BD082653.1 GI:22628263   |
| SOURCE                | JP 2001523092-A/13.  |
| ORGANISM              | unidentified   |
| REFERENCE             | unclassified.  |
| AUTHORS               | 1 (bases 1 to 1686)  |
| TITLE                 | Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.   |
| JOURNAL               | Methods and compositions for synthesis of long chain   |
| COMMENT               | polyunsaturated fatty acids<br>Patent: JP 2001523092-A 13 20-NOV-2001;<br>CALGENE LLC, ABBOTT LABORATORIES<br>PN JP 2001523092-A/13<br>PD 20-NOV-2001<br>PF 10-APR-1998 JP 1998544176<br>PR 11-APR-1997 US 08/833610<br>PI DEBORAH KNUZZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND.<br>PI SUNITA CHAUDHARY, AVANDA EUN YEONG LEONARD<br>PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/PC 30, A23K1/00<br>CC Strandedness: Single;<br>CC Topology: Linear;<br>FH Key Location/Qualifiers. |
| FEATURES              | Location/Qualifiers.   |
| source                | 1..1686<br>/organism="unidentified"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:32644"   |
| BASE COUNT            | 322 a 551 c 435 g 378 t  |
| ORIGIN                |  |
| Query Match           | 52.6%; Score 1675; DB 6; Length 1686;  |
| Best Local Similarity | 99.9%; Pred. No. 0;  |
| Matches 1686;         | Conservative 0; Mismatches 0; Indels 1; Gaps 1;  |
| QY 787                | GCCACTTAAAGGGTGCCCTCCCAACTGGTGGATCATGCCACTTCACGACCAAGCCCA 846  |
| DB 1                  | GCCACTTAAAGGGTGCCCTCCCAACTGGTGGATCATGCCACTTCACGACCAAGCCCA 60   |
| QY 847                | AGCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACGTGTGTTGTTCTGGCG 906   |
| DB 61                 | AGCCTAACATCTTCCACAAGGATCCGATGTGAACATGCTGACGTGTGTTGTTCTGGCG 120   |
| QY 907                | AATGCGACCCATCGAGTACGGCAAGAGAGAGCTGAAATACCTGCCCTCAATCAACAGC 966   |
| DB 121                | AATGCGACCCATCGAGTACGGCAAGAGAGAGCTGAAATACCTGCCCTCAATCAACAGC 180   |
| QY 967                | ACGAATACCTTCTTCTGATTGGGCGCGCGTGTCTATCCCTCATGTATTTCCAGTACCAGA 1026  |
| DB 181                | ACGAATACCTTCTTCTGATTGGGCGCGCGTGTCTATCCCTCATGTATTTCCAGTACCAGA 240   |
| QY 1027               | TCATCATGACCATATGCTGCATPAAGAACTGGGTGACCTGGCGTGGCGCGTCACTACT 1086  |
| DB 241                | TCATCATGACCATATGCTGCATPAAGAACTGGGTGACCTGGCGTGGCGCGTCACTACT 300   |
| QY 1087               | ACATCCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTTGGAGGCCCTCTTTTC 1146   |
| DB 301                | ACATCCCGGTCTTTCATCACCTACATCCCTTTCTACGGCATCTTGGAGGCCCTCTTTTC 360  |
| QY 1147               | TCACATTCATCAGTTCTCTGAGAGGCCACTGGTTGTGGGTACACAGATGAATCACA 1206  |
| DB 361                | TCACATTCATCAGTTCTCTGAGAGGCCACTGGTTGTGGGTACACAGATGAATCACA 420   |
| QY 1207               | TCGTCATGGAGATTGACAGAGGCCCTACCGTGCATGTTTCACTAGCCAGCTCAGACCA 1266  |
| DB 421                | TCGTCATGGAGATTGACAGAGGCCCTACCGTGCATGTTTCACTAGCCAGCTCAGACCA 480   |
| QY 1267               | CTTGCAACGTTGGAGCACTCCTTCTTCAACGACTGGTTCACTGAGACACCTTAACCTCCAGA 1326  |
| DB 481                | CTTGCAACGTTGGAGCACTCCTTCTTCAACGACTGGTTCACTGAGACACCTTAACCTCCAGA 540   |
| QY 1327               | TTGAGCACCACTCTTCCCCACCATCCCGGCACAACTTACACAAAGATCGCCCGCTGG 1386   |
| DB 541                | TTGAGCACCACTCTTCCCCACCATCCCGGCACAACTTACACAAAGATCGCCCGCTGG 600  |
| QY 1387               | TGAAGTCTCTATGTGCAAGCATGGCAATTAATACAGAGAGCGCTACTTGAGGGCCC 1446  |
| DB 601                | TGAAGTCTCTATGTGCAAGCATGGCAATTAATACAGAGAGCGCTACTTGAGGGCCC 660   |
| QY 1447               | TGCTGACATCATACAGTCCCTGAAGAGCTGTGGGAAGCTGTGGGTGGAGCGCTACTTTC 1506   |
| DB 661                | TGCTGACATCATACAGTCCCTGAAGAGCTGTGGGAAGCTGTGGGTGGAGCGCTACTTTC 720  |
| QY 1507               | ACAAATGAAGCACACCGCCCGGCACACCGTGGGAGGGGTGCAGTGGGTGATGGCC 1566   |
| DB 721                | ACAAATGAAGCACACCGCCCGGCACACCGTGGGAGGGGTGCAGTGGGTGATGGCC 780  |
| QY 1567               | AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGTGTATGCACTGCTCA 1626  |
| DB 781                | AGAGGAATGATGGGCTTTTGTCTGAGGGGTGTCCGAGAGGCTGTGTATGCACTGCTCA 840   |
| QY 1627               | CGACCCCATGTGGATCTTCTCCCTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1686  |
| DB 841                | CGACCCCATGTGGATCTTCTCCCTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900   |
| QY 1687               | ATAGCACCCCTGCCCTCATGGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGGCC 1746  |
| DB 901                | ATAGCACCCCTGCCCTCATGGGACCTGCCCTCCCTCAGCGCTCAGCCATCAGCCATGGCC 960   |
| QY 1747               | TCCAGTGGCTCTAGCCCTTCTTCCAGAGAGCAGAGGTGGCCACCGGGGTGGCTC 1806  |
| DB 961                | TCCAGTGGCTCTAGCCCTTCTTCCAGAGAGCAGAGGTGGCCACCGGGGTGGCTC 1020  |
| QY 1807               | TGTCTACCTCCACTCTCTGCCCTTAAAGATGGGAGAGACCGAGGGTCCATGCTCTCG 1866   |
| DB 1021               | TGTCTACCTCCACTCTCTGCCCTTAAAGATGGGAGAGACCGAGGGTCCATGCTCTCG 1080   |
| QY 1867               | CTGTGAGTCTCCCTTTCAGGCTGGTCACTAGGATCACCCCGCTTGTGTTCTTCA 1926  |
| DB 1081               | CTGTGAGTCTCCCTTTCAGGCTGGTCACTAGGATCACCCCGCTTGTGTTCTTCA 1140  |
| QY 1927               | TGCTCTTGGGTTTATAGGGCAGTCTCTAGTGGGAGGGGCTTACCCCTCCCGGCT 1986  |
| DB 1141               | TGCTCTTGGGTTTATAGGGCAGTCTCTAGTGGGAGGGGCTTACCCCTCCCGGCT 1200  |
| QY 1987               | GGCTTCACTCTCCCTGACGGCTGCCATTTGTCTCCACCTTTTCATAGAGAGGCTCTGTTGT 2046   |
| DB 1201               | GGCTTCACTCTCCCTGACGGCTGCCATTTGTCTCCACCTTTTCATAGAGAGGCTCTGTTGT 1260   |
| QY 2047               | TACAAAGCTCGGGTCTCCCTCCTGAGCTCGGTTAAGTACCGAGGCTCTCTTAAGATG 2106   |
| DB 1261               | TACAAAGCTCGGGTCTCCCTCCTGAGCTCGGTTAAGTACCGAGGCTCTCTTAAGATG 1320   |
| QY 2107               | TCCAGGGCCCAAGGCCCGCGGCGCACAGCCAGCCCAAACTTTGGGCTTGGAGAGTCCCT 2166   |
| DB 1321               | TCCAGGGCCCAAGGCCCGCGGCGCACAGCCAGCCCAAACTTTGGGCTTGGAGAGTCCCT 1380   |
| QY 2167               | CACCCCATCACTAGAGTCTCTGACCTTGGGCTTTCAGGGGCCCATTCACCGCTCCC 2226  |
| DB 1381               | CACCCCATCACTAGAGTCTCTGACCTTGGGCTTTCAGGGGCCCATTCACCGCTCCC 1440  |
| QY 2227               | CAACTTGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTTCGCTCTCTTGTGACTCAGCA 2286   |
| DB 1441               | CAACTTGAGCTGTGACCTTGGGACCAAGGGGAGTCCCTTCGCTCTCTTGTGACTCAGCA 1500   |
| QY 2287               | GAGGAGTGGCCAGTTTCAGGGAGGGGCGCGCTGGCTTGAGGCTCAGCCACCTCCAG 2346  |
| DB 1501               | GAGGAGTGGCCAGTTTCAGGGAGGGGCGCGCTGGCTTGAGGCTCAGCCACCTCCAG 1560  |
| QY 2347               | CTTTCTCTCAGGGTGTCTGAGGTCCAAAGATTCTGGAGCAATCTGACCTCTTCCAAAGG 2406   |

|                       |   |  |                    |
|-----------------------|---|--|--------------------|
| Dd                    | 1561  | CTTTCTCCTCAGGGTGCTCTGAGGTCCAAAGATCTCTGGAGCAATCTGAGACCAATCTGACCCCTTCTCAAAGG | 1620               |
| Qy                    | 2407  | CTCTGTTATCATGCTGGGCAGTGCACGCAATCCCTGGCCATTTGGCCCCAGGGGACGTG                | 2466               |
| Dd                    | 1621  | CTCTGTTATCATGCTGGGCAGTGCACGCAATCCCTGGCCATTTGGCCCCA-GGGACGTG                | 1679               |
| Qy                    | 2467  | GGCCCTG 2473   |                    |
| Dd                    | 1680  | GGCCCTG 1686   |                    |
| RESULT 36             |   |  |                    |
| LOCUS                 | BD092932  |  |                    |
| DEFINITION            | 1886 bp DNA linear PAT 27-AUG-2002  |  |                    |
| ACCESSION             | BD092932  |  |                    |
| VERSION               | BD092932.1 GI:22638543  |  |                    |
| KEYWORDS              | JP 2001527395-A/19.   |  |                    |
| SOURCE                | synthetic construct   |  |                    |
| ORGANISM              | artificial sequences.   |  |                    |
| REFERENCE             | 1 (bases 1 to 1686)   |  |                    |
| AUTHORS               | Knutzon, D., Mukerji, P., Huang, Y. S., Thurmond, J., Chaudhary, S. and Leonard, A. E. Y.   |  |                    |
| TITLE                 | Methods and compositions for synthesis of long chain  |  |                    |
| JOURNAL               | polyunsaturated fatty acids in plants   |  |                    |
| COMMENT               | Patent: JP 2001527395-A 19 25-DEC-2001;<br>CALGENE LLC, ABBOTT LABORATORIES<br>PN JP 2001527395-A/19<br>PD 25-DEC-2001<br>PF 10-APR-1998 JP 1998544175<br>PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR<br>11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI<br>DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI<br>THURMOND,<br>PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD<br>PC<br>C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC<br>30, A23K1/00<br>CC Strandedness: Single;<br>CC Topology: Linear;<br>FH Key Location/Qualifiers<br>1. .1686<br>/organism="synthetic construct"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:32630"<br>BASE COUNT 322 a 551 c 435 g 378 t<br>ORIGIN |  |                    |
| Query Match           | 52.6%   | Score 1675;  | DB 6; Length 1686; |
| Best Local Similarity | 99.9%   | Pred. No. 0;   |                    |
| Matches 1686;         | Conservative 0;   | Mismatches 0;  | Indels 1; Gaps 1;  |
| Qy                    | 787   | GCACCTTAAAGGGTGCTCTGCGCAACGTGGTGAATCATCGCCACTTCGACGACACGACCA               | 845                |
| Dd                    | 1   | GCCACTTAAGGGTGCTCTGCGCAACGTGGTGAATCATCGCCACTTCGACGACACGACCA                | 60                 |
| Qy                    | 847   | AGCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTGTTTGTCTTGGCG                 | 906                |
| Dd                    | 61  | AGCCTAACATCTTCCCAAGGATCCCGATGTGAACATGCTGCACGTGTTTGTCTTGGCG                 | 120                |
| Qy                    | 907   | AATGGGAGCCCATCGAGTAGCGGAGAGAGAGCTGAATACCTGCCCTCAATCACGAC                   | 966                |
| Dd                    | 121   | AATGGGAGCCCATCGAGTAGCGGAGAGAGAGCTGAATACCTGCCCTCAATCACGAC                   | 180                |
| Qy                    | 967   | ACGAATACTCTTCTCCTGATTGGGCGCGCTGCTCATCCCCCATGTATTTCCAGTACCAGA               | 1026               |
| Dd                    | 181   | ACGAATACTCTTCTCCTGATTGGGCGCGCTGCTCATCCCCCATGTATTTCCAGTACCAGA               | 240                |
| Qy                    | 1027  | TCATCATGACCATGATCGTCCATAGAACTGGGTGGACCTTGGGCTGGCGCTGAGTACT                 | 1086               |



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RESULT 38
BC009011
LOCUS
DEFINITION
Homo sapiens, fatty acid desaturase 2, clone MGC:17124
IMAGE:4181037, mRNA, complete cds.

ACCESSION
BC009011
VERSION
BC009011.1 GI:14290485
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strasbourg, R.
Direct Submission
Submitted (30-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 12 Row: k Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4406527.
FEATURES
Location/Qualifiers
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MYFQIIMTIVHNKNDLAWANSYIRFFITIPFYGILGALLFNIRFLSHWF
VWVTQMNHVMEIQEAYRDFSSQLTATCNVEQSFNDMFSFGLNFQIEHQ"

BASE COUNT
372 a 504 c 455 g 365 t
ORIGIN
Query Match 39.0%; Score 1242.6; DB 9; Length 1696;
Best Local Similarity 99.7%; Pred. No. 3.2e-253;
Matches 1245; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

98 CTGCACACACCGCTGGGAGGAGCGCTCTGTGCAGCAGCAGCGCGCGGAGGCGG 147

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1 CCACACACACCGCTGGGAGGAGCGCTCTGTGCAGCAGCAGCGCGCGGAGGCGG 60
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61 CAGTCACCGGGCGTCACAGTCGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
208 GGCGCCGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 267
121 GGCGCCGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
268 ACCTGCGCACCGACACTGGGCTGCTCATTCAGCGGAGGAGGAGGAGGAGGAGGAG 327
181 ACCTGCGCACCGACAGGTGGTGGTCAATTCAGCGGAGGAGGAGGAGGAGGAGGAG 240
328 CCATCCAGCACCGCGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 387
241 CCATCCAGCACCGCGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
388 ATGCTTTCGCGGCTTCCACCTGACCTGGAAATTCGTGGGCAAGTTCCTTGAACCCCTGC 447
301 ATGCTTTCGCGGCTTCCACCTGACCTGGAAATTCGTGGGCAAGTTCCTTGAACCCCTGC 360
448 TGATTGGTGAACCTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 507
361 TGATTGGTGAACCTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
508 CTGAGGACTTCCGCGGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 567
421 CTGAGGACTTCCGCGGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
568 ACCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 627
481 ACCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
628 CTCTCTTCTACTTTGGCAATGGCTGATTCCTACCTCTCTCTCTCTCTCTCTCTCT 687
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688 CTTCTCAGGCCCMAGCTGGATGGCTGCAACATGATTAATGCGCACCTGTCTGTCTACAGAA 747
601 CTTCTCAGGCCCMAGCTGGATGGCTGCAACATGATTAATGCGCACCTGTCTGTCTACAGAA 660
748 AACCCAAAGTGGAAACACCTTGTCCACAAATTCGTGATTCGGCCACTTAAGGGGTGCTCTG 807
661 AACCCAAAGTGGAAACACCTTGTCCACAAATTCGTGATTCGGCCACTTAAGGGGTGCTCTG 720
808 CCAACTGGTGGAAATCATCGCCACTTCCAGCACCAAGCCCAAGCTTAACATCTTCCACAAGG 867
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841 GCAAGAAGAAGCTGAAATACCTGCCCTCAATACACAGCAGCAATACCTTCTCTGATGG 900
988 GGCGCGCGCTGCTCATCCCCATGATTTCCAGTACAGATCATCATGACCATGATGCTCC 1047
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1108 ACATCCCTTCTACGGCATCTGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1167
1021 ACATCCCTTCTACGGCATCTGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
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QY 1192 CACAGATGAATCAGATCGTCTATGGAGATTGACAGAGGAGGCTACCGTGACTGGTTTCAGTA 1251  
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QY 1087 CACAGATGAACCACTTGTCTATGGAGATTGATCTTGATCACTACCGGAGCTGGTTTCAGCA 1146  
Db |||||  
QY 1252 GCCAGCTGACAGCCACCTGCAACGTTGGAGCAGTCTCTTCTTCAACGACTGGTTTCAGTGGAC 1311  
Db |||||  
QY 1147 GCCAGCTGGCAGCCACCTGCAATGTGGAGCAGTCTCTTCTTCAATGACTGGTTTCAGCGGC 1206  
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QY 1312 ACCTTAATTCAGATTGAGCAGCACCCTCTTCCCAACCATGCCCCGGCAGCAACTTACACA 1371  
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QY 1207 ACCTCAATTTCCAGATTGAGCAGCACCCTCTTCCCACTATGCCACGTCAACACCTGCACA 1266  
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QY 1372 AGATCGCCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCATTGAATACCAGGAGAGC 1431  
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QY 1267 AGATGCCCCACTGGTGAAGTCTCTCTGCGCAAGCATGGCATTGAATACCAGGAGAGC 1326  
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QY 1432 CGTACTGAGGCGCCTGTGGACATCATCAGTCCCTGAAGAAGTCTGGGAAGCTGTGGC 1491  
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QY 1327 CGTTGCTGAGGCGCCTGTGACATTTGACATTTGAGTTCACTCAAGAAGTCTGGGAGCTGTGGC 1386  
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QY 1492 TGGAGCCTTACTTACAAATGAGCCACAGCCCGCGGACACCGTGGGAAGGGGTGCA 1551  
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QY 1552 GGTGGGGTGATGGCCAGA-GGAATGATGGGCTTTTGTTCGAGGGGTGTCCGAGAGGCTG 1610  
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QY 1447 TGTTGGGTGACAGCCAGAGGAGGGGGCTTTTGTTCGAGGGTTCTCATGAGACTG 1506  
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Search completed: December 10, 2003, 15:11:08  
Job time : 7626 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 10:17:36 ; Search time 21 seconds  
(without alignments)  
894.572 Million cell updates/sec

Title: US-09-719-601-5  
Perfect score: 2438  
Sequence: 1 MGKGNQGEAAREVSVPVPT.....DIIRSLKSGKWLWDVILHK 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/aa/5A COMB.pcp:\*  
2: /cgn2\_6/ptodata/1/aa/5B COMB.pcp:\*  
3: /cgn2\_6/ptodata/1/aa/6A COMB.pcp:\*  
4: /cgn2\_6/ptodata/1/aa/6B COMB.pcp:\*  
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6: /cgn2\_6/ptodata/1/aa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description      |
|------------|--------|-------------|--------|----|------------------|
| 1          | 1940.5 | 79.6        | 432    | 4  | US-09-439-261-9  |
| 2          | 1940.5 | 79.6        | 432    | 4  | US-09-227-613-9  |
| 3          | 1940.5 | 79.6        | 465    | 4  | US-09-439-261-40 |
| 4          | 1940.5 | 79.6        | 465    | 4  | US-09-227-613-38 |
| 5          | 1628.5 | 66.8        | 356    | 4  | US-09-439-261-19 |
| 6          | 1628.5 | 66.8        | 356    | 4  | US-09-227-613-18 |
| 7          | 1560.5 | 64.0        | 445    | 4  | US-09-048-888-1  |
| 8          | 1515   | 62.1        | 444    | 4  | US-09-048-888-3  |
| 9          | 1508   | 61.9        | 444    | 4  | US-09-439-261-11 |
| 10         | 1508   | 61.9        | 444    | 4  | US-09-227-613-12 |
| 11         | 1508   | 61.9        | 445    | 4  | US-09-439-261-39 |
| 12         | 1508   | 61.9        | 445    | 4  | US-09-439-261-45 |
| 13         | 1493.5 | 61.3        | 444    | 4  | US-09-439-261-43 |
| 14         | 1493.5 | 61.3        | 444    | 4  | US-09-227-613-42 |
| 15         | 1128   | 46.3        | 360    | 4  | US-09-439-261-41 |
| 16         | 1128   | 46.3        | 360    | 4  | US-09-227-613-39 |
| 17         | 1103   | 45.2        | 287    | 4  | US-09-439-261-13 |
| 18         | 1103   | 45.2        | 287    | 4  | US-09-227-613-14 |
| 19         | 1103   | 45.2        | 288    | 4  | US-09-439-261-14 |
| 20         | 1103   | 45.2        | 288    | 4  | US-09-439-261-16 |
| 21         | 1103   | 45.2        | 288    | 4  | US-09-439-261-18 |
| 22         | 1103   | 45.2        | 288    | 4  | US-09-227-613-15 |
| 23         | 909.5  | 37.3        | 347    | 4  | US-09-439-261-42 |
| 24         | 909.5  | 37.3        | 347    | 4  | US-09-227-613-40 |
| 25         | 784    | 32.2        | 219    | 4  | US-09-439-261-20 |
| 26         | 784    | 32.2        | 219    | 4  | US-09-227-613-19 |
| 27         | 587.5  | 24.1        | 182    | 4  | US-09-439-261-21 |

28 587.5 24.1 182 4 US-09-227-613-20 Sequence 20, Appl  
29 502 20.6 131 2 US-08-834-655-9 Sequence 9, Appl  
30 502 20.6 131 3 US-08-834-033A-10 Sequence 10, Appl  
31 502 20.6 131 3 US-09-363-574-9 Sequence 9, Appl  
32 502 20.6 131 4 US-09-363-526-9 Sequence 9, Appl  
33 496 20.3 143 2 US-08-834-655-11 Sequence 11, Appl  
34 496 20.3 143 3 US-08-834-033A-12 Sequence 12, Appl  
35 496 20.3 143 3 US-09-363-574-11 Sequence 11, Appl  
36 496 20.3 143 4 US-09-363-526-11 Sequence 11, Appl  
37 459 18.8 457 2 US-08-834-655-2 Sequence 2, Appl  
38 459 18.8 457 3 US-08-834-033A-2 Sequence 2, Appl  
39 459 18.8 457 3 US-09-363-574-2 Sequence 2, Appl  
40 459 18.8 457 4 US-09-363-526-2 Sequence 2, Appl  
41 459 18.8 457 4 US-09-330-235-18 Sequence 18, Appl  
42 459 18.8 458 4 US-09-439-261-10 Sequence 10, Appl  
43 459 18.8 458 4 US-09-439-261-44 Sequence 44, Appl  
44 459 18.8 458 4 US-09-227-613-11 Sequence 11, Appl  
45 459 18.8 458 4 US-09-227-613-41 Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-439-261-9  
; Sequence 9, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; TYPE: PRT  
; LENGTH: 432  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (432)...(432)  
; OTHER INFORMATION: Xaa = Unknown or other at position 432  
US-09-439-261-9

Query Match 79.6%; Score 1940.5; DB 4; Length 432;  
Best Local Similarity 81.8%; Pred. No. 1-2e-207;  
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;  
Qy 19 PT---FSWEIQHNURDTSGLVIDRKYNITKMSIQHPGQGVICHYAGEDATDAFRAF 75  
Db 3 PTPRYTDEVAQRSGCEERWLVIDRKYNISSEFTRRHFGGSRVISHYAGQDATDPFVAF 62  
Qy 76 HPDLRFVGKFLKLLIGELAPPEPSODHGKSKITEDFRALKTAEDNNLKTNNHVFLL 135  
Db 63 HINKGLVKYMSLLIGELSPQPSPEPTKNKELTDEFRELATVERMGLMKANHVFFLL 122  
Qy 136 LLAHIIALDSIAWFTVYFGNGWIFLITAFVLATSQAQAGWLQHDYGHLSYVRKPKWNH 195  
Db 123 YLLHILLDGAAWLTWVFGTSFLPFLLCVLLSAVQAQAGWLQHDYGHLSYVRKPKWNH 182  
Qy 196 LVHKFVYGHLCASANNWNRHFFQHAKENIFHKOPDNNMLHVFVLGEWQPIEYKCKLK 255  
Db 183 LVHKFVYGHLCASANNWNRHFFQHAKENIFHKOPDNNMLHVFVLGEWQPIEYKCKLK 242

QY 256 YLPYNHQHEFFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAVSYIRFFITIPFYG 315  
DB 243 YLPYNHQHEFFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAVSYIRFFITIPFYG 302  
QY 316 ILGALLFLNFIRESLHFWVWVQNMHI VMEIDOEAYRDWFSQLTATCNVEQSFNDWF 375  
DB 303 ILGALLFLNFIRESLHFWVWVQNMHI VMEIDOEAYRDWFSQLTATCNVEQSFNDWF 362  
QY 376 SCHLNFOIEHLLPFTMPRHNLKIAPLVKSCLKAGHIEYQEKPLLRALLDIIRSLKXSGK 435  
DB 363 SCHLNFOIEHLLPFTMPRHNLKIAPLVKSCLKAGHIEYQEKPLLRALLDIIRSLKXSGK 422  
QY 436 LWLDAYLHK 444  
DB 423 LWLDAYLHK 431

## RESULT 2

US-09-227-613-9  
; Sequence 9, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295, US P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 432 is unknown or other.  
US-09-227-613-9

Query Match 79.6%; Score 1940.5; DB 4; Length 432;  
Best Local Similarity 81.8%; Pred. No. 1.2e-207;  
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

QY 19 PT---FSWEEIQKHLNLTDSGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATDAFRAF 75  
DB 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHGPGSRVISHYAGQDATDPFVAF 62  
QY 76 HPDLEFVKGKFLKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADMLFKTNHVFLL 135  
DB 63 HINKGLVKYKYNLSLIGELSPQSPFPTKNKELTDEFRELRAVVERMGLMKANHVFFLL 122  
QY 136 LLAHIIALESIAFTVYFGNGWIPITLITAFVLTSAQAQAGWLQHDYGHLSVYRKPKNH 195  
DB 123 YLLHILLDGAAMLTLVFGTSLPFLLCVLLSAVQAQAGWLQHDYGHLSVYRKPKNH 182  
QY 196 LVHKFVIGHLKGASANNWNRHFOHAKPNI FHKDPDVMNMLHVFLVGEWQPIEYGGKKLK 255  
DB 183 LVHKFVIGHLKGASANNWNRHFOHAKPNI FHKDPDVMNMLHVFLVGEWQPIEYGGKKLK 242  
QY 256 YLPYNHQHEFFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAVSYIRFFITIPFYG 315  
DB 243 YLPYNHQHEFFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAVSYIRFFITIPFYG 302  
QY 316 ILGALLFLNFIRESLHFWVWVQNMHI VMEIDOEAYRDWFSQLTATCNVEQSFNDWF 375  
DB 303 ILGALLFLNFIRESLHFWVWVQNMHI VMEIDOEAYRDWFSQLTATCNVEQSFNDWF 362  
QY 376 SCHLNFOIEHLLPFTMPRHNLKIAPLVKSCLKAGHIEYQEKPLLRALLDIIRSLKXSGK 435  
DB 363 SCHLNFOIEHLLPFTMPRHNLKIAPLVKSCLKAGHIEYQEKPLLRALLDIIRSLKXSGK 422

QY 436 LWLDAYLHK 444  
DB 423 LWLDAYLHK 431  
RESULT 3  
US-09-439-261-40  
; Sequence 40, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295, US P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (432)...(432)  
; OTHER INFORMATION: Xaa = Unknown or other at position 432  
; NAME/KEY: VARIANT  
; LOCATION: (459)...(459)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-09-439-261-40

Query Match 79.6%; Score 1940.5; DB 4; Length 465;  
Best Local Similarity 81.8%; Pred. No. 1.3e-207;  
Matches 351; Conservative 31; Mismatches 44; Indels 3; Gaps 1;

QY 19 PT---FSWEEIQKHLNLTDSGLVIDRKVYNITKWSIQHPGQGVIGHYAGEDATDAFRAF 75  
DB 3 PTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHGPGSRVISHYAGQDATDPFVAF 62  
QY 76 HPDLEFVKGKFLKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADMLFKTNHVFLL 135  
DB 63 HINKGLVKYKYNLSLIGELSPQSPFPTKNKELTDEFRELRAVVERMGLMKANHVFFLL 122  
QY 136 LLAHIIALESIAFTVYFGNGWIPITLITAFVLTSAQAQAGWLQHDYGHLSVYRKPKNH 195  
DB 123 YLLHILLDGAAMLTLVFGTSLPFLLCVLLSAVQAQAGWLQHDYGHLSVYRKPKNH 182  
QY 196 LVHKFVIGHLKGASANNWNRHFOHAKPNI FHKDPDVMNMLHVFLVGEWQPIEYGGKKLK 255  
DB 183 LVHKFVIGHLKGASANNWNRHFOHAKPNI FHKDPDVMNMLHVFLVGEWQPIEYGGKKLK 242  
QY 256 YLPYNHQHEFFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAVSYIRFFITIPFYG 315  
DB 243 YLPYNHQHEFFLLIGPPLIPMYFOYQIIMTIVHKNWVDLAWAVSYIRFFITIPFYG 302  
QY 316 ILGALLFLNFIRESLHFWVWVQNMHI VMEIDOEAYRDWFSQLTATCNVEQSFNDWF 375  
DB 303 ILGALLFLNFIRESLHFWVWVQNMHI VMEIDOEAYRDWFSQLTATCNVEQSFNDWF 362  
QY 376 SCHLNFOIEHLLPFTMPRHNLKIAPLVKSCLKAGHIEYQEKPLLRALLDIIRSLKXSGK 435  
DB 363 SCHLNFOIEHLLPFTMPRHNLKIAPLVKSCLKAGHIEYQEKPLLRALLDIIRSLKXSGK 422  
QY 436 LWLDAYLHK 444



OTHER INFORMATION: Xaa at position 320 is unknown or other.  
US-09-227-613-18

Query Match 66.8%; Score 1628.5; DB 4; Length 356;  
Best Local Similarity 99.7%; Pred. No. 5.6e-173;  
Matches 293; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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DB 1 VFYFNGMPTLITAFVLTATSAQAAGLQHDYGLSVYRKPNHVLHVKFVIGHLKASA 60  
QY 211 NWNHRRHFQHAHAKPNI FHKPDVNNMLHVFLGEMQPIEYGGKKLKYLPYNHQQHEFFLIG 270  
DB 61 NWNHRRHFQHAHAKPNI FHKPDVNNMLHVFLGEMQPIEYGGKKLKYLPYNHQQHEFFLIG 120  
QY 271 PLLLPMTYFOYQIIMTMIVHKNWDLAWAVSYIRFFIT-IPFYGILGALLFLNFIRFLE 330  
DB 121 PLLLPMTYFOYQIIMTMIVHKNWDLAWAVSYIRFFIT-IPFYGILGALLFLNFIRFLE 179  
QY 331 SHWFVMTOMNHVMEIDQAYRDFWSSQLTATCNVEQSFNDWFSGLNFQIEHHLPPT 390  
DB 180 SHWFVMTOMNHVMEIDQAYRDFWSSQLTATCNVEQSFNDWFSGLNFQIEHHLPPT 239  
QY 391 MPRHNLKTAPLVKSICAKHGIEYQEKPLLRALLDIIRSLKSGKGLMDAYLHK 444  
DB 240 MPRHNLKTAPLVKSICAKHGIEYQEKPLLRALLDIIRSLKSGKGLMDAYLHK 293

RESULT 7

US-09-048-888-1  
Sequence 1, Application US/09048888  
Patent No. 6492108  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/048,888  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0494 US  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: ENDANOT01

CLONE: 2451043  
US-09-048-888-1

Query Match 64.0%; Score 1560.5; DB 4; Length 445;  
Best Local Similarity 62.3%; Pred. No. 3e-165;  
Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;  
QY 1 MGGKGNQG--EGAAAREVSVPFTFSWBEIQKNLRLDGLVIDRKVYNITKNSIQHPGGOR 58  
DB 1 MGGVGEPGREGAQPAGPLTFCEWQIRAHQDPQDKWLVIRRVVVISRWQRHPGGSR 60  
QY 59 VIGHYAGEDATDAFRAHPDLEFVGKFLKPLIGELABEPPSOHQKSKITEDRALAK 118  
DB 61 LIGHGAEDATDAFRAHQDLNFRKFLQPLIGELABEPPSOHQKSKITEDRALAK 120  
QY 119 TADNMLFKTNHVFLLLAHIALESIAWFTVFYFGNGWIPTLITAFVLTATSAQAAGWL 178  
DB 121 AEDMKLPDASPTFFAFLLGHILAMEVLAWLLIYLLGPGWPSALAAFIATSAQSWCL 180  
QY 179 QHDYGHLSVYRKPNHVLHVKFVIGHLKASANNWNRHFFQHAHAKPNI FHKPDVNNMLHV 238  
DB 181 QHDLGHASIFKKSNNHVAQKFMGQKGFSAHNNFRHFFQHAHAKPNI FHKPDVNVAPV 240  
QY 239 FVLGEMQPIEYGGKKLKYLPYNHQQHEFFLIGPPLIIPMYFOYQIIMTMIVHKNWVDLAW 298  
DB 241 FLIGE--SSVEYGGKKRYPYNQOHLFFLIGPPLIIPMYFOYQIIMTMIVHKNWVDLAW 299  
QY 299 AVSYIRFFIT-IPFYGILGALLFLNFIRFLESHVFWVTOMNHVMEIDQAYRDFWSS 358  
DB 300 AASFYARFSLYLPFYGVFVLLFFVAVRVLESHVFWVTOMNHVMEIDQAYRDFWSS 359  
QY 359 QLTATCNVEQSFNDWFSGLNFQIEHHLPPTMPRHNLKTAPLVKSICAKHGIEYQEK 418  
DB 360 QLTATCNVEQSFNDWFSGLNFQIEHHLPPTMPRHNLKTAPLVKSICAKHGIEYQEK 419  
QY 419 LRLALLDIIRSLKSGKGLMDAYLHK 444  
DB 420 FLTALVDIVRSLKSGDMDLADYLHQ 445

RESULT 8

US-09-048-888-3  
Sequence 3, Application US/09048888  
Patent No. 6492108  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/048,888  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C.  
REGISTRATION NUMBER: 39,132

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/ REFERENCE/DOCKET NUMBER: PF-0494 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BSPINOT01
/ CLONE: 2056310
/
US-09-048-889-3

Query Match
Best Local Similarity 62.1%; Score 1515; DB 4; Length 444;
Matches 272; Conservative 62; Mismatches 99; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKNLRTDGLVIDRKVYNITKWSIOHPGQQRVIGHYAGED 67
Db 7 AAETAAQGPTRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHYAGD 66
QY 68 ATDAFRAHPDLEFVGKFLKPLLLIGELAPEESQDHGKNSKITEDFRALRKTAEDMNLFX 127
Db 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSFPEFTKNKELTDFRELRATVERMGLMK 126
QY 128 TNHVFFLLLAHIIALESIAWTFVYFGNGWIPTLITAFVLATSQAQAGWLQHDYGHLSV 187
Db 127 ANHVFFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHVLVHKFVIGHLKGASANNWNRHFOHAKPNIFHKDPDVMNLH--VFVLGEWQ 245
Db 187 FSTSKNHLHLHFVIGHLKGASANNWNRHFOHAKPNCFKDPDINM-HPFSFALGKIL 245
QY 246 PIYKGGKLYLPYNHQHYFFLIGPPLIIPMYFOYQIIMTWIHKWVDLAWAVSYIIR 305
Db 246 SVELGKQKKKMPYNHQHYFFLIGPPLIIPMYFOYQIIMTWIHKWVDLAWAVSYIIR 305
QY 306 FIITYIPFGILGALLFLNFIPLSHFWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 306 FIITYVPLGLKAFGLFFIVFPLESNWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365
QY 366 VEQSFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQKPLLRALLD 425
Db 366 VHKSAFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKHGIEYQKPLLSAFAD 425
QY 426 IIRSLKSKGLMDAYLHK 444
Db 426 IHSLSKESQLMDAYLHQ 444

RESULT 9
US-09-439-261-11
/ Sequence 11, Application US/09439261
/ Patent No. 6428990
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Mukerji, Pardeep
/ APPLICANT: Leonard, Amanda E.
/ APPLICANT: Huang, Yung-Sheng
/ TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
/ FILE REFERENCE: 6295.US.P1
/ CURRENT APPLICATION NUMBER: US/09/439,261
/ CURRENT FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: US 08/833,610
/ PRIOR FILING DATE: 1997-04-11
/ PRIOR APPLICATION NUMBER: PCT/US98/07422
/ PRIOR FILING DATE: 1998-04-10
/ PRIOR APPLICATION NUMBER: US 09/227,613
/ PRIOR FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: FastSeq for Windows Version 4.0

Query Match
Best Local Similarity 61.9%; Score 1508; DB 4; Length 444;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKNLRTDGLVIDRKVYNITKWSIOHPGQQRVIGHYAGED 67
Db 7 AAETAAQGPTRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHYAGD 66
QY 68 ATDAFRAHPDLEFVGKFLKPLLLIGELAPEESQDHGKNSKITEDFRALRKTAEDMNLFX 127
Db 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSFPEFTKNKELTDFRELRATVERMGLMK 126
QY 128 TNHVFFLLLAHIIALESIAWTFVYFGNGWIPTLITAFVLATSQAQAGWLQHDYGHLSV 187
Db 127 ANHVFFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHVLVHKFVIGHLKGASANNWNRHFOHAKPNIFHKDPDVMNLH--VFVLGEWQ 245
Db 187 FSTSKNHLHLHFVIGHLKGASANNWNRHFOHAKPNCFKDPDINM-HPFSFALGKIL 245
QY 246 PIYKGGKLYLPYNHQHYFFLIGPPLIIPMYFOYQIIMTWIHKWVDLAWAVSYIIR 305
Db 246 SVELGKQKKKMPYNHQHYFFLIGPPLIIPMYFOYQIIMTWIHKWVDLAWAVSYIIR 305
QY 306 FIITYIPFGILGALLFLNFIPLSHFWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365
Db 306 FIITYVPLGLKAFGLFFIVFPLESNWVWVWQNNHIVMEIDQAYRDWFSQLTATCN 365
QY 366 VEQSFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQKPLLRALLD 425
Db 366 VHKSAFNDWFSGLNFQIEHLLFPTMPRNLHKAIPLVQSLCAKHGIEYQKPLLSAFAD 425
QY 426 IIRSLKSKGLMDAYLHK 444
Db 426 IHSLSKESQLMDAYLHQ 444

RESULT 10
US-09-227-613-12
/ Sequence 12, Application US/09227613A
/ Patent No. 6432684
/ GENERAL INFORMATION:
/ APPLICANT: Mukerji, Pardeep
/ APPLICANT: Leonard, Amanda E.
/ APPLICANT: Huang, Yung-Sheng
/ TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
/ FILE REFERENCE: 6295.US.P1
/ CURRENT APPLICATION NUMBER: US/09/227,613A
/ CURRENT FILING DATE: 1999-01-08
/ PRIOR APPLICATION NUMBER: 08/833,610
/ PRIOR FILING DATE: 1997-04-11
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 12
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/
US-09-227-613-12

Query Match
Best Local Similarity 61.7%; Pred. No. 2.2e-159;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIQKNLRTDGLVIDRKVYNITKWSIOHPGQQRVIGHYAGED 67
Db 7 AAETAAQGPTRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHYAGD 66
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QY 68 ATDAFRAPDLFEVKGKFLKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFK 127
DB 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSPPTKTKELTDFRELRATVERMGLMK 126
QY 128 TNHVFLLLAHIIALESIAWFTVYFGNGWPTLITAFVLATSAQAQAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHLVHKFVIGHLKASANNWNRHFRHAKPNFHKDPDNNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLHHEVIGHLKAPASANNWNRHFRHAKPNCFRDPDNNM-HPFFALGKLL 245
QY 246 PIEYGGKKLYLPYNHQBHEFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIR 305
DB 245 SVELGKQKKYMPYNEHQHYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIR 305
QY 306 FETTYIPFYGILGALLFLANFIRELSHFWVWVQNMHIWMEIDQAYRDFWESSQATCN 365
DB 306 FETTYIPFYGILGALLFLANFIRELSHFWVWVQNMHIWMEIDQAYRDFWESSQATCN 365
QY 366 VHSKAFNDFSGHLNFQIEHHLFPTWPRHNYHKAFLVQSLCAKRGIEYQSKPLLSAFAD 425
DB 366 VHSKAFNDFSGHLNFQIEHHLFPTWPRHNYHKAFLVQSLCAKRGIEYQSKPLLSAFAD 425
QY 426 IIRSLKSGKLWLDAYLHK 444
DB 426 IIRSLKSGKLWLDAYLHK 444

```

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RESULT 11
US-09-439-261-39
; Sequence 39, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (445)...(445)
; OTHER INFORMATION: Xaa = Unknown or other at position 445
US-09-439-261-39

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Query Match 61.9%; Score 1508; DB 4; Length 445;
Best Local Similarity 61.7%; Pred. No. 2.2e-159;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

QY 11 AAAREVSVPT---FSWEEIQHNLRDTSGLVIDRKVNITKWSIQHPGGQVIGHYAGED 67
DB 7 AAATAAQGTPTPRYFTWDEVAQSGCEERWLVIDRKVNISEFTRRHPGGSRVISHYAGQ 66
QY 68 ATDAFRAPDLFEVKGKFLKLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEADNLFK 127
DB 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSPPTKTKELTDFRELRATVERMGLMK 126
QY 128 TNHVFLLLAHIIALESIAWFTVYFGNGWPTLITAFVLATSAQAQAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHLVHKFVIGHLKASANNWNRHFRHAKPNFHKDPDNNMLH--VFVLGEWQ 245

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DB 127 ANHVFLLYLLHLLDGAALTLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKPKNHLVHKFVIGHLKASANNWNRHFRHAKPNFHKDPDNNMLH--VFVLGEWQ 245
DB 187 FSTSKNNHLHHEVIGHLKAPASANNWNRHFRHAKPNCFRDPDNNM-HPFFALGKLL 245
QY 246 PIEYGGKKLYLPYNHQBHEFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIR 305
DB 245 SVELGKQKKYMPYNEHQHYFFLIGPPLIPMYFOYQIIMTMVHKWVDLAWAVSYIR 305
QY 306 FETTYIPFYGILGALLFLANFIRELSHFWVWVQNMHIWMEIDQAYRDFWESSQATCN 365
DB 306 FETTYIPFYGILGALLFLANFIRELSHFWVWVQNMHIWMEIDQAYRDFWESSQATCN 365
QY 366 VHSKAFNDFSGHLNFQIEHHLFPTWPRHNYHKAFLVQSLCAKRGIEYQSKPLLSAFAD 425
DB 366 VHSKAFNDFSGHLNFQIEHHLFPTWPRHNYHKAFLVQSLCAKRGIEYQSKPLLSAFAD 425
QY 426 IIRSLKSGKLWLDAYLHK 444
DB 426 IIRSLKSGKLWLDAYLHK 444

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RESULT 12
US-09-439-261-45
; Sequence 45, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US-P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (445)...(445)
; OTHER INFORMATION: Xaa = Unknown or other at position 445
US-09-439-261-45

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Query Match 61.9%; Score 1508; DB 4; Length 445;
Best Local Similarity 61.7%; Pred. No. 2.2e-159;
Matches 271; Conservative 62; Mismatches 100; Indels 6; Gaps 3;

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Db 187 FSTSKNHLHFFVIGLKGAPASWNNHMFQHHAKPNCFRKDPDINN-HPFFALGKIL 245  
Qy 246 PIEYGGKLLKYLPHNQHHEFFLGPPLLIPMYFOYQIIMTMIVHKWVDLAWAVSYIR 305  
Db 246 SVELGKQKKYMPYNHGHKYPFLGPPALLPLFYQWIFYFVIOQRKXWVDLAWMITFYR 305  
Qy 306 FFITYIPFYGILGALLFLNFRFLESHWFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365  
Db 306 FFITVPLLLGLKAFGLGFLFVIRFLESNWFWVVTQNNHIVMEIDHNRNDWVSTQLTATCN 365  
Qy 366 VEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425  
Db 366 VKSAFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425  
Qy 426 IIRSLKSKGLWLDAYLHK 444  
Db 426 IIRSLKSKGLWLDAYLHQ 444

RESULT 13  
US-09-439-261-43  
; Sequence 43, Application US/09439261  
; Patent No. 6428930  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; TYPE: PRT  
; LENGTH: 444  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (444)...(444)  
; OTHER INFORMATION: Xaa = Unknown or other at position 444  
US-09-439-261-43

Query Match 61.3%; Score 1493.5; DB 4; Length 444;  
Best Local Similarity 61.5%; Pred. No. 98-158;  
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

Qy 11 AAREVSVPT---FSWEEIQKNLRDTSGLVIDRKYNIITKWSIQHPGQQRVIGHYAGED 67  
Db 7 AAEATAAGPTPRYFTWDEVAQRSGCEERWLVIDRKYNISFTRRHPGGSRVISHYAGQD 66  
Qy 68 ATDAFAPFPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEADNLFK 127  
Db 67 ATDPFVAFHINKGLVKYNNLSLIGELSPESQSFPTKNEKLTDFE-LRATVERMGLMK 125  
Qy 128 TNHVPFLLLAHIIALESIAWFTVFYFGNGWPTLTITAFVLATSAQAQWLDYGHLSV 187  
Db 126 ANHVFFLLYLLHLLDGAALTLWVFGTSPFLPCLLCAVLLSAVQAQAGWLDYGHLSV 185  
Qy 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFOHAKPNI FHKDPDNNMLH--VFVLGEWQ 245  
Db 186 FSTSKNHLHFFVIGLKGAPASWNNHMFQHHAKPNCFRKDPDINN-HPFFALGKIL 244  
Qy 246 PIEYGGKLLKYLPHNQHHEFFLGPPLLIPMYFOYQIIMTMIVHKWVDLAWAVSYIR 305  
Db 245 SVELGKQKKYMPYNHGHKYPFLGPPALLPLFYQWIFYFVIOQRKXWVDLAWMITFYR 304  
Qy 306 FFITYIPFYGILGALLFLNFRFLESHWFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365  
Db 306 FFITVPLLLGLKAFGLGFLFVIRFLESNWFWVVTQNNHIVMEIDHNRNDWVSTQLTATCN 364  
Qy 366 VEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425  
Db 366 VKSAFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 424  
Qy 426 IIRSLKSKGLWLDAYLHK 444  
Db 426 IIRSLKSKGLWLDAYLHQ 443

Qy 306 FFITYIPFYGILGALLFLNFRFLESHWFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365  
Db 306 FFITVPLLLGLKAFGLGFLFVIRFLESNWFWVVTQNNHIVMEIDHNRNDWVSTQLTATCN 364  
Qy 366 VEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425  
Db 366 VKSAFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 424  
Qy 426 IIRSLKSKGLWLDAYLHK 444  
Db 426 IIRSLKSKGLWLDAYLHQ 443

RESULT 14  
US-09-227-613-42  
; Sequence 42, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 444 is unknown or other.  
US-09-227-613-42

Query Match 61.3%; Score 1493.5; DB 4; Length 444;  
Best Local Similarity 61.5%; Pred. No. 98-159;  
Matches 270; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

Qy 11 AAREVSVPT---FSWEEIQKNLRDTSGLVIDRKYNIITKWSIQHPGQQRVIGHYAGED 67  
Db 7 AAEATAAGPTPRYFTWDEVAQRSGCEERWLVIDRKYNISFTRRHPGGSRVISHYAGQD 66  
Qy 68 ATDAFAPFPDLEFVGKFLKPLLIGELAPEPSQDHGKNSKITEDFRALRKTAEADNLFK 127  
Db 67 ATDPFVAFHINKGLVKYNNLSLIGELSPESQSFPTKNEKLTDFE-LRATVERMGLMK 125  
Qy 128 TNHVPFLLLAHIIALESIAWFTVFYFGNGWPTLTITAFVLATSAQAQWLDYGHLSV 187  
Db 126 ANHVFFLLYLLHLLDGAALTLWVFGTSPFLPCLLCAVLLSAVQAQAGWLDYGHLSV 185  
Qy 188 YRKPKNHLVHKFVIGHLKGASANNWNRHFOHAKPNI FHKDPDNNMLH--VFVLGEWQ 245  
Db 186 FSTSKNHLHFFVIGLKGAPASWNNHMFQHHAKPNCFRKDPDINN-HPFFALGKIL 244  
Qy 246 PIEYGGKLLKYLPHNQHHEFFLGPPLLIPMYFOYQIIMTMIVHKWVDLAWAVSYIR 305  
Db 245 SVELGKQKKYMPYNHGHKYPFLGPPALLPLFYQWIFYFVIOQRKXWVDLAWMITFYR 304  
Qy 306 FFITYIPFYGILGALLFLNFRFLESHWFWVVTQNNHIVMEIDQAYRDWPSQLTATCN 365  
Db 306 FFITVPLLLGLKAFGLGFLFVIRFLESNWFWVVTQNNHIVMEIDHNRNDWVSTQLTATCN 364  
Qy 366 VEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 425  
Db 366 VKSAFNDWFSGLHNFQIEHLLFPTMPRNLHKAIPLVKSLCAKHGIEYQEKPLLRALLD 424  
Qy 426 IIRSLKSKGLWLDAYLHK 444  
Db 426 IIRSLKSKGLWLDAYLHQ 443

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RESULT 15
US-09-439-261-41
; Sequence 41, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-41

Query Match 46.3%; Score 1128; DB 4; Length 360;
Best Local Similarity 57.2%; Pred. No. 3.8e-117;
Matches 203; Conservative 56; Mismatches 90; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIOXNLRDGLVIRKYNITKMSIQHPGQGVIGHVAGED 67
DB 7 AATAAAGCTPRYFTWDEVAQRSGCEERWLVIRKYNISEFTRRHPGGSRVISHYAGQD 66
QY 68 ATDAFRAFPDLEFVGKFLKPLLIGELAPEPSQDHGSKSKITEDFRALRKAEDMNLFK 127
DB 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSPFETPKNKLDELFRERATVERMGLMK 126
QY 128 TNHVFLLLAHIIAIESIAWTFVYFGNGWIITLITAFVLATSOAAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHILLDGAALTLWVFGTSLFPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKEPKNHLVHKFVIGHLKASANNMNRHFQHHAKENIFHKDPDVNMLH--VFVLGEWQ 245
DB 187 PSTSKNHLHFFVIGHLKAPASWNNMNFQHHAKENCFRKPDPDINN-HPFFALGKIL 245
QY 246 PIEYKKKLYLPYNHGHYFFLIGPPELLIPMYFQYQIINTMIVHKWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHGHYFFLIGPPELLIPMYFQYFVYFVIOQKQWDLAWMITFYVR 305
QY 306 FFITYIPYGLGALLFNIRFLESNFWVVTOMNHVMEIDQAYRDWFSOL 360
DB 306 FFITYVPLGLKAFGLFFIVRFLESNFWVVTOMNHIPMHIDHRNDWVSTQL 360

RESULT 16
US-09-227-613-39
; Sequence 39, Application US/09227613A
; Patent No. 6432884
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pardeep
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-13

Query Match 45.2%; Score 1103; DB 4; Length 287;
Best Local Similarity 66.9%; Pred. No. 1.6e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSOAAGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANNMNRH 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVFSKWNHLLHFFVIGHLKAPASWNNHM 58
QY 217 HFQHHAKNIFHKDPDVNMLH--VFVLGEWQPIEGKKLYLPYNHGHYFFLIGPQL 274
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-613-39

Query Match 46.3%; Score 1128; DB 4; Length 360;
Best Local Similarity 57.2%; Pred. No. 3.8e-117;
Matches 203; Conservative 56; Mismatches 90; Indels 6; Gaps 3;

QY 11 AAREVSVPT---FSWEEIOXNLRDGLVIRKYNITKMSIQHPGQGVIGHVAGED 67
DB 7 AATAAAGCTPRYFTWDEVAQRSGCEERWLVIRKYNISEFTRRHPGGSRVISHYAGQD 66
QY 68 ATDAFRAFPDLEFVGKFLKPLLIGELAPEPSQDHGSKSKITEDFRALRKAEDMNLFX 127
DB 67 ATDPFVAFHINKGLVKYKNSLLIGELSPQSPFETPKNKLDELFRERATVERMGLMK 126
QY 128 TNHVFLLLAHIIAIESIAWTFVYFGNGWIITLITAFVLATSOAAGWLQHDYGHLSV 187
DB 127 ANHVFLLYLLHILLDGAALTLWVFGTSLFPFLCAVLLSAVQAQAGWLQHDYGHLSV 186
QY 188 YRKEPKNHLVHKFVIGHLKASANNMNRHFQHHAKENIFHKDPDVNMLH--VFVLGEWQ 245
DB 187 PSTSKNHLHFFVIGHLKAPASWNNMNFQHHAKENCFRKPDPDINN-HPFFALGKIL 245
QY 246 PIEYKKKLYLPYNHGHYFFLIGPPELLIPMYFQYQIINTMIVHKWVDLAWAVSYIR 305
DB 246 SVELGKQKKYMPYNHGHYFFLIGPPELLIPMYFQYFVYFVIOQKQWDLAWMITFYVR 305
QY 306 FFITYIPYGLGALLFNIRFLESNFWVVTOMNHVMEIDQAYRDWFSOL 360
DB 306 FFITYVPLGLKAFGLFFIVRFLESNFWVVTOMNHIPMHIDHRNDWVSTQL 360

RESULT 17
US-09-439-261-13
; Sequence 13, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-13

Query Match 45.2%; Score 1103; DB 4; Length 287;
Best Local Similarity 66.9%; Pred. No. 1.6e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSOAAGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANNMNRH 216
DB 8 GGIPAV-----QAQAGWLQHDYGHLSVFSKWNHLLHFFVIGHLKAPASWNNHM 58
QY 217 HFQHHAKNIFHKDPDVNMLH--VFVLGEWQPIEGKKLYLPYNHGHYFFLIGPQL 274
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Db 59 HFQHAKEPNCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 117  
Qy 275 IPMYFOYQIIMTMIVHKNWVDLAWAVSYIRPFTYIPFYGILGALLFLNFIRESHWF 334  
Db 118 LPLYFQWYIFYVIOKKWVDLAWMITFVVRFFLTYPVLLGKAFGLGFFIVRFLSNWF 177  
Qy 335 VVWVTQNNHIVMEIDQEAAYRDWFSQSQTATCNVEQSFNDWFSGLNFOIEHHLFPTMPRH 394  
Db 178 VVWVTQNNHIVMEIDQEAAYRDWFSQSQTATCNVEQSFNDWFSGLNFOIEHHLFPTMPRH 237  
Qy 395 NLHKAIPVLSLCAKHGIEYQSKPLLRALLDIIRSLKSGKWLWDAYLHK 444  
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLRALLDIIRSLKSGKWLWDAYLHQ 287

## RESULT 18

US-09-719-601-14  
; Sequence 14, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
; US-09-719-601-14

Query Match 45.2%; Score 1103; DB 4; Length 287;  
Best Local Similarity 66.9%; Pred. No. 1.6e-114; Indels 12; Gaps 3;  
Matches 194; Conservative 32; Mismatches 52

Qy 157 GMIPTLITAFVLATSOAQAQWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNR 216  
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNR 58  
Qy 217 HFQHAKEPNCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 274  
Db 59 HFQHAKEPNCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 117  
Qy 275 IPMYFOYQIIMTMIVHKNWVDLAWAVSYIRPFTYIPFYGILGALLFLNFIRESHWF 334  
Db 118 LPLYFQWYIFYVIOKKWVDLAWMITFVVRFFLTYPVLLGKAFGLGFFIVRFLSNWF 177  
Qy 335 VVWVTQNNHIVMEIDQEAAYRDWFSQSQTATCNVEQSFNDWFSGLNFOIEHHLFPTMPRH 394  
Db 178 VVWVTQNNHIVMEIDQEAAYRDWFSQSQTATCNVEQSFNDWFSGLNFOIEHHLFPTMPRH 237  
Qy 395 NLHKAIPVLSLCAKHGIEYQSKPLLRALLDIIRSLKSGKWLWDAYLHK 444  
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLRALLDIIRSLKSGKWLWDAYLHQ 287

## RESULT 19

US-09-719-601-14  
; Sequence 14, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2

; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (288)...(288)  
; OTHER INFORMATION: Xaa = Unknown or other at position 288  
; US-09-439-261-14

Query Match 45.2%; Score 1103; DB 4; Length 288;  
Best Local Similarity 66.9%; Pred. No. 1.7e-114;  
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;  
Qy 157 GMIPTLITAFVLATSOAQAQWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNR 216  
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANNWNR 58  
Qy 217 HFQHAKEPNCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 274  
Db 59 HFQHAKEPNCFRKPDINN--HPFFALGKILSVLGGKQKKYMPYNNHQHYFFLIGPPAL 117  
Qy 275 IPMYFOYQIIMTMIVHKNWVDLAWAVSYIRPFTYIPFYGILGALLFLNFIRESHWF 334  
Db 118 LPLYFQWYIFYVIOKKWVDLAWMITFVVRFFLTYPVLLGKAFGLGFFIVRFLSNWF 177  
Qy 335 VVWVTQNNHIVMEIDQEAAYRDWFSQSQTATCNVEQSFNDWFSGLNFOIEHHLFPTMPRH 394  
Db 178 VVWVTQNNHIVMEIDQEAAYRDWFSQSQTATCNVEQSFNDWFSGLNFOIEHHLFPTMPRH 237  
Qy 395 NLHKAIPVLSLCAKHGIEYQSKPLLRALLDIIRSLKSGKWLWDAYLHK 444  
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLRALLDIIRSLKSGKWLWDAYLHQ 287

RESULT 20  
US-09-439-261-16  
; Sequence 16, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (288)...(288)

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; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-09-439-261-16

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANWNHR 216
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANWNHR 58

QY 217 HFQHHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHQHEYFFLIGPPLL 274
Db 59 HFQHHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHQHEYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
Db 118 LPLYEQWYIFVYVQIRKQKVDLAWMITFYVFFVYVPLGLKAPLGLFFVIRFLESNW 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQSQTATCNVEQSFNDWFSGLNFQIEHHLFPTMPRH 394
Db 178 VVVTQNMHIHVEIDQAYRDWFSQSQTATCNVEQSFNDWFSGLNFQIEHHLFPTMPRH 237

QY 395 NLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKWLDAYLHK 444
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLSAPADIIHSLKESQGLWLDAYLHQ 287

RESULT 21
US-09-439-261-18
; Sequence 18, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paradi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US.P2
; CURRENT FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (288)...(288)
; OTHER INFORMATION: Xaa = Unknown or other at position 288
US-09-439-261-18

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANWNHR 216
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANWNHR 58

QY 217 HFQHHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHQHEYFFLIGPPLL 274
Db 59 HFQHHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHQHEYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
Db 118 LPLYEQWYIFVYVQIRKQKVDLAWMITFYVFFVYVPLGLKAPLGLFFVIRFLESNW 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQSQTATCNVEQSFNDWFSGLNFQIEHHLFPTMPRH 394
Db 178 VVVTQNMHIHVEIDQAYRDWFSQSQTATCNVEQSFNDWFSGLNFQIEHHLFPTMPRH 237

QY 395 NLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKWLDAYLHK 444
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLSAPADIIHSLKESQGLWLDAYLHQ 287

RESULT 22
US-09-439-261-15
; Sequence 15, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Pradi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US.P1
; CURRENT FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US/09/227,613A
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 288 is unknown or other.
US-09-227-613-15

Query Match      45.2%; Score 1103; DB 4; Length 288;
Best Local Similarity 66.9%; Pred. No. 1.7e-114;
Matches 194; Conservative 32; Mismatches 52; Indels 12; Gaps 3;

QY 157 GWIPTLITAFVLATSAQAAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANWNHR 216
Db 8 GGIPAV-----QAQAGWLOHDYGHLSVYRKPKNHLVHKFVIGHLKGASANWNHR 58

QY 217 HFQHHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHQHEYFFLIGPPLL 274
Db 59 HFQHHAKENIFHKDPDVMNLH--VFVLGEMQPIEYGGKKLKYLPYNHQHEYFFLIGPPLL 117

QY 275 IPMYFOYQIIMTMIVHKWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRESHW 334
Db 118 LPLYEQWYIFVYVQIRKQKVDLAWMITFYVFFVYVPLGLKAPLGLFFVIRFLESNW 177

QY 335 VVVTQNMHIHVEIDQAYRDWFSQSQTATCNVEQSFNDWFSGLNFQIEHHLFPTMPRH 394
Db 178 VVVTQNMHIHVEIDQAYRDWFSQSQTATCNVEQSFNDWFSGLNFQIEHHLFPTMPRH 237

QY 395 NLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKSGKWLDAYLHK 444
Db 238 NYHKVAPLVQSLCAKHGIEYQSKPLLSAPADIIHSLKESQGLWLDAYLHQ 287

RESULT 23
US-09-439-261-42
; Sequence 42, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paradi
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295-US.P2
; CURRENT FILING DATE: 1999-11-12
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; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (251)...(251)
; OTHER INFORMATION: Xaa = Unknown or other at position 251
; NAME/KEY: VARIANT
; LOCATION: (329)...(330)
; OTHER INFORMATION: Xaa = Unknown or other at these positions
US-09-439-261-42
Query Match 37.3%; Score 909.5; DB 4; Length 347;
Best Local Similarity 58.6%; Pred. No. 8.4e-93;
Matches 167; Conservative 43; Mismatches 68; Indels 7; Gaps 4;
Qy 19 PT---FSWEEIOKHNLRDTSGLVIDRKVYNTKWSIQHPGGORVIGHVAGSDATDAFRAP 75
Db 3 FTPTFTWDEVAQRSCGERWLVIDRKVYNISEFTRRHPGGSRVISHVAGQDADPFVAP 62
Qy 76 HPDLFVGVKFLKPLIGELAPEEPSQDGHGKSKITEDFRALKTAEDNMFLKTNHVPFLL 135
Db 63 HINKGLVKYKMSLLIGLSPEQSPFETPKNKELTDFEFLRATVVERMGLMKAHVFPFL 122
Qy 136 LLAHIIALESIAWFTVYFVNGWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNH 195
Db 123 YLLHILLDGAARLWLVFGTSFLPFLCAVLLSAVQAQAGWLQHD-GHLSVFTSKWNH 181
Qy 196 LVHKEFVIGHLKGASANNWNRHFOHAKENIFHKPDVNNMLH--VFVLGEMQPIEYGGKK 253
Db 182 LLHHEFVIGHLKGAPASANNWNRHFOHAKENCFKPDINN-HPPFFALGKILSVELGKQK 240
Qy 254 LKYLPNYHGHVEFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAW 298
Db 241 KXTMPYHGHXHYFFLIGPPALLPFLYFQWYFYFVIOQRKKWVDLAW 285

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RESULT 25
US-09-439-261-20
; Sequence 20, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-261-20
Query Match 32.2%; Score 784; DB 4; Length 219;
Best Local Similarity 61.7%; Pred. No. 4.1e-79;
Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;
Qy 157 GWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHVLHVKFVIGHLKGASANNWNR 216
Db 8 GGIPAV-----QAQAGWLQHDYGHLSVFTSKWNHLLHFFVIGHLKGASANNWNR 58
Qy 217 HFQHAKPNIFHKPDVNNMLH--VFVLGEMQPIEYGGKKLKYLPYHGHVEFFLIGPPL 274
Db 59 HFQHAKPNCFKPDINN-HPPFFALGKILSVELGKQKPKYHGHVEFFLIGPPL 117
Qy 275 IPMYFOYQIIMTMIVHKWVDLAWVYVIRPITTYIPFVIGLIGALLFLNFIRELESWF 334
Db 118 LPFYFQWYFYFVIOQRKKWVDLAWMTTYFVRPFTTYVPLLLGKAFGLGLFIVRFLSNWF 177
Qy 335 VVYTMNHVMEIDQEAIRDFWSSQLTATCNVEQSFNDWFS 376
Db 178 VVYTMNHIPMHIDHRNDMDVSTQLQATCNVHKSAFNDWFS 219

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RESULT 26

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; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (251)...(251)
; OTHER INFORMATION: Xaa = Unknown or other at position 251
; NAME/KEY: VARIANT
; LOCATION: (329)...(330)
; OTHER INFORMATION: Xaa = Unknown or other at these positions
US-09-439-261-42
Query Match 37.3%; Score 909.5; DB 4; Length 347;
Best Local Similarity 58.6%; Pred. No. 8.4e-93;
Matches 167; Conservative 43; Mismatches 68; Indels 7; Gaps 4;
Qy 19 PT---FSWEEIOKHNLRDTSGLVIDRKVYNTKWSIQHPGGORVIGHVAGSDATDAFRAP 75
Db 3 FTPTFTWDEVAQRSCGERWLVIDRKVYNISEFTRRHPGGSRVISHVAGQDADPFVAP 62
Qy 76 HPDLFVGVKFLKPLIGELAPEEPSQDGHGKSKITEDFRALKTAEDNMFLKTNHVPFLL 135
Db 63 HINKGLVKYKMSLLIGLSPEQSPFETPKNKELTDFEFLRATVVERMGLMKAHVFPFL 122
Qy 136 LLAHIIALESIAWFTVYFVNGWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNH 195
Db 123 YLLHILLDGAARLWLVFGTSFLPFLCAVLLSAVQAQAGWLQHD-GHLSVFTSKWNH 181
Qy 196 LVHKEFVIGHLKGASANNWNRHFOHAKENIFHKPDVNNMLH--VFVLGEMQPIEYGGKK 253
Db 182 LLHHEFVIGHLKGAPASANNWNRHFOHAKENCFKPDINN-HPPFFALGKILSVELGKQK 240
Qy 254 LKYLPNYHGHVEFFLIGPPLIPMYFOYQIIMTMIVHKWVDLAW 298
Db 241 KXTMPYHGHXHYFFLIGPPALLPFLYFQWYFYFVIOQRKKWVDLAW 285

```

```

RESULT 24
US-09-227-613-40
; Sequence 40, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 251 is unknown or other.
; OTHER INFORMATION: Xaa at position 329 is unknown or other.
; OTHER INFORMATION: Xaa at position 330 is unknown or other.
US-09-227-613-40
Query Match 37.3%; Score 909.5; DB 4; Length 347;

```

```
US-09-227-613-19
; Sequence 19, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo Sapien
;
; Query Match 32.2%; Score 784; DB 4; Length 219;
; Best Local Similarity 61.7%; Pred. No. 4.1e-79;
; Matches 137; Conservative 27; Mismatches 46; Indels 12; Gaps 3;
;
Qy 157 GWTPLTITAFVLTSAQAAGWLOHDYCHLSVWEKPKNNHLVHKFVIGHLKGASANNWHR 216
Db 8 GGPAV-----QAAGWLOHDYCHLSVWEKPKNNHLVHKFVIGHLKGASANNWHR 58
Qy 217 HFQHAKPNIFHKDPDVMNLH--VFVLGEWQPIEYGGKKLKYLPYNNHQHEYFFLIGPPLL 274
Db 59 HFQHAKPNCFRKPDPDINN-HPFFALGKILSVELCKQKKYKYPYNNHQHKKYFFLIGPPAL 117
Qy 275 IPMYFQIQTMTMIVHKWDLAWVSYIRFTIYIPFYGLGALLFLNFIREFLSHWF 334
Db 118 LPLFYQIYFYFVQIRKQKWDLAAMITFYRFTYVPLGLKAFGLFVIRFLESNWF 177
Qy 335 VWTQNMHIVNEIDQAYRDFWSQLTATCNVQSPFNDFWS 376
Db 178 VWTQNMHIVPHIDRMDVETQLOATCNVHKSAPNDFWS 219

RESULT 27
US-09-439-261-21
; Sequence 21, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (128)...(128)
; OTHER INFORMATION: Xaa = Unknown or other at position 128
;
US-09-439-261-21

Query Match 24.1%; Score 587.5; DB 4; Length 182;
Best Local Similarity 62.3%; Pred. No. 2.6e-57;
Matches 101; Conservative 22; Mismatches 36; Indels 3; Gaps 2;

Qy 139 HIALESIAWTFYFNGWIPITLITAFVLTSAQAAGWLOHDYCHLSVVRKPKNNHLVH 198
Db 2 HILLDGAALTLWVFGTSFLPFLCAVLLSAVQAAGWLOHDYCHLSVSTSKNNHLH 61
Qy 199 KVVIGHLKGASANNWHRHFQHAKPNIFHKDPDVMNLH--VFVLGEWQPIEYGGKKLKY 256
Db 62 HFVIGHLKGAPASANNWHRHFQHAKPNCFRKPDPDINN-HPFFALGKILSVELCKQKKY 120
Qy 257 LPYNHQHEYFFLIGPPLLIPMYFQIQTMTMIVHKWDLAW 298
Db 121 MPYNHQHYFFLIGPPALLPLFYFQYIFVFIQKQKWDLA 162

RESULT 28
US-09-227-613-20
; Sequence 20, Application US/09227613A
; Patent No. 6432884
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 128 is unknown or other.
;
US-09-227-613-20

Query Match 24.1%; Score 587.5; DB 4; Length 182;
Best Local Similarity 62.3%; Pred. No. 2.6e-57;
Matches 101; Conservative 22; Mismatches 36; Indels 3; Gaps 2;

Qy 139 HIALESIAWTFYFNGWIPITLITAFVLTSAQAAGWLOHDYCHLSVVRKPKNNHLVH 198
Db 2 HILLDGAALTLWVFGTSFLPFLCAVLLSAVQAAGWLOHDYCHLSVSTSKNNHLH 61
Qy 199 KVVIGHLKGASANNWHRHFQHAKPNIFHKDPDVMNLH--VFVLGEWQPIEYGGKKLKY 256
Db 62 HFVIGHLKGAPASANNWHRHFQHAKPNCFRKPDPDINN-HPFFALGKILSVELCKQKKY 120
Qy 257 LPYNHQHEYFFLIGPPLLIPMYFQIQTMTMIVHKWDLAW 298
Db 121 MPYNHQHYFFLIGPPALLPLFYFQYIFVFIQKQKWDLA 162

RESULT 29
US-08-834-655-9
; Sequence 9, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
```





```

; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-9

Query Match          20.6%; Score 502; DB 3; Length 131;
Best Local Similarity 69.4%; Pred. No. 5.4e-48;
Matches 86; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY      296 LMAVSYIRFTTYPYGILGALLFNITRPLESHFWVTQMNHIVNEIDQEA YRDW 355
       ||| :||:||||:| | | | | | | | | | | | | | | | | | | |
Db      8 LAWMITFYVRPLTVPLGLGKAFGLFFIVRPLESNNFVVMTQMNHIPMHIDH RNM DW 67

QY      356 FSSQLTATCNVBQSFPNDWFSGHLNFQIEHHLPFTMPRHNLHKIAPLVKSLCAKHGI EYQ 415
       ||| :||:||||:| | | | | | | | | | | | | | | | | | | |
Db      68 VSTQIQATCNVHKSAFNDFWSGHLNFQIEHHLPFTMPRHNYHXVAPLVQSLCAKHGI EYQ 127

QY      416 EKPL 419
       |||
Db      128 SKPL 131

```

RESULT 32  
US-09-363-526-9  
; Sequence 9, Application US/09363526  
; Patent No. 6410288  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMEACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/363,526  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WARD, MICHAEL R.  
; REGISTRATION NUMBER: 38,651  
; REFERENCE/DOCKET NUMBER: CGAB-201 USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 433-4150  
; TELEFAX: (415) 433-8716  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-363-526-9

```
Query Match          20.6%; Score 502; DB 4; Length 131;  
Best Local Similarity    69.4%; Pred.No. 5.4e-48;  
Matches      86; Conservative   14; Mismatches     24; Indels       0; Gaps        0;
```

QY 296 LAWAVSYIRFFITVTPFYGIIGALLFLNFIRFLESHWFVVVTQMNHIVMEIDQEAYEDM 35S  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 8 LAWMITVFVRFFLTVVPVLGLKAFGLGFFIVRFLSNWFVVVTQMNHIPMHIDHORNMDW 67

QY 356 FSSQTATCNVEQSFFNDWSGHNLNQIEHHLPPTPRNHLKIAPLVKSICAKHGIEYQ 41S  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 68 VSTOQAQCYNHKGAFNDFSGHNLNQIEHHLPPTPRNYHXHVAPLVOSLCCKHGIEYQ 127

QY 416 EKPL 419  
DB ||||  
 128 SKPL 131

RESULT 33  
US-08-834-655-11 US-08-834-655-11 Application US/08834655  
Sequence 11, Patent No. 5968809  
GENERAL INFORMATION:  
Applicant: KNUTZON, DEBORAH  
ApplcAnt: MURKERJI, PRADIP  
ApplcAnt: HUANG, YUNG-SHENg  
ApplcAnt: THURNOND, JENNIFER  
ApplcAnt: CHAUDHARY, SUNITA  
Title Of Invention: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTy ACIDS IN PLANTS  
Number Of Sequences: 18  
Correspondence Address:  
Addresser: RAE-VENTER LAW GROUP, P.C.  
Street: 260 SHERIDAN AVENUE, P.O. BOX 60039  
City: PALO ALTO  
State: CA  
Country: USA  
Zip: 94306  
Computer Readable Form:  
Medium Type: Floppy disk  
Computer: IBM PC compatible  
Operating System: PC-DOS/MS-DOS  
Software: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
Application Number: US/08/834,655  
Filing Date: 11-APR-1997  
Classification: 435  
Attorney/Agent Information:  
Name: RAE-VENTER, BARBARA  
Registration Number: 32,750  
Reference/Docket Number: CGNE.124.00U\$  
TELECOMMUNICATION INFORMATION:  
Telephone: (650) 328-4400  
TeleFax: (650) 328-4477  
Telex: N/A  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 143 amino acids  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-834-655-11

|    | Query Match           | 20.3%   | Score 496;         | DB 2;     | Length 143; |
|----|-----------------------|---|--------------------|-----------|-------------|
|    | Best Local Similarity | 66.7%;  | Pred. No. 2.9e-47; |           |             |
|    | Matches 86;           | Conservative 11;  | Mismatches 32;     | Indels 0; | Gaps 0      |
| QY | 287                   | MIYKHWVDLAWVSYIRFTTTPYPIYGLGALLFNFTFRFLSHFWVVTQMHVME      | 346                |           |             |
|    |                       |   |                    |           |             |
| DB | 14                    | MLVCMQMTDLLAAAGFYGRFLF                                    | 73                 |           |             |
|    |                       |   |                    |           |             |
| QY | 347                   | IDGEAYRDWFSSQLCATCNVQSFPNDWFGSLHNFQIEHFLFTFMPRHNLKIAPVLKL | 406                |           |             |

```
Db 74 IGHEKXRDWASSQLAATCNVPSLFIDWFSGLNFOIEHHLPFTMTNRHNYXVAPLVKAF 133
QY 407 CAXHGIEYQ 415
Db 134 CAXHGLHYE 142

RESULT 34
US-08-834-033A-12
; Sequence 12, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834.033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-033A-12

Query Match 20.3%; Score 496; DB 3; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 287 MIVKXNVVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRFLESHFWVWVTQMHVME 346
Db 14 MLVCMQWTDLLWAAAFYSRFFLSYSPFYGATGTLFLFVAVRVLESHFWVWVTQMHIPKE 73

QY 347 IDOEAYRDMFSSQLATCNVPSLFIDWFSGLNFOIEHHLPFTMTNRHNLHKLAPLVKSL 406
Db 74 IGHEKXRDWASSQLAATCNVPSLFIDWFSGLNFOIEHHLPFTMTNRHNYXVAPLVKAF 133

QY 407 CAXHGIEYQ 415
Db 134 CAXHGLHYE 142

RESULT 35
US-09-363-574-11
; Sequence 11, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,574
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-363-574-11

Query Match 20.3%; Score 496; DB 3; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 287 MIVKXNVVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRFLESHFWVWVTQMHVME 346
Db 14 MLVCMQWTDLLWAAAFYSRFFLSYSPFYGATGTLFLFVAVRVLESHFWVWVTQMHIPKE 73

QY 347 IDOEAYRDMFSSQLATCNVPSLFIDWFSGLNFOIEHHLPFTMTNRHNLHKLAPLVKSL 406
Db 74 IGHEKXRDWASSQLAATCNVPSLFIDWFSGLNFOIEHHLPFTMTNRHNYXVAPLVKAF 133

QY 407 CAXHGIEYQ 415
Db 134 CAXHGLHYE 142

RESULT 36
US-09-363-526-11
; Sequence 11, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
```

```

;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-526-11

Query Match 20.3%; Score 496; DB 4; Length 143;
Best Local Similarity 66.7%; Pred. No. 2.9e-47;
Matches 86; Conservative 11; Mismatches 32; Indels 0; Caps 0;

QY 287 MIVHKNVVDLAWAYSVYIRPITYIPYIGILGALLFNFIRESHHFVWVWTONHIVME 346
DB 14 MLVCNQMTDLWAAFSYRSRFLSYSPYIGATGTLTLFVAVRVLESHEVFWITQNHIFRE 73
QY 347 IDQAYRDWFSQSQTATCNVQSFNDFWFSGLNLFQIEHILFPTMPRHNLKHIAPLVKSL 406
DB 74 IGHEKGRDWASQLAANCNVEPSLFDWFSGLNLFQIEHILFPTMTTEHNYEXVAPLVKAF 133
QY 407 CAKHGIEYQ 415
DB 134 CAKHGLHYE 142

RESULT 37
US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-2

Query Match 18.8%; Score 459; DB 2; Length 457;
Best Local Similarity 24.9%; Pred. No. 2.3e-42;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;

QY 17 SVYTFSSWEEI-----QKHNLRTDGLVIDRKVYNITKWSIQHPGQQRVIGHYAGEDA 68
DB 6 SVRTETRAEVLNAEALNEGKDAEAPFLMIIDNKVYDVREVPDPGGSVILTH-VGKDG 64
QY 69 TDAFRAHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLPKT 128
DB 65 TDVDFTHP--EAAWETLANFYVGI--DESDRI--KNDDFAAEVRKURTLFQSLGIYDS 119
QY 129 NHVFFLLLAHIIALESIAWFTVYFG-NGWIPITLITAFVLATSOAQAGW-QHDPYGHLSV 187
DB 120 SKAYAFKVSFNLICWGLSTVIVAKWGQSTLANVLSAALLGLEWQCGWLADFLHHQV 179
QY 189 YRKPKNHLVHKFVICHLGKASANNWHRHFQHAKNFIHKDDVDNMLHVFVLGEWQPI 247
DB 180 FQDRFWGLFGAFLGVCQGFSSSWKDKNTHAAPNVHGEDDDIDTPHLLTWSE----- 235
QY 248 EYGGKKLKYLPYNHCHYEFFLIGPPLLIPIYFQIIMTMIVHKW-----VDLAWA 299
DB 236 -----HALEMFSVDPBELTRMSRF-----MVLNQTFEYFPLSPARLSWC 277
QY 300 VSYIRPITYIPYIGILGALLFNFI--FLESHWFV-----FLESHWFV----- 336
DB 278 LQ-SILFVLPGQAHKPSGARVPISLVEQLSLAMHW-TWYLATWELFKDPVNMMLVYFLV 335
QY 337 -----VTOMNHIVMEI---DQAYRDWFSQSQTATCNVQSFNDFWFSGLNLFQ 382
DB 336 SOAVCGNLLAIVFSLNHNGMPVISKEAVDMDFFTKIITGRDVHPGLFANWFTGGLNYQ 395
QY 383 IEHLFPTMPRHNLKHIAPLVKSLCAKHGIEYQEKPLLRALLDIRSLKKGK 435
DB 396 IEHLFPPSPRHNFSKIOPAVETLCKKNVRVHTTGMIEGTAEVFSRLNEVSK 448

RESULT 38
US-08-834-033A-2
; Sequence 2, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-033A-2

Query Match 18.8%; Score 459; DB 3; Length 457;
Best Local Similarity 24.9%; Pred. No. 2.3e-42;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;

QY 17 SVPTFSWEI-----QKHNLRTDGLVDRKVNITKWSIQHPGGQVGHYAGEDA 68
DB 6 SVPTFTRAEVLNAEALNEGKDAEAPFLMIDNKYDVREFVDPHGGSVILTH-VGKDG 64

QY 69 TDAFRAHPDLEFVGKFLKPLLIGELAPEEPQDGHGKNSKITDFAALRKTAEADNMLFKT 128
DB 65 TDVFDTHP--EAAWETLANFYVGD--DESDRDI-KNDDFAAEVRKLTFLFQSLGYDS 119

QY 129 NHVEFLLLAHIIAIESIAWFTVYFG-NGWIPLTAFVLATSQAAQGLQHDYGHLSV 187
DB 120 SKAYYAFKVSFNLGSLSTVIVAKWGQSTLANVLSAALLGLFWQCGGLAHDPLHHQV 179

QY 188 YRKPKNHLVHKFVIGHLKGASANNWNHRRHFQHAKEPIFKDPDNNMLHVFVLGEWQPI 247
DB 180 FQDRFWGDLFGALGGVCCQFSSWKKDKHNTTHAAPNVHGEDPDIDTHTPLTWSE--- 235

QY 248 EYGGKKLKLPLYNHQAHEFFLIGPPLIIPMYFOYQIIMTVHKNW-----VDLAWA 299
DB 236 -----HALEMFSVDPEELTRWGRF-----MVLNQTWTFYPILSFARLSWC 277

QY 300 VSYIRFFITYIPFYGILGALLFLNPIR--FLESHWFVW----- 336
DB 278 LQ-SILFVLPNGQAHKPSGARVPISLVEQLSLAMHW-TWYLATMFLFIKDPVNNMLVYFLV 335

QY 337 -----VTQMHIVMEI---DOEAYRDFWSSQLTATCNVQSFNDFWGLNFQ 382
DB 336 SQAVCNLLAIVPSLNHNGMPVISKEEAVDMDFFTKQIITGDRVHGLFANFTGGLNYQ 395

QY 383 IEHLFPPTPRNHLNIAPLVSLCAKHGIEYQEKELLRALLDIIRSLKSKG 435
DB 396 IEHLFPSPRNFNFSKIQAVELCKKYNVRHTTGMIEGTAEVPSRLNEVSK 448

; Sequence 2, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,574
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-2

Query Match 18.8%; Score 459; DB 3; Length 457;
Best Local Similarity 24.9%; Pred. No. 2.3e-42;
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;

QY 17 SVPTFSWEI-----QKHNLRTDGLVDRKVNITKWSIQHPGGQVGHYAGEDA 68
DB 6 SVPTFTRAEVLNAEALNEGKDAEAPFLMIDNKYDVREFVDPHGGSVILTH-VGKDG 64

QY 69 TDAFRAHPDLEFVGKFLKPLLIGELAPEEPQDGHGKNSKITDFAALRKTAEADNMLFKT 128
DB 65 TDVFDTHP--EAAWETLANFYVGD--DESDRDI-KNDDFAAEVRKLTFLFQSLGYDS 119

QY 129 NHVEFLLLAHIIAIESIAWFTVYFG-NGWIPLTAFVLATSQAAQGLQHDYGHLSV 187
DB 120 SKAYYAFKVSFNLGSLSTVIVAKWGQSTLANVLSAALLGLFWQCGGLAHDPLHHQV 179

QY 188 YRKPKNHLVHKFVIGHLKGASANNWNHRRHFQHAKEPIFKDPDNNMLHVFVLGEWQPI 247
DB 180 FQDRFWGDLFGALGGVCCQFSSWKKDKHNTTHAAPNVHGEDPDIDTHTPLTWSE--- 235

QY 248 EYGGKKLKLPLYNHQAHEFFLIGPPLIIPMYFOYQIIMTVHKNW-----VDLAWA 299
DB 236 -----HALEMFSVDPEELTRWGRF-----MVLNQTWTFYPILSFARLSWC 277

QY 300 VSYIRFFITYIPFYGILGALLFLNPIR--FLESHWFVW----- 336
DB 278 LQ-SILFVLPNGQAHKPSGARVPISLVEQLSLAMHW-TWYLATMFLFIKDPVNNMLVYFLV 335

QY 337 -----VTQMHIVMEI---DOEAYRDFWSSQLTATCNVQSFNDFWGLNFQ 382
DB 336 SQAVCNLLAIVPSLNHNGMPVISKEEAVDMDFFTKQIITGDRVHGLFANFTGGLNYQ 395

QY 383 IEHLFPPTPRNHLNIAPLVSLCAKHGIEYQEKELLRALLDIIRSLKSKG 435
DB 396 IEHLFPSPRNFNFSKIQAVELCKKYNVRHTTGMIEGTAEVPSRLNEVSK 448

RESULT 39
US-09-363-574-2
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Db 336 SQAVCGNLLAIVPSLNHNGMPVISKEEAVDMDFTXQIITORDVHFGLPANFTGGLNYQ 395  
Qy 383 IEHHLFPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIIRSLKKS GK 435  
Db 396 IEHHLFSPMRHNFHSKIQPAVEILCKKYNVRYHTTGMIEGTAEVFSRLNEVSK 448

## RESULT 40

US-09-363-526-2  
; Sequence 2, Application US/09363526  
; Patent No. 6410288  
; GENERAL INFORMATION:  
; APPLICANT: KNUITZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/363,526  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WARD, MICHAEL R.  
; REGISTRATION NUMBER: 38,651  
; REFERENCE/DOCKET NUMBER: CGAB-201 USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 433-4150  
; TELEFAX: (415) 433-8716  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-363-526-2

Query Match 18.8%; Score 459; DB 4; Length 457;  
Best Local Similarity 24.9%; Pred. No. 2.3e-42;  
Matches 118; Conservative 88; Mismatches 183; Indels 84; Gaps 14;  
Qy 17 SVPTFSWEEI-----QKHLRTDSGLVIDRKVYNIWKSIQHPGQQRVIGHYAGEDA 68  
Db 6 SVRTFTRAEVLNABALNEGKDAEAPFLMIIDNKVYDVREVPDPHGGSVILTH-VGKDG 64  
Qy 59 TDAPRAFPDLEFVGKFKPLLIGELAPEEPSQHGKNSKITEDFRALRKTAEDMNLFKT 128  
Db 65 TDVPTTFHP--EAWETLNFANFYVGD--DESDRI-KNDPFAEVRKRLTFLFQSLGYDS 119  
Qy 129 NHVFFLLLLAHIIALESIAWFTTVYFG-NGWIPTLITAFVLATSCAQAGMLQHDYGLSLV 187  
Db 120 SKAYVAFKVSFNLCIWSGLSTVIVAKWGOTSTLANVLSAALLGLEFWQCGGLAHDFLHQV 179  
Qy 188 YRKPKWHLVHKFVICHKGSASAWNNRHHFQHHAKPNI FHKDPDVMNLHVFLVGEWQPI 247  
Db 180 FQDRFWGDLFGAFLGVCQGFSSSWWDKKNTHAAPNVHGEPDIDTHPLLTWSE---- 235

Qy 248 EYGGKKLKYPYNHQHHEFFLIGPEPLIPMYFYQYQIMTNIVHKW-----VDLAWA 299  
Db 236 -----HALEMFSDFDEELTRMWSRF-----MVLNQTFYFPILSFARLSWC 277  
Qy 300 VSYVIRFFITYIPFYGILGALLFNFR--FLESHMFVM----- 336  
Db 278 LQ-SILFVLPNGQAHKPSGARVPISLVEQSLAMHW-TWYLATMFLFIKDPVNMVYFLV 335  
Qy 337 -----VTQMNHIVMEI---DQAYRDWFSQLTATCNVQSFNDWFSGHNFQ 382  
Db 336 SQAVCGNLLAIVPSLNHNGMPVISKEEAVDMDFTXQIITORDVHFGLPANFTGGLNYQ 395  
Qy 383 IEHHLFPTMPRHNLHKAIPLVKSLCAKHGIEYQEKPLLRALLDIIIRSLKKS GK 435  
Db 396 IEHHLFSPMRHNFHSKIQPAVEILCKKYNVRYHTTGMIEGTAEVFSRLNEVSK 448

Search completed: December 9, 2003, 10:20:08  
Job time : 23 secs